Assessing drivers of coastal primary production in northern Marguerite Bay, Antarctica

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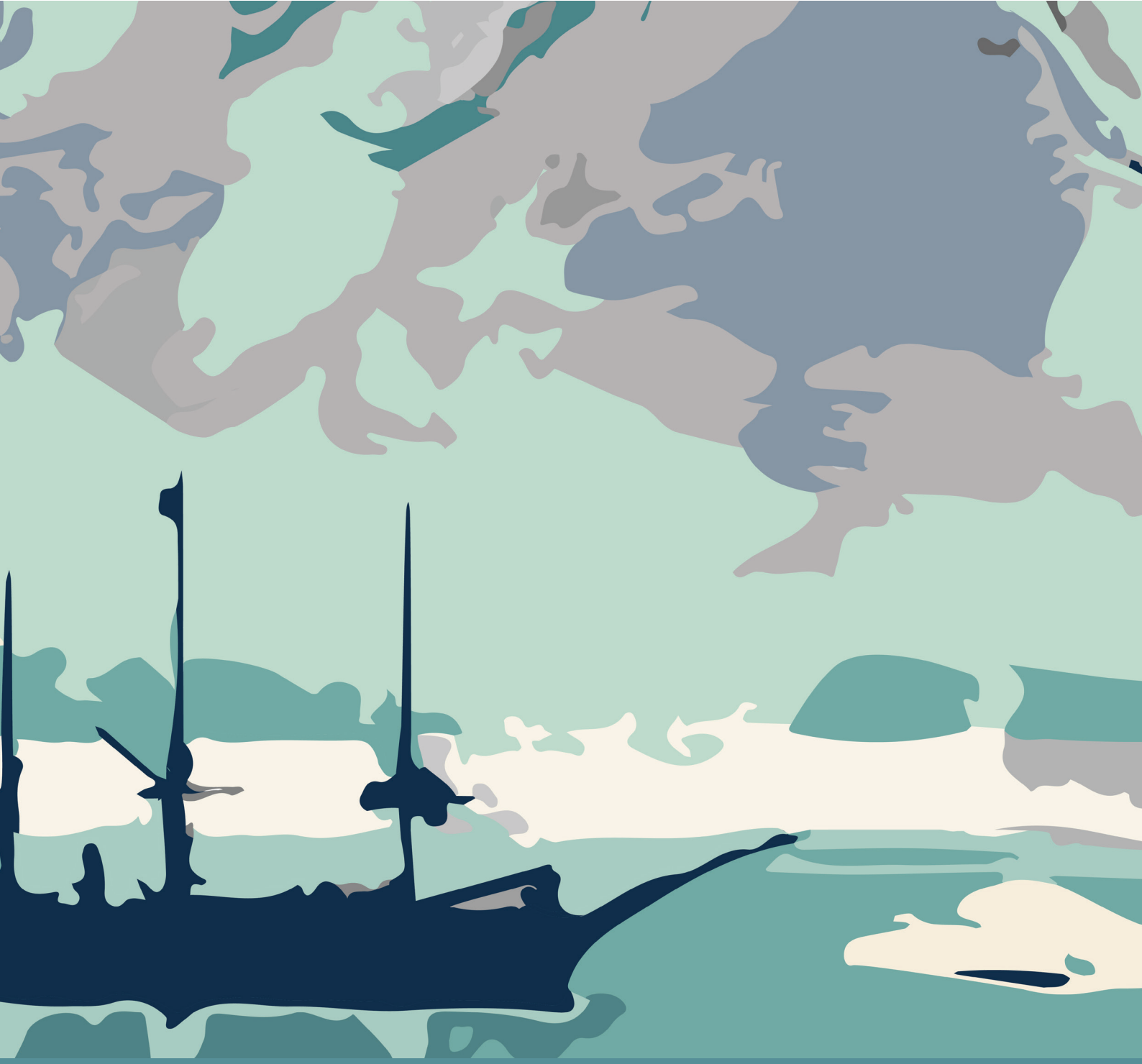

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Keynote Speakers

Penguin diplomacy - Brokering knowledge between science, society and policy makers in the Antarctic

Badhe Renuka[1]

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The extreme climatic regimes in the Southern Ocean and Antarctic ecosystems make them particularly vulnerable to any change in climate. On a global scale, changes in Antarctica such as melting of ice sheets have a potential to cause considerable damage especially to highly populated low lying coastal areas. On a regional scale, south of the polar front, there are high levels of endemism in the ecosystem, and changing climate, ocean acidification makes that area particularly vulnerable to introductions of non-native species, with consequent impacts on ecosystems. The Southern Ocean and Antarctica are governed by the Antarctic Treaty system agreements that enshrine the importance of science and scientific advice in Antarctic policy making. The Santiago declaration (2016) reaffirms the "commitment of the Consultative Parties to the comprehensive protection of the Antarctic environment and dependent and associated ecosystems, and the designation of Antarctica as a natural reserve, devoted to peace and science". It is well known that scientific advice for policy making can be time consuming and complex with increasing number of stakeholders involved. Knowledge brokering between the three pillars of science - society - policy making (Gluckman 2017) are also a key to an increased efficiency within the policy cycle. Engagement can start from science, societal input or from the policy process itself, and works on a continued feedback loop. Knowledge brokers can be organisations like ICSU, SCAR, EPB that ensure a continued flow of relevant scientific research into policy making. With recent technological advances, it is now becoming easier for individuals to take on the role of knowledge brokers between the three pillars of science, society and policymaking. The Antarctic Treaty system clearly recognises the roles of various stakeholders "including academia, decision makers and the general public - … and the global importance of scientific research in Antarctica" (Buenos Aires, 2011). So, how does science lead to policy making and implementation, and who and how are the stakeholders involved in this process? On the other hand, how can policymaking affect science in Antarctica? Understanding these various roles and processes, and harnessing the support from all relevant actors makes us much better prepared to protect and manage the Antarctic and it's fragile ecosystems for the future.

Global change impacts on Antarctic seabird and marine mammal populations

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The Southern Ocean is a location where major climate changes occurred over the last century, accompanied with an important level of human exploitation of natural living resources. These global changes can potentially lead to major perturbations of the Southern Ocean ecosystems up to marine top predators. Fisheries may also directly affect seabirds through accidental mortality in fishing gear (bycatch) and additional food resources provided by discards. The past 20 yr of research has seen an increasing number of studies investigating the effects of climate change and fisheries activities on Southern Ocean air-breathing predators. Long-term data of at sea observations and of populations with individually known animals were essential to detect these effects. Here, I give a rapid overview of the current knowledge, highlight new insights and give some perspectives on the impact of global changes on Southern Ocean air-breathing predator populations. Shifts in distribution and breeding phenology were documented in parallel to increases in sea surface temperatures and changes in sea ice cover. Species and region-specific population trends were observed in parallel with climate change. Warm sea surface temperatures seemed to mainly negatively affect demographic rates, although exceptions were found. Variations in sea ice cover affected demographic parameters and population dynamics of several populations. Relationships suggest non-linear effects, with optimum sea ice cover conditions appearing to be the rule. Fishing efforts were mainly negatively related to survival rates and positively related to breeding success, although the latter only concerns a few species. A few studies showed that climate factors and fisheries bycatch may affect simultaneously demographic parameters in a complex way, which can be integrated in population models to predict the impact on populations. Recent findings highlighted the potential effects of emerging threats on populations, such as contaminants, diseases and extreme climatic events, and pointed the role of inter-individual heterogeneity in the response of populations. Although in seabirds population growth rate is less sensitive to variations in juvenile survival than to variations in adult survival, chronic mortality of young individuals due to environmental changes may negatively affect populations. Needed are mechanistic studies that integrate the effects of multiple environmental stressors and foraging behaviour on demographic parameters and populations. This will allow taking into account the resilience of populations to environmental changes. Given the long life span of Southern Ocean air-breathing predators, and hence their relatively slow micro evolutionary responses to global change, we need studies assessing their phenotypic plasticity.

Biosketch: Christophe Barbraud is a researcher working at Centre d'Etudes Biologiques de Chizé, CNRS, France. After a PhD on the evolutionary ecology of the snow petrel in 1999, he has been investigating the impacts of climate change and human activities on the demographic processes and population dynamics of seabirds and marine mammals, mainly in the Southern Ocean. His work is essentially based on long-term studies of individually marked individuals, needed to monitor the long-term cycles and trends related to climate change. He regularly conducts fieldwork in Antarctica with the support of the French Polar Institute (IPEV).

Human Physiology research in Antarctica: the immune system under Stress

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Life in the Arctic and Antarctic environments means adaptation of biological systems to hostile conditions. In humans these processes are often accompanied by adverse physiological and psychological effects. But the extreme conditions on Earth are very similar and mimicking in their key elements also adaption to life in space and this link between polar research and manned space flight is of special interest. But what are the principles and most prominent environmental and social threats to physical and mental health during either long-duration space flight missions, overwintering in a hostile and exposed spot and how can we prevent and mitigate the adverse effects from these threats and ensure adequate adaptation? To now, the steps involved in such adaption are gradual and the biological system either builds up resistance to the stress and maintains a healthy physiological and psychological equilibrium (allostatic load), or succumbs to the stress, resulting in disequilibrium, cognitive or emotional dysfunction with a negative impact on performance and immunity, disease or even death (allostatic overload). These responses can induce either activation and/or paralyses of key immune responses. These questions have been addressed in projects implemented at Concordia and the Neumayer III-station. The overall context as well as the outcome and conclusions of these studies are reported and the next potential steps described.

Supported by European Space Agency(ESA), the French(IPEV), Italian(PNRA) and German (AWI) polar institutes, the German National Space Program(DLR, 50WB0719/WB0919/WB1317), by BELSPO/PROEDEX/ESA, NASA and the ESA Topical Team *Stress and Immunity*.

Scale matters (or does it?): Microbial communities in Antarctic terrestrial soils

Cowan Donald[1]

[1] University of Pretoria, Soutn Africa

The past one and a half decades have seen a dramatic increase in studies on Antarctic terrestrial microbiology, at scales ranging from the microscopic to the continental. These studies have led to substantial revisions of many of the existing paradigms relating to the diversity, distribution, function and physiological responses of soil microorganisms and microbial communities.

Metagenomic analyses have shown that the 'common' soil organisms are actually rare, and that the 'uncultured' members of the community are often the majority. The microbial species distribution in Antarctic soils is anything but homogeneous, with community composition being driven by numerous abiotic (and some biotic) factors, including substrate, physicochemical parameters (especially water availability), niche community structure and much more. The task of understanding the complexity of these drivers is increased by the fact that some are scale-dependent, while others are not.

In the absence of high plants in most Antarctic terrestrial soil habitats, microorganisms play a dominant role in ecosystem services. However, the extreme nature of these habitats has led to the general perception that microbial processes are extremely limited and that microbial communities will show limited capacity to adapt to changing environmental conditions. The latter is certainly a simplification, with both field and laboratory experiments suggesting that microbial community structures can be dynamic over relatively short timescales.

Deep metagenome sequence analyses suggest that Antarctic soil microbial communities encode metabolic and anabolic capacities as diverse as any other terrestrial soil community, with high levels of metabolic redundancy and a broad range of pathways and genes specifically targeting stress response and adaptation processes.

There are still extensive gaps in our knowledge: quantitative functional studies are few and generally limited (for obvious logistical and practical reasons), and little is yet known about the interactions between organisms and trophic tiers in Antarctic soil communities. The role of entire taxonomic clades, such as phage and viruses, is virtually unknown.

Protecting Antarctic marine ecosystems

Lochte Karin[1]

[1] Alfred Wegener Institute for Helmholtz Centre for Polar and Marine Research

The ecosystem of the Southern Ocean is subject to partly climatic and partly anthropogenic impacts, in particular at the Antarctic Peninsula, which can cause substantial changes in the Antarctic biodiversity and ecosystem functioning. These impacts range from ocean acidification and warming, changes in sea ice cover, introduction of alien species, to fishing and increased shipping. In contrast to the Arctic Ocean, the Southern Ocean is governed by a protective legal system (Antarctic Treaty, the Protocol on Environmental Protection, CCAMLR). It regulates human activities in Antarctica, but cannot prevent externally driven changes encroaching on the polar ecosystem. At present efforts are underway to develop Marine Protected Areas (MPA) around the Antarctic continent to protect the unique and vulnerable ecosystem. Several proposals are on the table for MPAs in the Ross Sea, the Weddell Sea and around East Antarctica. They are supported by large collections of biological data from many expeditions. But the proposals for MPAs also face political opposition. What are the reasons for or the problems of installing MPAs? How can we monitor the success of MPAs? What does it mean for biological sciences? These are important questions for biological research in Antarctica. It calls for international efforts to provide the necessary data for the implementation of MPAs, a joint data basis that interlinks physical, biological and human impact data, and a clear view on the long-term responsibility for the protection of the valuable marine ecosystem of Antarctica.

Keynote

What does phytoplankton tell us about global change?

Schloss Irene[1-2]

[1] Argentinian Antarctic Institute (IAA)
[2] National Council of the Research (CONICET) of Argentina

The ecosystem of the Southern Ocean is subject to partly climatic and partly anthropogenic impacts, in particular at the Antarctic Peninsula, which can cause substantial changes in the Antarctic biodiversity and ecosystem functioning. These impacts range from ocean acidification and warming, changes in sea ice cover, introduction of alien species, to fishing and increased shipping. In contrast to the Arctic Ocean, the Southern Ocean is governed by a protective legal system (Antarctic Treaty, the Protocol on Environmental Protection, CCAMLR). It regulates human activities in Antarctica, but cannot prevent externally driven changes encroaching on the polar ecosystem. At present efforts are underway to develop Marine Protected Areas (MPA) around the Antarctic continent to protect the unique and vulnerable ecosystem. Several proposals are on the table for MPAs in the Ross Sea, the Weddell Sea and around East Antarctica. They are supported by large collections of biological data from many expeditions. But the proposals for MPAs also face political opposition. What are the reasons for or the problems of installing MPAs? How can we monitor the success of MPAs? What does it mean for biological sciences? These are important questions for biological research in Antarctica. It calls for international efforts to provide the necessary data for the implementation of MPAs, a joint data basis that interlinks physical, biological and human impact data, and a clear view on the long-term responsibility for the protection of the valuable marine ecosystem of Antarctica.

Art as outreach: sharing Antarctic research through painting

Simonson Lily

Lily Simonson's ongoing collaborations with researchers aim to celebrate the longstanding tradition of art and science working in concert to expand knowledge and share new discoveries. Simonson's emphasis on painting from direct observation has led her to frequently embed in expeditions, from the deep sea to the Antarctic. Through a personal narrative, Simonson will describe the process that led her to these interdisciplinary collaborations. She will discuss the impacts of this synergy, with a specific focus on public outreach.

As the US National Science Foundation Antarctic Artist & Writers Program Awardee, Simonson spent more than three months on the ice. She completed 25 scuba dives beneath the sea ice in McMurdo Sound, observing the benthic communities of shimmering polychaetes, vibrant sea stars, unusual crustaceans, and other invertebrates flourishing in the Ross Sea. By diving under the ice or observing collected specimens, Simonson was able to study, draw, and paint the resident organisms alive, flush with natural pigment, and illuminated by the unique blue glow of sunlight filtered through the ice covering the ocean's surface. Simonson subsequently worked with field teams to investigate and capture on canvas the complex soil ecosystems of Taylor Valley and its resident nematodes, tardigrades, and rotifers extracted from the soil in and around the Valley's fascinating network of water tracks. These works aim to explore how warming temperatures might impact the diversity of invertebrates in the soils of the Dry Valleys.

During this SCAR Biology Symposium, Simonson will use her drawings and impressions from Antarctica to create a new painting. Symposium participants are invited to visit her during her process, to offer their perspectives and insights. During this presentation, Simonson will share the way that interacting with Antarctic researchers at the symposium shaped her process.

Taxon-specific sensitivity of Southern Ocean phytoplankton to climate change

Trimborn Scarlett[1-2]

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The Southern Ocean acts as a disproportional large atmospheric CO2 sink and thus affects climate at a global scale. Future biological CO2 sequestration will depend on how Southern Ocean phytoplankton will respond to climate change. Next to the on-going acidification, rising temperatures will alter surface ocean stratification, which in turn may alter vertical mixing with subsequent effects on light availability and nutrient input from deeper layers. How will these environmental changes affect future phytoplankton community structure and productivity? Shipboard manipulation experiments with natural phytoplankton assemblages of different locations of the Southern Ocean (Atlantic Antarctic Circumpolar Current, Western Antarctic Peninsula) were conducted simulating future climate change scenarios (CO2, irradiance, iron). In response to ocean acidification, phytoplankton community composition was sensitive. In particular, the use of natural iron sources (i.e. dust) was essential for a realistic projection of the biological carbon pump in the iron-limited Southern Ocean under ocean acidification. Interestingly, ocean acidification resulted in dominance of the prymnesiophyte Phaeocystis antarctica, irrespective of changes in iron availability or light regime, pointing out its tolerance to high pCO2. Laboratory experiments further underline the sensitivity of diatoms such as Chaetoceros debilis and Fragilariopsis kerguelensis to ocean acidification and high irradiance in contrast to the more tolerant P. antarctica. As the biological carbon pump is primarily driven by diatoms, a shift away from diatoms towards P. antarctica could potentially weaken the biological carbon pump and alter climate feedback mechanisms.

Theme 1
Distribution and trends

Spatial variability of microbenthos in intertidal waters of Scotia Bay (Laurie Island), with emphasis in benthic diatoms

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Besides contributing significantly to coastal primary production and providing a key source of food for both primary and secondary consumers, the importance of microbenthos lies also on its dampening sediment resuspension and serving as a shelter to algal propagules and larvae of invertebrates. The current study is the first one addressing the microbenthos of Scotia Bay (Laurie Island, South Orkney Islands), and its main goal was to detect differences between the communities living on rocky and sandy bottoms (epilithon and epipsammon, respectively). Samples of these two communities were taken by triplicate from four different sites within the intertidal zone during low tide conditions. Sites were selected based not only on the type of bottom but also on the degree of protection from wind and the influence of glacier melting runoff.

The richest site in terms of benthic fauna and macroalgae proved to be the most protected from wind (site S1), located near Mount Mossman and characterized by a bottom mostly made up of rocky blocks. At the inlet of the bay (S2 y S3) and next to the glacier (S4), the intertidal sea bottom was predominantly sandy. The communities living on both types of bottom included diatoms, flagellates, dinoflagellates, and unidentified cysts, while epipsammon also comprised ciliates and exoskeletons of silicoflagellates. Within the total area sampled, the epipsammic community reached average abundances over three times higher than the epilithic ($4.8\ 10^7$ cells.m^{-2} vs. $1.4\ 10^7$ cells.m^{-2}). Diatoms were the dominant group in both communities, with a majority of their taxa belonging to the genera *Navicula*, *Licmophora*, *Amphora*, and *Cocconeis*. Planktonic genera were mainly represented by *Thalassiosir*a, which occurred at all sampling sites, plus *Rhizosolenia*, *Chaetoceros*, and *Corethron*, which showed highest concentrations at sites S1, S2 and S3, respectively. Highest diatom abundances corresponded to the epipsammon from S4, in the vicinity of the glacier ($8.9\ 10^7$ cells.m^{-2}). Epilithic diatoms, on the other hand, showed maximum concentrations at S1 ($5.3\ 10^7$ cells.m^{-2}). Flagellates exhibited a similar trend, with higher numbers in the epipsammon (mean: $0.2\ 10^7$ cells.m^{-2} vs $0.06\ 10^7$ cells.m^{-2} for epilithon). The rest of the groups always showed abundances below $0.1\ 10^7$ cells.m^{-2} in both communities, although with highest figures at S1. The only exception was dinoflagellates, for which highest concentrations were found in the epipsammon of site S2. A comparative assessment of benthic vs. planktonic diatom species will be discussed.

Resolving internal relationships within Syllidae (Annelida) using a combined phylogenetic and morphological approach

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The family Syllidae constitutes one the largest and most diverse groups within 'polychaetes' annelids, but also one of the most complicated, with several taxonomical and phylogenetic problems still unsolved, since many of its genera seem to be paraphyletic (Álvarez-Campos *et al.* In press). Although Antarctic Syllidae have been relatively well studied in the past century (e.g. Hartman, 1991; San Martín & Parapar, 1997), most of the research only included brief diagnosis of the species, with none or few illustrations of commonly used diagnostic characters, which makes impossible to establish the true diversity or distribution of syllids in the area. In addition, as it has been already shown in the family, some of the morphological features traditionally used to identify species are homoplastic or ill-interpreted, which turns on the underestimation of the real biodiversity within Syllidae (Álvarez-Campos et al. 2017). Therefore, the combination of morphological (e.g. scanning electron microscopy -SEM-) and molecular techniques is essential to dig into these taxonomically problematic groups. Furthermore, the use of other recent methodological advances in morphological techniques is essential to provide further evidence of hidden differentiation among closely related species. One of these techniques is micro-computed tomography (micro-CT) scanning, which allows capturing high resolution details of internal structures of the organisms without damaging them. In our study, 97 specimens, belonging to the 4 main subfamilies within Syllidae, from twelve different localities of the Antarctic Peninsula and South Shetland Islands, were studied for the first time under a three-fold approach: internal (micro-CT) and external (SEM) morphology, combined with molecular data (28S rRNA, 18S rRNA, 16S rRNA and cytochrome c oxidase subunit I), in order to disentangle the chaotic taxonomical situation in the group. The sequenced genes were added to our existing database and were used for phylogenetic inference using both maximum likelihood and Bayesian inference methods, providing a phylogenetic hypothesis for the whole group and in particular for the Antarctic species. We also discuss the usefulness of the internal anatomical details obtained using micro-CT scanning techniques.

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In situ submersible observations of western Antarctic Peninsula deep sea fauna

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In January and February 2017 a submersible-based cruise was conducted along the western Antarctic Peninsula. The focus of the cruise, organized by Japanese NHK TV, was to obtain high-definition video footage of scientists exploring the deep waters of Antarctica for a documentary (Deep Antarctica). The three-person 1000m-capable submersible carried a scientist (CDB, MOA, or KSRB) in addition to the pilot and a cameraman. Logging a cumulative 100 hours of dive time, survey sites included an offshore continental break site (west of Smith Island), the Antarctic Sound, Fumarole Cove (Deception Island), Boyd Strait, Wilhelmina Bay, Buls Bay (Brabant Island), Fournier Bay (Anvers Island), and Palmer Deep. Numerous noteworthy pelagic and benthic observations were made during the eighteen dives. Two dives (Smith Is. and Boyd St.) were entirely water-column focused and included sightings of rarely seen swimming medusae and a lobate ctenophore, along with lengthy encounters with several species of squid, including one never before observed in the wild (KSRB). At all dive sites the water column was generally occupied by various species of fish, primarily *Neolepis coatsi*, and krill, chiefly *Euphausia superba*, but also *E. crystallorophias* (Antarctic Sound) and *E. triacantha* (Palmer Deep). Water temperature varied between the dive sites and at maximum dive depths ranged between -1.4 (Antarctic Sound) to 1.4°C (Palmer Deep). Video-based surveys of the seafloor communities were carried out at depths ranging from 180m at Buls Bay, Brabant Island, to 1000m at Palmer Deep. During the majority of the dives the biotic communities varied in terms of both species composition and relative abundances of taxa. Seafloor substrate was equally variable, encompassing featureless plains of soft sediment, rolling silty terrain with occasional dropstones, densely colonized vertical ledges and ice-scoured hard bottom. The dives also yielded in situ observations of gigantism, and both unknown or undocumented behaviors of crustaceans, echinoderms, and fish, recorded for the first time with high resolution cameras. Finally, a complete whale skeleton (probably a juvenile *Megaptera novaeangliae*) was discovered at 965m on the Palmer Deep slope. The intact skeleton is likely the southernmost discovery of its kind to date and possibly the best imaged natural whale fall in any ocean. Preliminary examination of the video footage revealed 30 different taxa (fishes, worms, crustaceans) on and around the bones and on the surface of the enriched sediments surrounding the whale skeleton.

Macroinvertebrate communities from the shallow soft-bottoms of Deception Island (Southern Ocean): a paradise for opportunists

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Deception Island (South Shetland Islands) is an atypical spot in its Antarctic context, being an active volcano with a submerged caldera. Although the sea-floor of its enclosed bay, Port Foster, has been extensively studied from 40 m down, little is known about the macrozoobenthic composition of its shallower areas. The aim of this study was to characterize the so far unexplored soft-bottom marine macroinvertebrate communities living within the first few meters depth in Port Foster. Eight sampling stations were selected, and three replicates per station and depth (5 and 15 m) were collected by SCUBA diving using 0.008 m^{-2} corers. Six clusters of samples were distinguished, showing a high variability in the composition of the shallow-water macrofauna. This heterogeneity did not appear to be related to the proximity of the sites to the open sea (entrance of the caldera) or depth, nor to the sediment type or the organic matter content. Overall, the assemblages within each cluster were generally dominated by highly abundant opportunistic species, including the annelids *Capitella perarmata*, *Mesospio moorei*, *Leitoscoloplos kerguelensis*, *Apistobranchus glacierae*, and *Tharyx cincinnata,* the amphipod *Cheirimedon femoratus*, and the bivalve *Aequiyoldia eightsii*. The remarkably high densities reported in several stations, suggest that the shallow-water environment of Port Foster is highly productive. In light of these results, we propose a general trophic web for the shallow waters of Port Foster linking the unusually high densities of macroinvertebrates with the also high occurrence of megafaunal echinoderms present in this area.

Antarctic marine chemical ecology, biodiversity, and more...

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The structure of marine benthic ecosystems is determined by both environmental and biological factors. Among the last ones, the phylogenetic history, the ecological relationships (symbiosis, competition, predation), the life-cycles, and the colonization rates of the organisms are crucial for the survival of their populations. In contrast to what happens in other regions of the planet, the Antarctic ecosystems are ruled by a strong environmental stability, only comparable to that observed in caves or abyssal regions, and thus the interactions between organisms play an important role in structuring the communities (Dayton et al., 1974; Paul et al., 2007). Since 1998, the Antarctic research projects ECOQUIM, ACTIQUIM, ACTIQUIMWHALES, and DISTANTCOM aimed at gaining a better understanding of the diversity and structure of Antarctic benthic marine communities, both at biological and chemical levels. To do so, we study the ecological activity of the marine natural products from benthic organisms, by carrying out *in situ* chemical ecology experiments. The chemical ecology of marine benthic organisms (local scale) includes, among others, repellence, toxicity, and antifouling activity assays, as well as the identification of the natural products and their potential bioactivities. However, over the years, our studies have diversified to include other related topics in marine ecology. Therefore, we also study the trophic relations, symbiosis and bioaccumulation in shallow Antarctic benthic communities. On the other hand, at a regional scale, we study the evolutionary history of selected Antarctic invertebrates: biodiversity, phylogeography, and genetic connectivity between populations. As further related topics arise, our team is also producing new methodologies to answer new questions about marine benthic invertebrates. This is made possible thanks to the collaboration of a multidisciplinary team of researchers, challenging our current knowledge in marine ecology in Antarctica at different levels. An update of the current developments in these studies is presented here, including the most recent results. Such knowledge will also contribute to provide the basis to identify and palliate threats to the diversity on these unique ecosystems, which also constitute a natural biological laboratory for ancient interactions, subjected to very particular conditions.

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A new genus within the remarkable and rare amphipod family Podosiridae

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The amphipod family Podosiridae (Lowry and Myers, 2012) is notable for its combination of morphological characters from the disparate amphipod families Podoceridae and Eusiridae. At present, Podosiridae is represented by only a single described species, Podosirus vaderi (Bellan-Santini, 2007), collected in 2002 from a vent community at 1680 metres water depth in the Azores Triple Junction zone. Based on its grasping pereopods, large gnathopods and elongate maxilliped, this species is hypothesised to be an epifaunal ambush predator.

However, a recent (February-March 2016) British Antarctic Survey research cruise (JR 15005, 'SO-AntEco' [https://www.bas.ac.uk/project/so-anteco/]) in the vicinity of the South Orkney Islands has yielded 4 additional specimens attributable to the family. Further, these individuals show high morphological similarity to an additional, as yet undescribed, specimen collected off Clarence Island (South Shetland Islands) in 1936 and presently residing in the Discovery Collections held at the National Oceanography Centre, Southampton (http://noc.ac.uk/facilities/discovery-collections).

These five specimens are clearly members of the Podosiridae, exhibiting the slender, compressed body, moderate rostrum, lack of accessory flagellum, extended, raptorial maxilliped, acuminate coxae, elongate urosomite 1 and entire telson that are together characteristic of the family. However, the specimens differ from Podosirus in the produced form of the lateral cephalic lobes, presence of eyes, ratio of antenna 1 articles, prehensile pereopods 3-7, shape of epimeral plate 3, and uropod 3 with extended peduncle. As such, it is proposed that these specimens represent a new genus within the family Podosiridae.

Here, the morphology of this new genus will be detailed using photography and scientific illustrations, whilst deductions will be made with regards to the ecology of this genus based on details of collection circumstance and functional morphology, with initial inspection suggestive of a similar predatory life-style to Podosirus. Further, rapid freezing and preservation in 96% ethanol upon collection has facilitated the extraction of high quality DNA from the specimens collected from the South Orkney Islands. Portions of 18S SSU rDNA, 16S rDNA, cytochrome c oxidase 1 (COI) and Histone H3 genes will be sequenced and added to a large (285 taxa) alignment of other peracarid taxa. This will be utilised to determine, with greater certainty, the possible phylogenetic placement of this remarkable family.

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Parasite fauna comparison among Nacella species inhabiting across Southern Ocean: evidence of isolation?

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The Southern Ocean (SO) is characterized by a high level of endemism related to the historical isolation from the Eocene. However, the actual isolation of the SO has been put in doubt due to the recent phylogeographic evidences. These studies have been showed that many species has been able to cross the Antarctic circumpolar current barrier many times (Patarnello et al. 1996; Billard et al. 2015, Hune et al. 2015). In this context, the SO marine benthic fauna has been shaped by the interaction of geological, oceanographic and climatic events (Aronson et al. 2007). Parasites need to live inside or on another living organism to survive and develop. Parasites are a good model to estimated the efficiency of the contemporary and historical barriers to dispersal in SO and their influence to form the current biodiversity in the area. In general, parasites with complex life cycle (those than need more than one host) are characterized by low potential to dispersal associated with the mobility of their host (Blasco-Costa et al. 2012). In addition, parasites are closely related to their host, and then they could share similar biogeographic history (Criscione 2008). Finally, the biogeographic history of the "preys" is considered as determinant in the community structure of endoparasites (González et al. 2006). The patellogastropod *Nacella concinna* is the most abundant invertebrate in the intertidal and subtidal environments in Antarctica an also has relative closed species inhabiting southern South America. These patellograstropods are intermediary hosts in the life cycle of many parasites species. In this study, we compare the parasite-fauna composition between *Nacella concinna* and *N. deaurata* (SA) to understand the current patterns of diversity and connectivity among these organisms in both environments. Three scenarios are postulated: (1) If the definitive host is a long distance migrant between A and SA, then both species could share at least one parasite species, (2) If A is a closed environment with an endemic fauna without connection with SA, then both species could have different parasite-fauna, and (3) If both *Nacella* species have highly specific parasites, they should follow the biogeographic and evolutionary history of their hosts. This work is the first intent to reveal the strength of the ACC as barrier to parasites and to understand the evolutionary history of these organisms in the SO.

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Spatial pattern of genetic diversity in the Antarctic and Subantarctic species of the bivalve *Kidderia* spp.

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The Antarctic continent is separated from other landmasses by sheer distance and in the marine realm the Polar Front acts as a barrier to dispersal. On fact, the Antarctic Circumpolar Current acts as an effective barrier for many invertebrate taxa, especially between Antarctic and sub-Antarctic provinces (Gonzalez et al. 2016). However, many benthic marine species from Antarctic remain poorly studied. The bivalve *Kidderia bicolor* (Marterns 1885) is a small organism (average size around 5 mm) and is highly abundant in the intertidal of Antarctic Peninsula and its genera have been registered in Patagonia, Falkland Island, South Georgia, South Shetland Island and the Antarctic Weddell sector (Zelaya 2005). Up today the taxonomic classification and relationship among species inside genus has been studied based exclusively on morphological traits. Its brooding reproduction and low dispersal capabilities predict limited gene flow between geographically isolated populations. Here we develop a phylogenetic and phylogeographic analysis in order to deal with the following questions: ¿Are the genera *Kidderia* composed by genetically different lineage? ¿What is the phylogenetic relationship between *Kidderia bicolor* and those *Kidderia* species described in subantarctic area? In the Antarctic realm, there is population genetic structure in *Kidderia bicolor*? The SSU rRNA gene was used to develop a phylogenetic analysis including samples from Antarctic Peninsula and Chilean Patagonia. Results confirm that Kidderia belong to the family Cyamiidae and showed that the taxonomic units *Kidderia bicolor* and *Kidderia subquadrata* (Pelseneer 1903) are related taxa separated by 13 mutational step. At population level, the mitochondrial DNA diversity was evaluated using the cytochrome c oxidase subunit I (COI) gene. Preliminary results are revealing high genetic diversity among spatially isolated populations of *Kidderia bicolor* in Antarctic Peninsula. The processes behind these patterns are yet unknown, however possible explanations lie in the recent oceanography history of Antarctic Circumpolar Current.

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DNA Barcoding of fishes collected off the South Orkney Islands

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A comprehensive description of benthic fauna is key for sound conservation and management plans. Biodiversity descriptions rely on species identification, which can be challenging when taxonomically relevant morphological characters are fragile, obscure or largely absent. Molecular methods such as DNA barcoding can complement specimen identification and furthermore hint at cryptic speciation, synonymies, or intraspecific phylogeographic patterns. The South Orkney Islands (SO) archipelago is located in the Scotia Sea, some 600km north-east of the tip of the Antarctic Peninsula. The waters around the SO feature exceptionally high marine Antarctic biodiversity and the first High Seas marine protected area worldwide.

Recently, a research expedition to the South Orkneys has been conducted in the framework of the SCAR program "State of the Antarctic Ecosystem" (AntEco). We here present the fish fauna collected during the SO-AntEco expedition. Morphological identifications of preserved specimens are compared to molecular identification obtained via DNA barcoding. Additionally, we examine distribution patterns of the fish fauna to compare different seafloor habitats across the SO archipelago and identify potential, important drivers of community composition. The fish fauna in turn may influence benthic invertebrate communities via top-down control as opposed to structuring processes directly driven by environmental conditions.

Our results advance the Antarctic DNA barcoding database and our understanding of benthic communities and its drivers in a biodiverse, marine Antarctic region. Thereby we contribute to the South Orkney Islands marine fauna management and preservation in the future.

Metagenomic sequencing of environmental DNA reveals marine faunal assemblages from the West Antarctic Peninsula

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Various human activities cause direct harm to aquatic ecosystems by loss of biodiversity. To mitigate these impacts, conservation initiatives rely upon accurate surveys of biological communities as indicators of ecosystem health. Environmental DNA (eDNA) - genetic material extracted from bulk environmental collections such as water or sediment (Taberlet et al. 2012; Thomsen and Willerslev 2015) - has become a widespread method for monitoring changes in communities. The growing popularity of eDNA is in part due to its sensitivity for detecting aquatic organisms and is often less costly when compared to conventional surveys. To determine the potential of eDNA for assessing animal biodiversity of the Antarctic marine biosphere, we collected water samples from four West Antarctic Peninsula shelf regions (< 300m) for eDNA extraction and metagenomic shotgun sequencing analyses. Processing the resulting 325 million sequence reads via a customized bioinformatics pipeline, we identified abundant signatures of common benthic invertebrate fauna and endemic notothenioid fishes. Further, we detected signatures of the lithodid king crabs, whose potential shoreward expansion to warming shelves has sparked concerns that the crabs may alter shallow benthic communities. The metagenomics approach also uncovered high species richness and diversity comparable to current biological inventories (Griffiths et al. 2011), supporting the efficacy of this eDNA methodology. Additionally, the rate of eDNA degradation impacts faunal detection sensitivity, thus we also quantified mitochondrial ND2 gene copies in eDNA derived from the icefish, *Chionodraco rastrospinosus*. Through this eDNA degradation experiment, we found that detectable numbers of ND2 copies persisted to at least 20 days in polar temperatures, which was longer than reported for a temperate environment (Thomsen et al. 2012). Overall, this work further supports the use of eDNA for numerous conservation initiatives. As these approaches frequently complement traditional surveys, the combination of both survey types will likely improve the comprehensiveness of biodiversity detection in the Southern Ocean. This study was supported by NSF Award ANT1142158 to CHCC and UIUC STEM postdoctoral fellowship to DAC.

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A new giant *Lipkius*-like shrimp from the Crozet Islands (Crustacea, Decapoda, Caridea)

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It is a well-known fact that the Southern Ocean is a cold spot of diversity for decapod crustaceans. Yet, at the beginning of the twenty-first century, new species continue to be described in the sub-Antarctic and Antarctic SCAR-MarBIN/RAMS Areas Of Interest (AOI), suggesting that this fauna remains incompletely known. A remarkable discovery presented herein confirms this. A strange and huge (total length of over 150mm) caridean shrimp was found in the biological material obtained by long line sub-Antarctic fisheries, preserved by the French fishery controllers (COPEC), and sorted during the Antarctic Biodiversity Workshop, Concarneau, autumn 2016. The unique specimen examined was collected on the steep slope of a seamount situated NW of the Crozet Islands: 44.6533°S 47.9415°E, 1889 m depth. It is suspected to have been hauled up on board with corals entangled in long lines. The shrimp exhibits no affinity with any previously known species from the Southern Ocean. A close examination reveals some similarities with *Lipkius holthuisi* Yaldwyn, 1960 from New Zealand and SE Australian bathyal waters, which was the only known species of the family Lipkiidae Burukovsky, 2012. However, important differences were observed as well. The characters of the new shrimp are presented. Its systematic position is discussed and hypotheses are proposed for explaining the occurrence of this very unusual taxon in sub-Antarctic waters. Just like campylonotid shrimps, thymopine lobsters and belliid crabs, *Lipkius*-like shrimps have a distribution centred on the cold and temperate waters of the southern hemisphere, and these species-poor taxa are suspected to be Gondwanan relicts.

Experimental evidence of chemical defence mechanisms in Antarctic bryozoans

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The role of bioactive metabolites in ecological interactions involving bryozoans, one of the most abundant and diverse members of the Antarctic benthos, has been scarcely studied. To extend our knowledge about the allelochemistry of Antarctic bryozoans, three ether extracts (EE) and three butanol extracts (BE) obtained from six samples belonging to two Antarctic common species (*Cornucopina pectogemma* and *Nematoflustra flagellata*), were tested for repellent and antibacterial activities. The Antarctic sea star *Odontaster validus* and the amphipod *Cheirimedon femoratus* were selected as sympatric predators to perform anti-predatory and substrate preference assays. The extracts were also screened for quorum quenching and antibacterial activities. The results showed that these species were not repellent against sea stars. In contrast, both species with the two extracts tested caused repellence to the amphipods in the feeding assays, suggesting that defence activities derive from lipophilic and hydrophilic metabolites. In the substrate preference assays, only one of the EE and BE from *C. pectogemma*, were active. No quorum quenching activity was detected in any of the extracts. Regarding antibacterial activity, all EE exhibited growth inhibition towards at least one bacterium strain. Our results showed intraspecific variability of chemical defences, and supported the fact that chemically mediated interactions are common in Antarctic bryozoans as means of protection to combat against predation and microbial invasions.

Autonomous reef monitoring structures in the Southern Ocean, a tool for the study of the understudied small fauna

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Autonomous Reef Monitoring Structures are standardized artificial largely used in shallow, tropical marine locations to assess the cryptofauna (Knowlton et al. 2010, Plaisance et al. 2011, Knowlton et al. 2015). These multilayer type I PVC structures offer a succession of closed and open layers for the small and very small fauna and flora to colonize. They are typically left attached underwater for one year in these warmer environments before recovery and analysis through classical taxonomy and metabarcoding approaches.

We present here the first results for ARMS in the Southern Ocean, close to the Dumont d'Urville french Antarctic station (REVOLTA II program, IPEV). The ARMS were immersed in 2014, and were either left at the locations for two years (recovery in January 2016) or three years (recovery in January 2017).

The plates were photographed, and specimens were sampled both one by one and in a mix for metabarcoding. Three molecular markers were used (mitochondrial genes COI and 16S, and nuclear 18S), as well as multiple wide-ranging primers pairs for each, to maximize the amplification and identification of a wide range of taxonomic groups.

The plates colonized for two years were rather sparse, maybe because of unusual ice conditions at the location, but the plates colonized for three years were richer. Sequence analysis of the three markers yielded generally congruent results, although some groups were not recovered with all. Expectedly, 18S was the less precise of the markers but corroborates attribution to higher taxonomic ranks. Bryozoans and tube worms dominated the plates, with several having close but no identical sequences in the reference databases (Barcode of Life database and GenBank).

Our ARMS were also included in outreach projects to school classes. These structures are a precious tool for the study of the understudied small fixed and sessile organisms in the shallow areas of Southern Ocean, especially if deployed as a network by a collaboration of research projects to cover a wider variety of spatial scales. They provide information on colonization and growth, and a simple but powerful monitoring tool for this changing environment.

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Criptic speciation in Southern Ocean *Aequiyoldia* (*Yoldia*) spp.

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The species of the genus *Yoldia* Möller, 1842 are common soft-bottomed nuculanid bivalves. In the Southern Ocean, *Yoldia eightsii* Jay, 1839 was originally described in Patagonia and Antarctica while *Y. woodwardi* Hanley, 1960 is distributed in the Falkland/Malvinas Islands and also in Tierra del Fuego (Rabarts & Whybow, 1979). Southern Ocean's *Yoldia* species have received little attention and their taxonomic status remains uncertain and have been recently grouped under the same species name *Aequiyoldia eightsii* (Sartori et al 2016). However, molecular analyses highlighted marked genetic divergence (> 7%) between mitochondrial haplotypes from Patagonian and Antarctic *Yoldia eightsii* which lead to suspect the presence of cryptic species within *Aequiyoldia eightsii* across the Drake passage (Gonzalez-Wevar et al. (2012).

In order to further understand the diversity pattern in *Aequiyoldia* spp., we expand the sampling area and collected specimens from the Magellanic Region, Falkland/Malvinas Islands, the West Antarctic Peninsula and the Kerguelen Islands. Samples were characterized by the most diagnostic morphological measurements defined by Rabarts & Whybow (1979), and their phylogenetical relationships were reconstructed from sequences of the mitochondrial locus cytochrome c oxidase subunit I (COI). The statistical analysis of the morphological data differentiates three morphogroups composed by (1) the samples from Falklands/Malvinas Islands that correspond to *Y. woodwardi*, (2) those from Patagonia-Antarctica-Kerguelen as representants of *Y. eightsii* and (3) samples found only in Kerguelen Islands and belonging to *Y. isonota* (now *Portlandia isonota*; Huber, 2015). The relationships among the COI haplotypes of Southern-Ocean *Aequiyoldia*, show several lineages including: (1) Falkland/Malvinas Islands clade, (2) Patagonian clade, (3) (4) (5) three distinct Antarctic clades, (6) Kerguelen clade. The three Antarctic clades being the closest together; Patagonia and Falkland Islands clades being separated by 4,5% of divergence, the Antarctic clades scoring around 7-8% divergence with Patagonian/Falkland islands clades, and finally Kerguelen clade being separated by nearly 30% divergence from the other clades. The intraclade diversities range from low to zero.

An unsuspected diversity represented by three mitochondrial lineages, was discovered in Antarctic *A. eightsii. Aequiyoldia eightsii* from Patagonia and Antarctica, reached reciprocal monophyly and accumulated 8% of mitochondrial divergence, but conserved similar morphology. *Aequiyoldia eightsii* from Patagonia acquired morphological differences, with only 4% of divergence with samples from Falkland Islands, so that *Aequiyoldia woordwardi* could be revalidated. In Kerguelen, *A. eightsii* shared similar morphology with those from Patagonia and Antarctica but the mitochondrial divergence of 30% suggests that they may belong to a different genus.

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Long-distance dispersal in higher latitude Siphonaria (Gastropoda: Euthyneura) species

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Biogeographical mechanisms explaining the distribution of southern temperate taxa have been debated since the XIX century but a consensus has been growing on the combined significance of vicariance and long-distance. In this study we present multi-locus phylogenetic and population-based analyses of high-latitude direct developing Siphonaria species. We include subantarctic Siphonaria populations from several subantarctic provinces (South America, Falkland/Malvinas Islands, South Georgia, the Kerguelen and Macquarie islands). Through molecular reconstructions we present a clear picture about 1) the evolutionary relationships within subantarctic Siphonaria 2) the number of valid taxonomic units and 3) the geographic distribution of each taxon. With this information it was possible to unveil the biogeography of the genus across the Southern Ocean. Phylogenetic reconstructions highlight the existence of two clearly discriminated and broadly distributed subantarctic lineages of Siphonaria identified as S. lateralis and S. fuegiensis. These cryptic and sympatric Siphonaria species were formerly recognized as Kerguelenella lateralis but their phylogenetic positions indicate that they are included in the genus Siphonaria. Divergence-time estimates suggest that the separation between S. lateralis and S. fuegiensis occurred ~ 4.0 million years ago (Ma) (between 3.0 - 8.0 Ma). After this cladogenetic process they followed different evolutionary pathways even when they are currently sympatric across Subantarctica. Extremely low levels of genetic diversity characterize subantarctic Siphonaria species reflecting the role of Quaternary glacial cycles in their respective demographic histories. The presence of dominant and broadly distributed haplotypes in both species suggests high levels of connectivity among geographically distant localities. Both, S. lateralis and S. fuegiensis, constitute sister cryptic species broadly distributed in Subantarctica, from southern South America to Macquarie islands. Transoceanic similarities, similar phylogeographic signals and very low levels of genetic diversity recorded in these direct-developing species reveal the prevalence of long-distance dispersal, probably mediated by rafting in circumpolar currents. We propose a biogeographic model for the Quaternary to explain the broad distributions of these higher latitude pulmonates, their presence on isolated subantarctic islands and their low genetic diversity and simple structure over thousands of kilometers.

Biogeographical patterns in Southern Ocean mollusks with contrasting developmental modes

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The biogeography of the Southern Ocean marine benthic biota and its current bioregionalization are the consequence of major tectonic, oceanographic and climate changes over the last 50 million years ago. Continental drift, major gateway openings, and temperature decrease shaped past and present oceanographic circulation in the region. Here, we present new biogeographical analyses based on nuclear and mitochondrial markers in different groups of near-shore benthic mollusks with contrasting developmental modes that are currently found in different provinces of the Southern Ocean. We used phylogenetic and phylogeographic approaches to further understand the role of historical and contemporary processes in the current patterns of genetic divergence, diversity, and structure across provinces of the Southern Ocean. We include in the analyses direct developers (Trophon/Trophonella, Margarella, and Siphonaria) and broadcast-spawners (Nacella, and Yoldia). We determined uncorrected p-distances, divergence times using strict Molecular Clock Hypothesis (MCH) and we constructed Maximum Parsimony genealogies. As general rule, low levels of genetic diversity characterize Antarctic and Subantarctic mollusks as a consequence of Quaternary glacial processes that deeply affected population sizes and the demography of the analyzed groups. Similarly, all the analyzed groups showed high degree of genetic divergence between Antarctic and Subantarctic provinces supporting the role of the Polar Front as an effective biogeographic barrier. The effective separation between Antarctic and Subantarctic lineages occurred between 3.7 and 14.5 Ma, long after the physical separation of the continental landmasses or to the initiation of the ACC. In this scheme, the geodynamic evolution of the Scotia Arc with the establishment of a full deep ACC during the middle Miocene may represent a key driver in the isolation of the marine Antarctic fauna. Surprisingly, direct developers like Margarella and Siphonaria exhibited high levels of genetic homogeneity across geographically distant Subantarctic areas. Such results support the role rafting as an important biogeographic mechanism in the Southern Ocean. In contrast, broadcast-spawners like Nacella and Yoldia showed marked genetic distinction among geographically distant Subantarctic provinces. In this case, life-history traits constrains prevent long-dispersal through larvae in these groups. Finally, current biogeographical patterns in Southern Ocean mollusks are not related to particular groups but to historical oceanographic/climatic processes, as well as contemporary ones including the likelihood of long-distance dispersal.

The knowns and known unknowns of the biogeography and ecology of a likely climate-change winner: the amphipod *Themisto gaudichaudii*

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The amphipod *Themisto gaudichaudii* is a so far neglected but key pelagic player in the Southern Ocean. This hyperiid amphipod species is found along a wide latitudinal gradient with temperatures differing by almost 20°C between its distributional limits. Due to its high abundances, swarm-forming behaviour and importance for higher trophic levels, it is often referred to as krill from the north. Whilst Antarctic krill (*Euphausia superba*) is more restricted to colder waters further south, *T. gaudichaudii* is more abundant in northern ice-free zones and is prone to extend its range southwards with the rising water temperatures observed in the Southwest Atlantic sector. In this region, density changes of salps and Antarctic krill have already been noted over the last decades, with krill decreasing whilst salps are on the increase. However, the interactions between the three key players – *Themisto*, krill and salps – are too little understood to evaluate cascading top-down effects and potential ecological shifts in the Southern Ocean pelagic realm. Knowledge gaps in the biology and ecology of *Themisto gaudichaudii* are being explored with a focus on its genetic and trophic connectivity. The scenario in which *Themisto* may be responsible for outcompeting or controlling the standing stock of other key pelagic players such as Antarctic krill and salps further south may only hold true if it represents a single, panmictic population across its wide geographic and associated temperature range. Phylogeographic analyses confirm its spreading potential, showing several well-supported genetic lineages occurring in sympatry and across a wide geographical range. An in-depth morphological study of the different *Themisto* populations is presented. *Themisto*'s feeding ecology is documented by reviewing literature data, behavioural observations and feeding experiments, to verify its opportunistic predatory habits and a preferred predation on krill or salps. Finally, consequences of these possible zooplankton range shifts on higher trophic levels are discussed.

Filter-feeding isopods (*Antarcturus cf. spinacoronatus*) conquer a major new habitat on the underside of the Antarctic shelf ice

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The colonization of a new habitat affords an important advantage to the successful pioneer species because competitors, predators and parasites are likely to be out of step. Here, we report the first retrieval and molecular characterization of a cryo-benthic community of isopod crustaceans that live at depths of 80-150m on the underside of a floating shelf-ice tongue at the Drescher Inlet (Riiser-Larsen Ice Shelf), Eastern Weddell Sea. The specimens were retrieved with a sampler mounted on a remotely operated vehicle (ROV) when video transsects were carried out.

The molecular analysis of mitochondrial and nuclear genes of four specimens spanning the size range of individuals collected confirmed that (1) all belonged to a single species and that (2) this species has previously been identified in benthic communities in the Eastern Weddell Sea as *Antarcturus cf. spinacoronatus* (Baltzer et al 2000). The molecular phylogeny shows that the cryo-benthic *A. cf. spinacoronatus* are deeply nested in a family of isopods characterized by increasing complexity of morphological and behavioural adaptations to the acquisition of detrital and planktonic food particles. This demonstrates that the floating shelf-ice was likely colonized from the seafloor and not vice versa and that the filter-feeding life style of *A. cf. spinacoronatus* formed a predisposition playing a key role in the colonization of the new habitat.

Density estimates of *A. spinacoronatus* under the floating shelf-ice (25 adults and 190 juveniles per square meter) are significantly higher than on the seafloor, suggesting that the transition to the new habitat devoid of any macrofaunal competition or predation provides a major advantage to the species and thus may be a geographically more widespread phenomenon.

Our results are an indication that earlier reports of increased mid-water foraging of Weddell Seals (Liebsch et al. 2007) and the identification of filter-feeding isopods on seal-mounted still images from the underside of the shelf ice (Watanabe et al. 2006) are causally linked.

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Freezing abilities of Antarctic rotifers: clues for biogeography?

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Rotifers are microscopic multicellular animals that in Antarctica inhabit both inland waterbodies and thin water films covering soil and terrestrial moss. In such environment, rotifers (along with other micromeazoans like tardigrades and nematodes) should undergo multiple and rapid cycles of freezing and thawing. It is known that rotifers can survive freezing to -80ºC, often for several years, either inside the collected samples, or being dried in the experiment prior to freezing (Caprioli & Ricci, 2001; Newsham et al., 2006). There is an evidence of active rotifers surviving experimentally induced freezing in liquid nitrogen with the subsequent rapid thawing (Koehler & Johnson, 1969). However, it is not clear how Antarctic rotifers cope with relatively slow freezing under lower temperatures in the natural environment, neither the differences in freezing survival were compared between species from different regions.

In the 1st experiment we used 8 species from maritime Antarctica (MA, Argentine archipelago, Antarctic Peninsula, James Ross Island) and 12 species from continental Antarctica (CA, Victoria Land, Dronning Maud Land). Rotifers (4 replicates with 12 individuals each) were put alive and active into 1 ml of mineral water and slowly frozen under -15ºC (average time of freezing ATF=43 min), kept for 1 week under this temperature, and then gradually thawed in a thermostat under +8ºC. In the 2nd experiment, 2 species from MA and 2 from CA were frozen under -80ºC (ATF=13 min) and then thawed by short exposure to +37 ºC.

In both experiments, no species had 100% mortality, and some cohorts had 100% survival after freezing at -15ºC (*Philodina gregaria, Adineta editae*). Average survival rates were 8.3-72.9% for MA and 37.5-85% for CA, with no significant differences in survival between two experiments, but statistically significant difference between two biogeographical regions. We hypothesize that the differences in freezing survival in rotifers from MA and SA might be connected with the evolutionary history of adaptation to the Antarctic environment, and thus explain biogeography of Antarctic rotifers.

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Sponge communities of the Antarctic Peninsula: influence of environmental variables on species composition and richness

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Main objective of this study conducted at the tip of the Antarctic Peninsula was to investigate whether the species composition and species richness of Southern Ocean sponge communities in the area of the Antarctic Peninsula are significantly influenced by environmental variables. Two hundred and sixty-three sponge samples, and 81 species of 33 genera from all Porifera classes were were analyzed, the studied material was sampled during the expedition ANT-XXIX/3 by RV Polarstern.

Samples were collected in three large-scale areas in the vicinity of the Antarctic Peninsula: Bransfield Strait, Drake Passage and Weddell Sea. Following six environmental variables were measured from bottom water samples (except for sea-ice cover): depth (m), light transmission (%), oxygen (lmol.kg^{-1}), salinity, sea-ice cover (%) and temperature (°C). identified. Total numbers of sponge species per sample station ranged from 1 to 29. A detrended correspondence analysis and a backward-stepwise model selection were performed to check whether species composition and richness were significantly influenced by environmental variables.

The analyses revealed that none of the measured environmental variables significantly influenced species composition but that species richness was significantly influenced by (1) temperature and (2) the combination of temperature and depth. Results of this study are of crucial importance for development, performance and assessment of future protection strategies in case of ongoing climatic changes at the Antarctic Peninsula.

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The past is the key to the future: Ecology and Holocene evolution of freshwater diatom communities in Esmeralda lake, Antarctica.

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Topographically and climatically, the Antarctic Peninsula (AP) differs significantly from Continental Antarctica. The AP has experienced one of the highest temperature increases on Earth in the second half of the 20th century as a response to the ongoing global warming. The extreme sensitivity of the area to climate change represents an exceptional potential for AP palaeoclimatic records. Vega Island (63°50‘S/57°25‘W), located in the northern Weddell Sea just north of the larger James Ross Island, belongs to a biogeographic transition zone between the Maritime and Continental Antarctic regions. More than 80% of the island is covered with permanent ice, leaving only small parts ice-free.

To evaluate regional changes since the onset of the Holocene, we collected sediment cores from Esmeralda lake (the biggest lake) at Cape Lamb on the southern coast of Vega Island over the summer of 2014, and analysed them for diatom community structure. This lake was chosen because it formed as a result of the last deglaciation during the Pleistocene/Holocene transition, and we focus on the longest (176cm) core with excellently preserved organoclastic laminae that could record environmental changes of the past millennia. Only the top 40cm of the sediment core contained sufficient diatom remains for community characterization. In order to facilitate explaining variation in diatom communities, elemental composition, magnetic susceptibility, grain size, cation exchange capacity, and biological pigments were also determined. This combination of methods gives us a unique insight into the past environmental changes in the lake catchment as well as in the lake body.

A diverse diatom flora of at least 75 different taxa have been observed in the core. The flora is dominated by *Microcostatus australoshetlandicus* and several *Psammothidium*, *Nitzschia* and *Pinnularia* taxa. Aerophilic genera such as *Luticola*, *Humidophila* and *Muelleria* are present, but never dominate the flora. This observation might indicate the presence of a large, temporally stable waterbody. Several taxa could not be identified at present using the currently available literature and will be subject to further taxonomic analysis.

This poster presents a general overview of the project with the results of the diatom analysis together with a preliminary interpretation of their paleo-environment. The results will be completed with an age-depth model resulting in a high resolution, multi-proxy record that will contribute to a detailed picture of the past climatic and environmental changes in the north-eastern AP region through identifying periods of enhanced weathering and climatic fluctuations.

Diversity and community structures of prokaryotes in Antarctic fresh water lakes revealed by high-throughput sequencing

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The pioneering study of Franzmann (1996) showed Antarctic prokaryotes are remarkably diverse and represent most major evolutionary groups. Later studies by Bowman et al. (2000a, 2000b) using analysis of 16S rDNA clones revealed that the prokaryotic communities in Antarctic lakes consisted of both archaea and bacteria, including over 200 distinct phylotypes. We have also revealed diverged prokaryotic community in the Antarctic lake sediment (Kurosawa et al., 2010). These studies implied that the comprehensive prokaryotic communities in Antarctic lakes could not be revealed sufficiently by traditional Sanger sequencing, and high-throughput (next generation) method might be more appropriate. In this study, we have revealed the prokaryotic diversity and community structures of three Antarctic fresh water lakes by high-throughput sequencing.

The water samples including surface sediments were collected at Lake Yukidori-Ike, Lake Hotoke-Ike, and Lake Skallen-Oike located in the coastal region of Lützow–Holm Bay, East Antarctica in December 2012 through January 2013 during the 54th Japanese Antarctic Research Expedition. The water temperature and pH of the lakes were 5.4˚C-pH8.4, 5.5˚C-pH7.9, and 6.1-pH7.8, respectively. The environmental DNA was extracted and applied to PCR amplification of V3-V4 region of 16S rDNA using the prokaryote universal primer set (Pro341F-Pro806R). The PCR products were sequenced using Illumina MiSeq. The microbial diversity was analysed by using MacQIIME v.2.6.1 and related software.

The final number of sequences of three lakes after removing low quality ones were as follows: Yukidori-Ike, 65,815 reads, 812 OTUs; Hotoke-Ike, 64,466 reads, 651 OTUs; Skallen-Oike, 84,326 reads, 698 OTUs. The coverage was more than 0.98 in each lake. In all the lakes, Proteobacteria and Bacteroidetes were the most dominated phyla that were the most prevalent and present at all the locations and often constituted the top two dominant groups of bacteria also in Arctic and Antarctic lakes. In general, the class Betaproteobacteria is one of abundant group in the polar freshwater ecosystems, and Alphaproteobacteria is one in the saline ecosystems. However, this trend could not be seen in the three lakes. It is interesting that the ratio of Alphaproteobacteria and Gammaproteobacteria to Betaproteobacteria was 2.3 in Skallen-Oike that is marine relic not like other two lakes. Any effects of this history may reflect current bacterial community structure in this lake. Other comprehended features prokaryotic communities of three Antarctic fresh water lakes have been also successfully investigated. These results might help us to understand Antarctic biosphere more deeply.

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In search of marine Antarctic cyanobacteria

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Cyanobacteria are among the most ancient prokaryotic phyla present on the planet. They are thought to be responsible of two major geological changes and evolutionary process, the Great Oxygenation Event and the Endosymbiosis, which supported modern Life. In Polar freshwater and terrestrial ecosystems, cyanobacteria often constitute the major carbon fixers and the base of the food web. They are present in a wide range of habitat from hypersaline lakes to cryoconites. Nevertheless, their presence between the Polar front and Antarctic coast remains enigmatic. For a long time, it has been accepted that they were not present in Antarctic waters (Wilkins et al., 2012). However, they were found in low abundances in two publications, which were investigated the water column (Wilmotte et al., 2002; Wilkins et al., 2013). There is still a lack of information regarding their presence and role in Antarctic coastal waters.

In order to investigate the presence of cyanobacteria in Antarctic marine benthos, samples were collected by scuba diving during two expeditions (2015, 2016) in the Lion's channel, (Terre Adélie, Antarctica). Samples were directly frozen, dried or fixed with formaldehyde. DNA was extracted from one frozen sample and two dried samples. Then, 16S rRNA V3-V4 region was amplified using cyanobacteria-specific primers. Amplicons were sequenced using MiSeq Illumina technology. In parallel, fixed and frozen samples were scrutinized by microscopy.

We obtained 14 558 reads, which were related to Cyanobacteria. They clustered into 97 OTUs and belong to six orders (Chroococcales, Nostocales, Oscillatoriales, Pseudanabaenales, Stigonematales, Synechococcales) with a large dominance of Pseudanabaenales. Thirty-one of the cyanobacterial OTUs were 100% identical to sequences of strains isolated from freshwater environment, and air samples from both temperate and Polar regions.

Microscope observations revealed the presence of at least 3 cyanobacterial morphotypes including thin filaments, large Oscillatoriales, and a potential symbiotic or opportunist Nostocales.
Albeit the low abundance of reads attributed to cyanobacteria, it remains necessary to assess their ecological role in Antarctic coastal waters.

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Population connectivity of *Dendrilla antarctica* Topsent, 1905 (Porifera, Demospongiae) from west Antarctica shallow bottoms using Genome-wide SNPs obtained from RADseq techniques

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In the marine realm, ocean circulation, past geological events, and the dispersal capabilities of organisms largely influence the distribution of genetic diversity among populations. In the particular case of the Southern Ocean, glacial-interglacial cycles have had great impact on shallow- water benthic fauna, being the main factor driving their distribution and population structure [1]. Even though sponges are major components of the Antarctic benthic fauna, their genetic diversity and gene flow between populations is poorly known, as few reliable genetic markers are normally available. Recent population genetic studies have greatly benefitted from RADseq approaches that allow sampling of hundreds to thousands of loci across the genome of non-model taxa at relatively low cost. Here, we developed ddRADseq markers for 71 individuals from 7 populations to assess the genetic structure of the marine sponge *Dendrilla antarctica* along the Western Antarctic Peninsula and the South Shetland Islands. Our initial dataset consisted of 115 million raw reads, with 2,600 to 11 million reads per specimen. Our analysis of population assignment identified 4 major clusters without clear geographic structure, indicating high levels of admixture. Population differentiation based on Fst estimates was relatively low when compared to sponges from other latitudes [2]. Highest levels of population differentiation were observed between King George Island and Paradise Bay in the Antarctic Peninsula, separated by 335 km, but also among King George Island and O'Higgins base, which are only separated by 150 km. Pattern of genetic differentiation among populations could not be explained by a stepping stone model of isolation by distance, and in turn, oceanographic currents might be driving the divergence. Relatively high levels of gene flow among the populations of the Shetland Islands and the Western Peninsula are also found in other benthic invertebrates [see 3]. However, sponges usually show higher levels of genetic differentiation than observed here, possibly indicating enhanced dispersal capabilities of the larva of *Dendrilla antarctica*, among other possible reasons.

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Population structure and phylogenetic relationships of a new phyllodocid from the shallow-water Southern Ocean

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Despite the fact that shallow-water polychaetes have been widely studied in the Southern Ocean, still new species that are relatively common are often discovered. Here, we report the discovery of a new and abundant upper-infralitoral Antarctic phyllodocid of the genus *Eulalia*. Morphologically, this species mixes features of different genera, not matching completely with any phyllodocid genus previously described. Its most remarkable morphological trait is the lack of a nuchal organ, the absence of which is reported, to our knowledge, for the first time in the family Phyllodocidae. Although its generic status is not clear yet, we assigned the new phyllodocid to the genus *Eulalia* in concordance with our Maximum Likelihood and Bayesian Inference phylogenetic analyses, based on two nuclear (*18S* and *28S*) and two mitochondrial (*COI* and *16S*) markers. Using the *COI* and 16S of 91 and 83 individuals, respectively, from 5 populations across the South Shetland Islands and the Antarctic Peninsula, we investigated the genetic connectivity of this new species. The haplotype networks obtained suggest that all populations present panmixis, likely due to the presence of planktotrophic larvae allowing for the long-distance dispersal of the species. Another hypothesis explaining panmixis is passive transport of adults through the algae they inhabit and that are drifted away by marine currents. Future studies will be directed to clarify the phylogenetic status of the new *Eulalia*, to enlarge the sampling to test its dispersal abilities through larger distances, and to establish a robust phylogeographic hypothesis for the species in the light of past climatic events.

Diversification of Waldo (Bivalvia: Galeommatoidea) commensal epibionts of irregular echinoids from Antarctic and Subantarctic water determined from molecular analysis

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The marine benthic fauna of the Antarctic continental shelf is considered as the most isolated on the planet, due to extreme environmental conditions and surrounding barriers such as geographic distances, oceanic currents and deep waters. The current Antarctic biodiversity results from biogeographic and evolutionary processes driven by tectonic and climatic events since the Mesozoic. The study of diversification of taxa characterized by low dispersal capacities represents an important source of information to understand the biogeography of the Southern Ocean from an historic perspective. The genus *Waldo* (Bivalvia) is an epibiont "commensal" that lives on irregular echinoids. *Waldo* produce large and non planktotrophic eggs, which are incubated and the embryos are brooded within maternal gills up to an advanced development stage, being released as little juveniles. *Waldo* lives between the spines in the ambulacral areas of numerous irregular echinoids from Antarctic and Subantarctic areas, being the original description from Kerguelen Islands. Up to date, four species have been described in Antarctic and Subantarctic water. In this study, we compared Waldo specimens collected on *Abatus cavernosus* from Patagonia, *A. cordatus*, from Kerguelen Island, and *A. agassizii* from South Shetland islands. Moreover, Waldo were also collected on another brooding schizasteridae *Trypilus abatoides* that is found together with *A. agassizii* in King George Island. All specimens were photographed and sequenced for 28S and 16S genes. Phylogenetic trees were reconstructed with Maximum Likelihood algorithm. Our phylogenetic reconstruction showed 4 clades: the first clade encompassed all sequences from Magellan Straits, the second clade grouped all sequences from Kerguelen while the third and fourth clades clustered sequences from individuals of *Abatus* and *Trypilus* from Antarctic. This study confirmed the presence of previously described species of *Waldo* and probably new species inhabiting on sea urchins from Antarctic, suggesting, moreover, that the richness of *Waldo* species may be greater than actually known. Our results also support that geographic isolation has been the main driver of Waldo diversification rather than host specificity.

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A new genus of endolithic microalga from McMurdo Dry Valleys (East Antarctica)

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The McMurdo Dry Valleys constitute the largest ice-free region of Antarctica (c.a. 0.03% of the continent) and one of the world's most extreme deserts. Typically, cold desert soils from Dry Valleys have low levels of carbon and nitrogen and have small amounts of clay. Despite the low temperatures, dry and poor soils and katabatic winds, life exists. Milder microclimate conditions of the subsurface soil ease the growth of microbial life on such harsh environments. Soil acts as a refuge, protecting life from intense solar radiation and desiccation. In fact, some microbes are able to take advantage of those microenvironments, inhabiting the pore spaces of soil - frequently in porous rocks such as sandstones -, and constituting photosynthesis-based endolithic communities. In addition, to cyanobacteria and microalgae (primary producers), other organisms present in such consortia play important, complementary ecological functions that contribute to sustain life in these environments.

In this study, a green microalga was isolated from an endolithic sample collected in McMurdo Dry Valleys (Victoria Land, East Antarctica) during the K020 expedition, in January 2013. The non-axenic eukaryotic isolate (LEGE Z-009) was characterized by morphology- and molecular-based methods, namely cell morphometry and phylogenetic analyses of nuclear and chloroplast SSU rRNA genes. which indicated a significant phylogenetic distance, allowing to conclude that the microalgae represents a novel chlorophyte genus. Advanced morphologic features such as cup-shaped chloroplasts and polyphosphate granules were then detected by electron and confocal microscopy.
This new genus identification represents an important taxonomic novelty and it is in line with recent studies that point towards a much more extensive and interesting biodiversity in Antarctica than previously thought (Chown et al., 2015).

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Hidden diversity in the freshwater copepod genus Boeckella from Antarctic and Patagonian regions

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Species within the copepod crustacean genus Boeckella are found in several types of freshwater habitat across Australia, New Zealand, Argentina, Chile, the sub-Antarctic islands and Antarctica itself. The species Boeckella poppei is exceptional in being the only freshwater copepod that is currently reported from all of the main Antarctic biogeographic regions, including both the peri-Antarctic islands (maritime and sub-Antarctic) and continental Antarctica (East and West Antarctica), as well as from southern South America. In this study, we set out to (a) confirm B. poppei as a valid species through taxonomic, systematic and molecular approaches, (b) describe the evolutionary relationships among the related species that co-occur with B. poppei in Patagonia and the sub-Antarctic, (c) describe genetic diversity, population structuring and demographic patterns across Antarctic and Patagonian locations at both local/regional and intercontinental geographic scales. We used a combination of molecular sequencing techniques and classical taxonomic approaches based on morphological description to identify the different species within Boeckella across a geographic range including Patagonia, South Georgia, Signy Island (South Orkney Islands), South Shetlands Islands and west coast of the Antarctic Peninsula. Sampling was conducted in low altitude ponds and lakes using a zooplankton net (250□m mesh), where individuals were recognized by their bright red colour. Taxonomic identification was performed for each location based on the available literature (Bayly 1992a,b). Characteristics of the fifth leg were used as the diagnostic character for species recognition. After morphological identification, DNA extraction was carried out. Two fast-evolving mitochondrial loci (COI and 16S) and two nuclear loci (28S and ITS) were amplified using PCR in order to generate a more complete evolutionary history of these copepods. Preliminary data and analyses indicate that some of the haplogroups in Chilean Patagonia shown a very restricted geographic distribution, whereas others showed a wider range, covering most of the sampling regions. Antarctic haplogroups were highly divergent from Patagonia, with high genetic diversity and significant evidence of population expansion. This study is the first phylogeographic study in Antarctic freshwater ecosystems, testing key questions regarding the persistence or extinction of freshwater biota during the Last Glacial Maximum and previous glacial advances in the sub-Antarctic and Antarctic regions.

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Life abounds in the intertidal sub-Antarctic Auckland Islands

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The Auckland Islands, due south of New Zealand at 50°S, are positioned at the northern extent of the Antarctic Circumpolar Current[1,2]. It is predicted that as southern high-latitudes warm, the polar influence will contract causing the oceanic fronts and westerly wind belt to migrate southwards[3]. The biological assemblages of the sub-Antarctic islands provide sentinels for monitoring change associated with an evolving climate[4]. However, as is characteristic of many of the sub-Antarctic islands, scientific understanding of biodiversity on the Auckland Islands, particularly in the marine environment, is scarce.

In order to monitor ecosystem response to changing oceanic conditions, we have begun to establish a baseline understanding of the composition of key assemblages. In February 2016 we conducted what is believed to be the first quantitative survey of intertidal macroalgae and macrofauna at the Auckland Islands[5]. Assisted by a group of young environmental leaders, we surveyed the rocky intertidal at wave sheltered and exposed sites on the mid-eastern coastline of Auckland Island. Specimens of fleshy and coralline macroalgae were also collected, pressed and preserved for identification in New Zealand.

The macrofaunal and macroalgal assemblages of sheltered, inner fiord sites contrasted with an outer coast, wave exposed site. It was particularly challenging to identify taxa to genera or species level, due to a limited amount of taxonomic work in the region. For example, the majority of the 8 distinct specimens of coralline algae collected are thought to be undescribed species, and for some of these, undescribed genera. Similarly, multiple macroalgae specimens found are undescribed. In order to understand the diversity and ecology of these habitats we must work to build taxonomic knowledge of the assemblages. This will enable a comparison of assemblages in the Auckland Islands with those of other sub-Antarctic islands. This work comprises one of the first steps towards establishing a long term ecological research and monitoring programme at the Auckland Islands.

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Benthic hydroids (Cnidaria: Hydrozoa) off Adélie Land (Antarctica)

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Hydrozoans are one of the main and more characteristic zoological groups of Antarctic benthic communities, yet there are Antarctic areas where the hydrozoan fauna is either completely unknown or, as in Adélie Land (East Antarctica), scarcely known. Hitherto, only one study on hydrozoans inhabiting marine bottoms off Adélie Land has been published by Naumov & Stepanjants in 1972. The present study contributes to increase the knowledge about the benthic hydroid fauna off Adélie Land by studying material collected between 2007–2013, during sampling surveys associated to the CEAMARC and REVOLTA projects as well as by carrying out a comprehensive revision of previous studies in the area. A total of 33 species of benthic hydroids, belonging to 13 families and 21 genera, was found in the new material. Thirty-two species, including *Schizotricha auroraustralis* sp. nov., were identified to specific level; 16 of them represent new records. Thus, the number of benthic hydroids known off Adélie Land is raised to 45. In the studied collection, Leptothecata is the dominant order with 27 species, while Anthoathecata is only represented by six species. Symplectoscyphidae (21%) is the most speciose family, with 7 species (21%), whereas Kirchenpaueriidae has the highest biomass because of the presence of *Oswaldella stepanjantsae*, the species with the highest abundance and biomass. Most of the studied species (94%) are restricted to Antarctic and/or sub-Antarctic waters, twenty of them (63%) being endemic to the Antarctic region. Only two species are also found outside Antarctic and sub-Antarctic waters. The fauna is dominated by eurybathic species (41%), followed by those restricted to the continental shelf (34%).

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Bathymetric distribution of Antarctic benthic hydroids and the influence of this extreme environment: how do they respond?

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Benthic hydroids are an important component of the Antarctic benthic ecosystem. This system is characterized by extreme environmental conditions that undoubtedly affect the distribution of the organisms. In some cases, these conditions are related to depth (e.g. Anchorice or Iceberg Scouring). The Antarctic depth profile has special characteristics that reflect glacial erosion as well as depression of the crust by isostatic loading during ice sheet expansion. Indeed, Antarctic continental shelf is deeper than others elsewhere in the world. The shelf-break can exceed 1000 m in depth while the world average is 100-200 m. This fact, along with the dynamic ice formation, affects *a priori* the distribution of Antarctic benthic hydroids. Stepanjants, in 1979, first studied the bathymetric distribution of Antarctic benthic hydroids, and Peña Cantero, in 2004, summarized all available bathymetric information for Antarctic benthic hydroids, and established a series of bathymetric groups according to ecological features.

The aim of this study is to review and complete knowledge on the bathymetric distribution of Antarctic benthic hydroids with recent data in order to define hydrozoan bathymetric assemblages and depth indicator species. For this, we have compiled all valid records for the known species of benthic hydroids from the Antarctic (including Scotia Arc) and included them in a depth range division. Using similarity matrices (Sørensen coefficient), a hierarchical cluster with SIMPROF test was performed. With this, we assessed similarity between established bathymetric ranges. Our results suggest the bathymetric division of the Antarctic benthic hydroids into three main groups. The first one, which corresponds to the Continental Shelf, expands between 0 to 700 m, and is clearly characterized by Eudendriidae and Campanulinidae. The second one, which is associated with the continental slope, extends between 700 and 1500 m and it is characterized by a few exclusive species, like *Halisiphonia prolifica*, a rare species described from East Antarctica by Peña Cantero in 2014. Finally, the third group, here named Abyss, extends beyond 2000 m, depths where few species of benthic hydroids have been described [(e.g. *Branchiocerianthus norvegicus* (3987 m)]. Additionally, our results indicate a further division of the Continental Shelf group. The results show distinct boundaries between divisions, which could be linked to environmental factors, some of them likely related to the influence of ice.

Complex biological research conducted in Eastern Antarctica (Thala Hills oasis, Enderby Land)

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Targeted investigations of biodiversity in Antarctica were started by Belarusian specialists in 2007 after joining of the Republic of Belarus to the Antarctic Treaty. Collection of materials and observations are carried out mainly in the location of the field base "Gora Vechernyaya", the eastern part of the Molodezhniy region (Enderby Land, Tall hills) and in the area of 7 Russian stations.

Currently, investigations are carried out in the following fields:

1. Microbiological. Created collection of pure cultures of microorganisms obtained by seeding of different samples on the substrate surface. More than 300 isolates of pure cultures of microorganisms were allocated. Identification and searching for microorganisms, which may be a potential source of biologically active substances and enzymes with biotechnological importance are being carried out now. Works on definition of biomass and some morphometric parameters of bacterioplankton for freshwater lakes is implemented.

2. Botanical. Selection and identification of Micromycetes growing on natural and artificial substrates and resistant to low temperatures are being carried out in different regions.
Investigation of the algae taxonomic diversity of lake and terrestrial ecosystems allowed us to register about 150 species of algae belonging to 8 types, 15 classes, 35 orders, 51 families and 72 genera. In the process of analysis of herbarium specimens from Antarctica we identified 43 species of lichens from 28 genera and 16 families.

3. Zoological. Zoological investigations cover almost all groups of vertebrates and invertebrates inhabiting marine, freshwater and terrestrial ecosystems.
Rrepresentatives of zooplankton in freshwater ecosystems were studied. Among those the rotifers is undoubtedly dominant group. 7 species of rotifers: 5 of them belong to *Monogononta* and 2 - to *Bdelloidea* were found in aquatic habitats. Among the other members of the zooplankton we have noted *Daphniidae*, nematodes and tardigrades. Marine zoobenthos in the subtidal zone are represented by almost all types and groups of macroinvertebrates.

4. Biochemical. Allocation of melanin from foliated and bushy lichen of East Antarctica is carrying out, as well as a comparative study of their elemental composition. Identification of calorie variety of different representatives of marine fauna is currently in progress.

5. Monitoring. An important element of the Antarctic environment protection is the assessment of environmental impact of carrying out or planned activities. To assess the state of environment in the area of Belarusian Antarctic expedition we carried out samples of water from freshwater ponds and seasonal streams, snow, sediments, from coastal and freshwater loose substrate.

The importance of gastropod-macroalgal interactions in benthic communities along the western Antarctic Peninsula

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Coastal communities along the western Antarctic Peninsula (WAP) are dominated by dense forests of large brown macroalgae (seaweeds) which support remarkably high densities of small crustaceans known as amphipods (Amsler et al. 2014). The macroalgae are chemically defended from predation by amphipods and by fish. Amphipods end up gaining a refuge in chemically defended algae from fish which are their major predators (Zamzow et al. 2010). In turn, the amphipods benefit the macroalgae by keeping them free of small competing epiphytic algae (Amsler et al. 2014). Because macroalgae and amphipods are the two most abundant groups of organisms in the community, this has been described as a "community wide mutualism" (Amsler et al. 2014). However, amphipods are not the only important small grazers in these communities. Macroalgae can support an abundance of gastropods such as snails in addition to the existing amphipod assemblages studied to date (Amsler et al. 2015). Additionally, qualitative observations suggest that gastropods are more abundant than amphipods on other algae, such as large blade forming macroalgae, that have not yet been included in previous studies (M Amsler and C Amsler 2015, pers. comm.). To date, only one study has been done to quantitatively determine gastropod abundance and diversity in the WAP and this study did not include large blade forming macroalgae nor did it include a big enough sample size of algal collections to determine accurate gastropod community assemblages (Amsler et al. 2015). Due to qualitative observations suggesting that gastropods are relatively more abundant than amphipods on large blade forming alga such as *Himantothallus grandifolius* the following study will determine if gastropods have a host specific association with macroalgae. Scuba divers will collect a total of 8 macroalgal species (4 ecologically important large blades, 4 other) from multiple sites and depths off ice-free islands near Palmer Station, Antartica. All epibionts, including gastropods, will be removed from the algae by a combination of thallus shaking, repeated seawater rinses, and hand picking. The gastropods will be identified to the lowest possible taxon and enumerated. Using ANOVA, gastropod abundance, number of species and species diversity will be compared across agal taxa.

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Distributions of larval and juvenile/adult stages of the Antarctic myctophid fish, Electrona antarctica, off Wilkes Land in East Antarctica

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Mesopelagic fish represent a vast amount of biomass in the Southern Ocean ecosystem, and lanternfish (Myctophidae) are a dominant family of these fish. Of the 35 myctophid species recorded in the Southern Ocean, *Electrona antarctica* has the largest biomass and is broadly distributed in the Southern Ocean, across a wide range of latitudes from the Antarctic Polar Front (APF) to the high Antarctic zone This study investigated the larval and juvenile/adult spatial distributions of the Antarctic myctophid *E. antarctica*. Fish were sampled in January 2011 and January 2012 on a transect along 140°E and in January 2013 along 110°E using two different opening/closing net systems. In total, 1,075 *E. antarctica* were collected: 948 larvae, 121 juveniles/adults, and 6 in the transformation stage. Most larvae were collected at 5–200m depth, with diel vertical migration (DVM) not apparent. Larvae were mainly distributed in the Modified Circumpolar Deep Water (−1.5°C to 2.0°C). By contrast, an analysis of the echogram at 38 kHz and discrete depth samples implied that juveniles/adults undertook DVM except in the continental slope area (65.5°S). As the distribution of krill is limited to the cold water mass (<−1.5°C) along the continental slope, *E. antarctica* and krill populations are spatially separated off Wilkes Land during summer. According to the previously estimated larval period of 30–47 days, *E. antarctica* may spawn in late November to December in the marginal ice zone or near the sea ice edge. This study implies that the environment related to sea ice provides a nursery ground for early stage larvae of *E. antarctica*, suggesting that sea ice changes could impact on the population dynamics of adult fish, which is important prey for higher trophic animals in the Southern Ocean, through annual fluctuation of the early survival.

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Break away from Antarctica: quaternary diversification of Harpagifer genus in the Southern Ocean

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The evolution of benthic marine fauna in the Southern Ocean (SO) has been modelled by climatic, oceanographic and geological factors. The geographic isolation of the Antarctic continent and the subsequent formation and intensification of the Circumpolar Antarctic Current (ACC) in the late Miocene are determinant factors for understanding the evolutionary relations between Antarctic and sub-Antarctic fauna Recent studies indicate that the level of connectivity maintained by populations of marine organisms from shallow habitats, after the separation of the Antarctic and South American continents, could be related to reproductive strategies and linked to the intensification of the ACC. In this context, the evolution of cold-adapted notothenioid fish is an interesting model of diversification processes in SO. While most of the teleost groups were eradicated from Antarctica, this suborder dominates in diversity and abundance. The adaptive radiation of this group has been a case study to understand the evolution of Antarctic fauna and the biography of the SO marine fauna. However, most of these studies have been biased toward the relationships within the Antarctic clade rather than in the association among closely related phylogenetic taxa found inside and outside the Polar Front. We used phylogeographic and phylogenetic approaches to evaluate the impact of Quaternary glacial cycles on the biogeography of Harpagifer lineages. This genus, with 12 nominal species, has representatives in South America, Antarctic Peninsula and sub-Antarctic islands. Phylogenetic reconstructions within the genus were performed using mitochondrial markers (D-loop and COI) and nuclear markers (Rhodopsin and ITS). These reconstructions support the Antarctic origin of Harpagifer recognizing two lineages ($\Phi st = 0.7633$; $p < 0.001$). Results allowed to recover the monophyly of Harpagiferinae and the reciprocal monophyly of the South American clade and the Antarctic-sub-Antarctic clade. The divergence between these two clades occurred 1.66 Ma (95% HPD 0.82-2.62 Ma), a more recent separation than expected under vicariance hypothesis, and consistent with climatic and oceanographic variations that occurred during the cold periods of the Quaternary. Finally, the relationships within the Antarctic-sub-Antarctic clade were not entirely resolved using the previous genetic markers, suggesting that the diversification of Harpagifer from Antarctic Peninsula to sub-Antarctic islands occurred 0,59 Ma (95 % HPD 0,25–0,95 Ma). In this context, we are exploring a GBS approach to estimate contemporary genetic structure and population connectivity within the sub-Antarctic area.

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"Black gold" exploration around Falkland Islands represents a "goldmine" of opportunity for benthic research: Pilot study of polychaete worms

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Benthic environmental impact assessments (BEIS) and monitoring programmes accompanying hydrocarbons industry activities result in large collections of benthic organisms. Such collections offer great potential for systematics and biogeography research, but sadly these opportunities are only rarely realized, as exemplified by the experience from the West African margin. Recently, hydrocarbons companies began exploration activities in offshore waters of Falkland Islands. A large collection of around 25 000 polychaete specimens, representing at least 220 morphological species was processed at the Natural History Museum London as part of a BEIS. Additional funding enabled us to enter these specimens into the museum's collection, thus making them available to the wider research community. An online taxonomic guide (http://falklands.myspecies.info) was created to provide a single taxonomic source to standardize identification across different contractors, which should lead to generation of comparable datasets in the future. This comprehensive polychaete collection has already led to preparation of peer-reviewed publications ranging from taxonomy (large number of species are new to science and some are currently under formal description) to ecology (500m and 1000m depth horizons support very different polychaete assemblages) and biogeography (offshore waters of Falkland Islands harbour polychaete fauna more similar to Southern Ocean and other deep oceans rather than Magellanic province as is case for shallow water and terrestrial fauna). This pilot project on polychaetes has successfully demonstrated the value of such collections for research as well as supporting BEIS. The next stage is to gain further funding for other taxonomic groups. The objective is to make the waters of Falkland Islands one of the best understood marine provinces.

Inordinate fondness of deep-sea Polynoidae – discoveries from depths of Southern and Pacific Oceans

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Polynoidae (Annelida: Polychaeta) are marine worms known for bearing often ornamental scales. They are highly diverse with around 1000 species recognised world-wide, although most of these records are from shallow waters. Deep-sea macrofaunal benthos has traditionally been sampled with coring devices, in which highly mobile epibenthic organisms like Polynoidae were rarely captured. Recent deployments of an epibenthic sledge in Southern Ocean (ANDEEP and BIOPEARL cruises to Weddell, Scotia and Amundsen Seas) and abyssal Pacific Ocean (JPIO cruise to Clarion-Clipperton Fracture Zone (CCFZ)) offered new insights into the contribution of polynoid worms to diversity of deep-sea benthos. Combined cruise efforts resulted in collection of around 100 polynoid species (around 40 from the deep Southern Ocean and around 60 from the investigated area of abyssal Pacific). There are no known records of Polynoidae from CCFZ (Pacific Ocean), an area currently undergoing exploration due to concentration of polymetallic nodules. In the Southern Ocean, there are currently about 65 known polynoid species, mostly from the shelf depths and concentrated in subfamily Polynoinae. However most of polynoid diversity presented here lies in the exclusively deep-sea subfamilies Macellicephalinae, Macellicephaloidinae, Bathyedithinae and Polaruschakovinae with a majority of species new to science. The only systematic review of these deep-sea groups dates to mid-1970s, when a number of monotypic genera were established. Most species were represented by few type specimens or holotype only, which mirrors the rarity of material at the time. The polynoid collection presented here increases diversity of these deep-sea groups by 400% and at least 30 new species are currently under description. Combined DNA data (CO1, 16S and 18S genes) provides an insight into the phylogeny of these poorly understood deep-sea groups. Molecular data suggests that the subfamilies Macellicephalinae and Bathyedithinae are paraphyletic, but Polaruschakovinae is monophyletic. Many genera, which are no longer monotypic following discovery of material presented here, appear to be justified forming distinct and monophyletic groups. Given our findings of high diversity of deep-sea Polynoidae, it is important that other studies widen the types of sampling gear employed to investigate the deep-sea biodiversity comprehensively.

Evaluation of intra and interspecific divergence in penguins

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The penguins' species are widely distributed in the southern hemisphere. About 18 species and several sub-species have been described, however, there are taxonomic debate and doubt about the extant number of species/sub-species. For example, the *Eudyptes* genera presents the greatest debate. Although around seven species have been recognized for *Eudyptes* genera (Garcia-Borboroglu & Boersma 2013), some authors debate if the sub-species of *Eudyptes chrysolophus* should be considered as different species or not. Banks et al. (2006) using mtDNA markers elevate all three subspecies described based on morphology from to species level, morphology from *E. chrysolophus*, to species level. Nevertheless, Baker et al. (2009) using the sequences of COI suggest to maintain the *E. chrysolophus* lineages as subspecies. In the case of *Pygoscelis papua*, two subspecies has been described based on morphology: *P. papua papua* from sub-Antarctic province and *P. papua ellsworthi* from Antarctic region.

However, a recent genetic study showed divergent clades for each Sub-Antarctic Island studied and the Antarctica (Vianna et al. 2017). We amplified the mitochondrial regions cytochrome c oxidase I (COI) and cytochrome b (Cyt b) from about 300 samples of penguins from different localities, covering different areas within the distribution of each species. The phylogeny of the group maintained the topology described by other authors using different molecular markers, however, in some species we found a high intraspecific divergence, as in *P. papua* between Antarctic and sub-Antarctic islands, which is not concordant with the subspecies previously defined by morphology. When comparing between species, we found that the divergence between populations of *P. papua* is deep and it is compared to the recent divergence time between *Spheniscus* species. In contrast, between Humboldt and Galapagos penguins there is no divergence, in fact they presented the same sequence for COI. In the case of chinstrap penguin, no difference were observed between Antarctic populations and the sub-Antarctic island Bouvet. In the case of *S. humboldti* and *S. magellanicus* no divergent lineages were observed along its range of distribution.

This work provides relevant information about the existence of cryptic species within the Spheniscidae family. Moreover, the sub-species description based on morphological trait for other penguins' species is not completely supported by molecular data. We suggest that more detailed study using other markers in the genome should be carried out in order to completely clarify the taxonomic of Spheniscidae.

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Genetic identity of the two physonect siphonophores – an enigmatic taxon Mica micula and Pyrostephos vanhoeffeni from the Southern Ocean waters

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The greatest challenge in the study of Siphonophora lies in the identification of all parts of the fragile colonies which usually separated during net sampling. Species identity within the group is typically based on the morphology of at least one swimming bell. But a link between a larva, or a eudoxid stage and its polygastric stage has only so far been shown using molecular markers. *Pyrostephos vanhoeffeni* was first identified by Moser (1925). Although not abundant, is widely distributed throughout the Southern Ocean.

Colonies comprising a single small nectophore (2 mm in length) and stem was collected by Margulis (1982) from Antarctic waters and introduced as *Mica micula*. The colonies collected so far indicate that this species is limited only to the Southern Ocean region. *M. micula* colonies showed some characteristics associated with the family Pyrostephidae (Mapstone, 2009), but the problem is to ascertain the identity of this siphonula. Pagès and Gili (1989) collected more than one physonects, but of these only *Bargmannia elongata* bears a certain resemblance to the siphonula. Therefore, they concluded that *Mica micula* is not a valid species but represents a siphonula/post-larval stages of a physonect species, perhaps *B. elongata.*

Recently Grossman et al. (2013) published a redescription of *Mica micula*, with notes on its distribution and identity. However, no *Bargmannia* nectophores or bracts were found in the same area.

In recent years the importance of using molecular studies to resolve taxonomically challenging problems has grown significantly. Therefore, the aim of the present study was to use the molecular methods to check genetic affinity of *M. micula* to *P. vanhoeffeni*. In the present study 34 nectophores of *P. vanhoeffeni* and 4 colonies of *M. micula* collected from three areas in the Southern Ocean were analysed for the 16S rRNA gene. The results allowed to distinguish five haplotypes. Three of them were found exclusively in Admiralty Bay and were shared by individuals of both studied taxa, confirming the assumption that *M. micula* is the post-larval stage of *P. vanhoeffeni*. The two additional haplotypes were found in open ocean localities and in Admiralty Bay. What is more, the barcoding gap observed between these two haplotypes and the haplotypes from Admiralty Bay suggests the existence of two cryptic species within the species *P. vanhoeffeni*.

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Non-Antarctic notothenioids: phylogenetic history and contemporary phylogeographic implications in the face of environmental changes

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Most attention is presently paid to Antarctic notothenioids for their purportedly limited physiological tolerance to climate change and increased temperatures. However, three non-Antarctic Notothenioidei families, Bovichtidae, Pseudaphritidae and Eleginopsidae, diverged early from the main notothenioid lineage and have never established populations on the Antarctic shelf. While it is expected that early-diverged notothenioid species may appear to be more robust to effects of climate change than high-Antarctic congeners, it is difficult to predict how they will cope with future conditions. Possible strategies may affect distribution, (i.e. altering the geographic range), behavior, phenology and ultimately, genetic variability of these species. It is possible that the high degree of endemism and the dependence of life history stages on local environmental specificities might enhance vulnerability in the non-Antarctic species. Various factors involved in the species response to environmental changes including dispersal capacity, fitness (growth rate, reproductive output, age–size-ratios at first reproduction), ecotype, and genetic variability (gene pool modification rate) are crucial to understanding population structure and connectivity, and hence vulnerability to local extinctions. The integration of these factors with life history traits and molecular genetic footprints left by past and present demographic events (e.g. population size changes or migration) provide key tools to disentangle the biotic and abiotic factors that drive differentiation of populations. These tools can be used to model and project future population viability. Through a review of major life history traits that are characteristic of the three non-Antarctic early-diverged notothenioid taxa and by discussing what genetic resources and population differentiation information is available (Papetti et al. 2016), we emphasise the population fitness and dynamics of these taxa to strengthen resource management and conservation through an integrative approach. Finally, we suggest an integrated approach within a phylogeographic framework that could build on existing knowledge, and provide information on key components of the species adaptation potential.

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In (white) cold blood: speciation, introgression and hybridization in Antarctic fish

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Correct species identification is essential to assess biodiversity and species richness in ecosystems threatened by environmental changes. This is particularly important when secondary contacts between phylogenetically closely related species occur and hybridization is a potential outcome. Several recent examples of cryptic speciation and hybridization posit that we have just begun to appreciate the complexity of notothenioid species. In this study, we investigate these issues in the genus *Chionodraco* (Channichthyidae, Notothenioidei, Perciformes) in the Weddell Sea, the Ross Sea and the Antarctic Peninsula. The three species are the only representatives of the genus *Chionodraco* and have a different distribution on the Antarctic continental shelf. Two species are sympatric (*C. hamatus* and *C. myersi*, primarily with a circum-High-Antarctic distribution) and one is largely allopatric (*C. rastrospinosus*, off the Antarctic Peninsula and along the southern Scotia Arc). Our goal is to draw an overall picture of the genus *Chionodraco* in terms of distribution and genetic structure providing tools and protocols to assist the identification of species and hybrids and to be possibly applied to other Antarctic notothenioid fishes. The huge ambiguity in the morphological identification of both larvae and adults of the three species and the documented occurrence of hybrids between *Chionodraco* species pairs require that multidisciplinary tools are developed for a straightforward species identification. We have therefore considered several life history traits for the three *Chionodraco* species, such as geographic distribution and otolith morphology, and related them to genetic structure and phylogeography patterns. These studies are relevant to better describe the Antarctic marine biodiversity, a prerequisite to properly establish management and conservation measures.

An integrative approach to construct terrestrial ciliate community in Antarctica

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Extreme environmental constraints in Antarctica allow only microfauna such as bacteria, protists, and nematodes to survive as dominant organisms. Terrestrial protozoa in maritime Antarctica are important primary producers due to their high biomass and respiration. Of them, ciliates are considered to be an important group in food web and nutrient cycling in Antarctic soil ecosystems (Bamforth et al., 2005; Petz, 1997).

The ciliate, microscopic eukaryotes are unicellular organism with two kinds of nuclei - diploid micronuclei and selectively polyplopid macronuclei within each cell. They contain 10,000 species in 11 classes and live in a variety of habitats such as soil, freshwater, seawater worldwide (Lynn, 2008; Russell et al., 2016; Small and Lynn 1985). However, few studies of ciliates in Antarctic terrestrial habitats have been performed due to difficulty of the culture and access to Antarctica. Up to date, only 70 ciliate species have been reported from Antarctic soils (Foissner, 1998; Sudzuki, 1979). To build an integrative information on ciliate diversity and community structure in Antarctic soil, we have accumulated morphological, molecular, and ecological data of ciliates from over 200 spots on King George Island and Terranova bay, Antarctica. So far, we published one new genus (*Pseudonotohymena antarctica*), three new species (*Anteholostica rectangula*, *Metaurostylopsis antarctica*, *Urosomoida sejongensis*) and redescription of three species (*Neokeronopsis asiatica*, *Paraholosticha musicola*, and *Keronopsis helluo*) and discovered seven species (*Gonostomum affine*, *Gonostomum* cf. *strenuum*, *Halteria grandinella*, *Hemiurosomoida longa*, *Lamtostyloides edaphoni*, *Oxytricha* cf. *balladyna*, *Parasterkiella thompsoni*).

By expanding our research data to the evaluation of environmental impacts on biodiversity and community structures, we plan to create Antarctic ciliate database for meta-barcoding, and will be attempted; 1) Discovery of presence of non-culturable ciliates, 2) Determination of the environmental factors influencing to the population of ciliates based on the relationship between spatial patterns and environmental data, and 3) Monitoring of ciliate communities by annually analyzing the samples and environmental data.

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Advances in Antarctic fish cytogenetics: from embryonated eggs to karyotype characterization of the Antarctic silverfish Pleuragramma antarctica (Boulenger 1902)

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As the morphological manifestation of a species genome at cell level, chromosomes provide characters traditionally used in inter- and intra-specific comparative analyses for taxonomic purposes (cytotaxonomy).

Since the early 80s, cytogenetic approaches have been applied to the study of Antarctic fish suborder Notothenioidei. This led to valuable information used to decode specific *in situ* genome architectural features and changes in the frame of Antarctic species diversification and evolution. In almost three decades, the bulk of cytogenetic data has expanded, and now covers half of the known species inhabiting the high Antarctic waters (reviewed in Ghigliotti et al. 2015).

However, the cytogenetics of one of the most ecologically important species, the Antarctic silverfish *Pleuragramma antarctica* (Boulenger 1902), abundant and widely distributed along Antarctic coasts, remained poorly studied. This is mainly due to the difficulties of keeping adult specimens alive and in good condition, as required for cytogenetic procedures. Prior to present report, only five adult specimens were studied from the Weddell Sea (Ozouf-Costaz et al. 1991), and only basic information was available on the chromosomal number (2n= 48) and karyotype formula (8m+22sm+8a). The occurrence of a nursery area in Terra Nova Bay (Western Ross Sea), where embryos of Antarctic silverfish develop in the platelet ice layer under the sea ice surface (Vacchi et al. 2012), provided a great opportunity for developing alternative protocols using embryos as source of chromosomes.

To optimize the protocol, various ontogenetic stages of Antarctic silverfish were cultured in the aquaria at Mario Zucchelli Station and tested. Embryos at their latest developmental stage were found to be most suitable for obtaining high number of mitotic cells and metaphase chromosomes. The quality of the chromosomal preparations enabled in depth cytogenetic investigations including karyotype characterization, and *in situ* mapping of target genes (antifreeze protein genes, ribosomal genes) and DNA repeated sequences (telomeric sequences, LINEs). Furthermore, part of the cytogenetic material, in form of frozen fixed cell suspensions or slide chromosome preparations, are deposited with the new polar fish repository based at the Institute of Marine Sciences (ISMAR) - CNR (Genoa, Italy). This repository, launched in the frame of the PNRA (POLICY project) with participation from international collaborations, includes both Arctic and Antarctic fish cytogenetic samples, providing a new biological resource for the broad polar fish community.

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Stable Isotopic Analyses on Cephalopod Beaks: an approach to study ontogenic changes along cephalopods life

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Cephalopod beaks are hard chitinous structures resistant to digestion and that differ between species, being commonly used to identify cephalopod species from predators' stomach contents. These structures grow along the cephalopod life without replacement, which turns into a powerful tool to study the individual life. Stable isotopic analysis (SIA) of $\delta^{13}C$ and $\delta^{15}N$ is a technique that allows to study marine organisms' habitat and trophic ecology, respectively. The main objective of this study is to validate and establish SIA, applied to different beak parts, as a routine method to study habitat and trophic ecology along the individuals' life. As model species, we used the endemic Southern Ocean squid *Kondakovia longimana,* one of the main cephalopod prey of Antarctic top predators. Several upper (UB) and lower beaks (LB) were sectioned in tip of the rostrum and a section along the hood and crest (UB) and tip of the rostrum, a section along the lateral wall and the wing (LB). Sections were posteriorly sectioned into four equal subsections and all the pieces analysed for $\delta^{13}C$ and $\delta^{15}N$. Values of $\delta^{13}C$ (-26.3 to -20.6‰) remain stable along the beak. In opposite, $\delta^{15}N$ values (3.2 to 8.2‰) show an increase along the beak, with tip of the rostrum presenting the lowest values and the farthest subsection, relatively to the tip of the rostrum, and wing the highest. Our results show that the tip of the rostrum gives information about the individual earliest life-stages and the farthest regions about the latest individual life-stage.

This study confirms SIA as a reliable technique to study habitat and trophic ecology of cephalopods. To study ontogenic changes along the cephalopod life we should use the tip of the rostrum and the section along the hood of the UB. However, to study changes between the young and adults of the same individual, we can only use the tip of the rostrum and the end of the hood in the upper beaks or the tip of the rostrum and the wing in the lower beaks.

Phylogeography and taxonomy of the Snow Petrel (*Pagodroma nivea s.l.*)

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Having undergone historic climatic changes, the Snow Petrel (*Pagodroma nivea s.l.*), a circumpolar Antarctic and Subantarctic seabird, is a well suited model organism to predict future scenarios resulting from future global changes. Nowadays, the taxonomic status of the Snow Petrel remains the subject of considerable controversy (Shirihai, 2007; del Hoyo & Collar, 2014), the current consensus treating it as two distinct subspecies (del Hoyo & Collar, 2014), the lesser and the greater Snow Petrel (respectively P. nivea nivea and P. n. major). Few "pure" parapatic populations of both "subspecies" are known whereas most colonies consist of hybrid morphotypes. The evolutionary history of the species is still uncertain and the existence of the two "subspecies" could be the result of different glacial refugia with the establishment of post glacial hybridization zones (Fraser et al., 2012). As one of the target species of the RECTO project (funded by BELSPO) we will assess the genetic diversity of the Snow Petrel to attempt to reconstruct its evolutionary history and phylogeography in order to link population histories and refugia to past climate changes. Biometrical variation (bill, tarsus, wing and tail length) will be measured and used to assess morphological variance among populations. For this purpose, we will obtain specimens from various locations of the Antarctic and the Scotia Arc, to be collected during field campaigns and from museum specimens. Levels of morphological variation will be compared to molecular diversity of highly variable mitochondrial regions (control region) and whole mitogenomes. The latter data will also be used to detect potential cryptic species. while the development of large numbers of single-nucleotide polymorphism (SNP's) from RAD sequencing techniques or microsatellites will provide suitable tools to untangle the complex genetic structures of these birds. Coalescent analysis of SNP's (or microsats) will reveal population expansion, bottlenecks and connectivity and Bayesian analysis will also reconstruct the phylogeography of the two "subspecies" present today.
Current global changes are quickly affecting our planet, and parts of Antarctica are among the fastest warming regions (Turner et al., 2009; Bromwich et al., 2013) while the Southern Ocean is also further endangered by ocean acidification. Future distributions of the Snow Petrel and its prey will be predicted under different scenarios by integrating spatial and trait distribution models based on physiological limits and ecological niches with state-of-the art models for ocean dynamics (Luyten, 2011), sea ice (Vancoppenolle et al., 2009) and Lagrangian particle models (Dulière et al., 2013).

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Diversity, ecology and specificity in Antarctic lichens

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The extreme climate conditions of the Antarctic continent provide an environment where only perfectly adapted organisms can survive. The terrestrial vegetation communities of the ice-free areas of this continent (ca. 2%) are mainly comprised of mosses, fungi and lichens.

However, the mechanisms that connect climate and life's diversity in Antarctica are still poorly understood owing to limited taxon and climate data sampling in many areas of the continent. The current study investigates the role of climatic factors driving lichen diversity, distribution and species specificity in Antarctica using saxicolous lecideoid lichens as a model system. These lichens are well adapted to the cold and severe habitats and abundant throughout the whole Antarctic continent.

Lecideoid lichens, characterised by a whitish to grey thallus and lecideine apothecia with eight hyaline ascospores, form a functional group of crustose lichens, placed in the genera *Carbonea, Lecanora*, *Lecidea, Lecidella* and *Rhizoplaca.* The mycobiontic partner of the lichenous mutualism depends on the availability of an appropriate photobiont, providing necessary carbohydrates. The various mycobiont species show variable degrees of specialisation on photobiont associations. But also the photobionts show an evidence for the influence of climatic factors on the distribution and genetic diversity of the *Trebouxia* species. Most *Trebouxia* species are cosmopolitan, but have preferences for special climate conditions and others are only to be found in restricted habitats like the recently identified species *T.* sp. URa1 at the most extreme cold deserts.

The distribution, genetic diversity and phylogenetic relationships were mapped to newly developed climate zones and revealed different specificity levels of the mycobiont/photobiont interactions under different climate conditions. Our recent work shows that a strong degree of specialisation often is associated with a restricted geographic distribution like *Lecidella greenii* only occurring in a few climate zones and combined with only one photobiont species, whereas more generalized myco- and photobionts associations are widespread like *Lecidea cancriformis,* abundant over the whole continent and connected to every available photobiont species.

Thus, physiological adaptation to the climate as well as the generalized association between the mutualistic partners in lichens facilitate the successful colonisation of lichens in Antarctica.

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A pragmatic approach to the assessment of South Georgia benthic diversity reveals a unique and vulnerable assemblage

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The implementation of the Convention on Biological Diversity (CBD) requires adequate monitoring of what biodiversity is present, and this in turn implies some prior knowledge of the biodiversity that is present. Recently the Government of South Georgia and the South Sandwich Islands has embraced the CBD and efforts are being made to continue to monitor the diversity in both the terrestrial and marine environments. A substantial obstacle often overlooked in these surveys is the time and cost involved in identifying the diversity present, and the accuracy of the end result. A major problem is defining a useable measure of diversity that is equal across taxa. The 'species' is the current standard and, we argue, should remain so as it is the taxonomic unit that has real biological and evolutionary meaning. As defining a species that adequately encompasses all of life has as yet to be achieved, and as formal taxonomic descriptions are occurring at a much slower rate than species discovery, a pragmatic approach is required to uncouple perceived diversity as presented in database, and actual diversity as uncovered by careful scientific observation and enquiry. Using ophiuroids as a model, we investigate the diversity of the South Georgia benthic assemblage and assess relationships and connectivity with conspecifics on the Patagonian and Antarctic continental shelves.

Inventory completeness and accuracy of taxonomic determination: outcomes of a large scale barcoding effort of echinoderms in Terra Nova Bay (Antarctica, Ross Sea)

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In 2010, the Italian National Antarctic Research Program (PNRA) funded a two-years pilot-project named "BAMBi" (Barcoding of Antarctic Marine Biodiversity) with the aim of creating a first data first set of DNA-barcoding COI sequences from the Terra Nova Bay (TNB) area for the highest possible number of invertebrates. This project was followed by others and, after several sampling expeditions, a large amount of samples from a variety of taxa has now been COI sequenced. In this contribution we focus on the results obtained for echinoderms, one of the most important group of invertebrates in the Antarctic benthos both in term of richness and abundance. The group was widely studied in the past in Terra Nova Bay and checklists, based on morphological classifications, are available for Ophiuroidea, Astroidea and Echinoidea. Holothuroidea and Crinoidea, instead, have never been subject of specific studies and determined despite their abundance in benthic samples.

Of the 535 specimens selected for barcoding from the above classes, COI sequences were successfully obtained for 468 of these. The analysis showed the existence of >14 species of Asteroidea, 14 of Ophiuroidea, 12 of Holoturoidea, 6 of Echinoidea and 3 species of Crinoidea. The barcoding approach enabled the recognition of several mistakes in the past classification based on morphology, even in the case of very common species. This has a wide relevance that goes beyond a correct classification since several of these species are also used as model organism in physiological tests. Two new records for the Ross Sea were also found. Several unexpected 'sister clades' were evidenced even in common species suggesting that our knowledge of the Terra Nova bay fauna was far to be complete and precise.

Direct observation of aeolian transport of diatoms in the McMurdo Dry Valleys: implications for microbial biogeography and landscape connectivity

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In the McMurdo Dry Valleys (MDVs), Antarctica desert, aeolian processes are major drivers of sediment transport and biogeochemical processes. Aeolian dispersal of microorganisms may also contribute to microbial community assembly processes in aquatic habitats in the MDVs (lakes, ephemeral streams, and glacier cryoconite). Diatoms are abundant in MDV stream and lake benthic microbial mats and are also common in glacier and lake ice cryoconite, with some taxonomic similarity between stream and glacier cryoconite communities. In an attempt to observe directly aeolian diatom dispersal, wind-blown sediments from Alatna, Miers, Taylor, and Victoria Valleys were collected one meter above the sediment surface during the 2013/2014 and 2014/2015 summers and winters. Aeolian sediments were examined using scanning electron microscopy for preliminary characterization with subsequent examination by light microscopy. Thus far, for the aeolian samples from Lake Fryxell basin, Taylor Valley, which contains numerous streams, the diatoms identified have been taxa that are often dominant taxa in stream microbial mats (*Hantzschia amphioxys* and *Humidophila arcuata* var. *parallela*) or are commonly present in stream mats (*Muelleria meridionalis* and *Muelleria peraustralis*). Local sourcing of diatoms is consistent with previous isotope sediment analysis that indicated a primarily local origin of the wind-blown sediments. In this study, we directly observed the aeolian transport of diatoms representative of stream microbial mats, thereby establishing an important link between previously observed taxonomic similarity between MDV stream and glacial cryoconite diatom communities. Our results suggest wind-mediated dispersal of microorganisms is an important driver of biological connectivity over the MDV landscape.

Species composition of scavenging amphipods (Crustacea: Lysianassoidea) in a rapidly changing environment (Potter Cove, King George Island, South Shetland Islands) revealed by DNA barcodes and morphology

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The crustacean amphipod superfamily Lysianassoidea plays an important role in Southern Ocean benthic food webs due to high biomass and abundance and their predominantly scavenging mode of feeding. However, their poorly differentiated morphology and their unsolved phylogenetic relationships impede our understanding of the lysianassoid fauna even in well-studied areas of the Western Antarctic Peninsula. Accurate species inventories, however, are essential for a multitude of downstream analyses in the context of ecology and biodiversity such as food web modelling and the detection of community shifts. This particularly holds true in areas highly affected by climate-driven environmental changes such as King George Island (KGI) where a remarkably retreat of the ice cap is detected since decades (Rückamp et al. 2011). In Potter Cove (KGI) calving events of the tidewater glacier (Fourcade Glacier) and its consequences such as freshwater runoff and high sedimentation has already led to shifts in biotic communities and their dynamics (e.g. Quartino et al. 2013; Pasotti et al. 2014; Schloss et al. 2014; Sahade et al. 2015; Fuentes et al. 2016). Here, we report the first inventory of the scavenging amphipod guild of Potter Cove using an integrative approach combining morphological and molecular species identification (COI barcoding) methods of more than 41,000 specimens from baited traps. For comparison, 2039 specimens from adjacent Marian Cove were analysed. Ten lysianassoid species were recorded in the deeper outer Potter Cove whereas the inner cove (<50m) was dominated by a single species, *Cheirimedon femoratus* Pfeffer, 1888 (99.44% relative abundance). It is hypothesized that the impoverished lysianassoid fauna inside the meltwater-influenced inner cove represents a model for future conditions along the Western Antarctic Peninsula under conditions of increased glacial melting. *Abyssorchomene charcoti* (Chevreux, 1912) and *Orchomenella pinguides* Walker, 1903 were recorded in KGI waters for the first time. Furthermore, one new lysianassoid amphipod species of the genus *Orchomenella* Sars, 1890 is described: *Orchomenella infinita* sp. n. First-time DNA barcode data was established for *Cheirimedon femoratus*, *Hippomedon kergueleni* Miers, 1875, *Orchomenella rotundifrons* K.H. Barnard, 1932 and *Orchomenella infinita* sp. n.

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Species frequency and new taxa of Antarctic cryptoendolithic black fungi by multi locus phylogeny

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Endolithism is a border life-style for microbes in Antarctica where they live in constant equilibrium between life and extinction. Rock black fungi are invariably present in these communities in spatial association with similarly extremotolerant organisms. The geographic and genetic isolation in the long term and the tremendous environmental pressure led to the evolution of unique and extremely adapted genotypes (Selbmann et al., 2005; 2008; Egidi et al., 2014), very resistant but sensitive to any variation. Polar ecosystems are prone to Climate Change (Steig et al., 2009) and the establishment of more permissive conditions may facilitate the settlement of competitive alloctonous species that, over the time, may outcompete highly adapted organisms, ending to genetic loss (Selbmann et al., 2013). A wide sampling was performed along the North Victoria Land in the frame of the XXVI Italian Antarctic campaign, where 48 locations and 72 sites were sampled for colonized rocks. Among the microorganisms isolated from the 201 rock samples analyzed, black fungi predominate with 56 isolates; five meristematic hyaline fungi and 5 yeasts were also isolated. Molecular analyses based on ITS comparison showed that the endemic species *Friedmanniomyces endolithicus* was the most frequent. Other isolates belonged to the species *Oleoguttula mirabilis*, *Extremus antarcticus*, *Elasticomyces elasticus*, *Cryomyces antarcticus*, *Hortaea thailandica* and *Exophiala mesophila*; yet, a big deal of the isolates belonged to still undescribed species.

Molecular phylogeny based on multi-locus analyses (ITS, SSU, LSU, RPB2) revealed the presence of 2 new species in the genus *Oleoguttula* and one new species in the genera *Constantinomyces*, *Vermiconia* and *Exophiala*, respectively. Also, a new genus of rock fungi from both Antarctic and Alps was found in the order Chaetothyriales. A well supported and phylogenetically isolated and still undescribed group, exclusively constituted of Antarctic endolithic fungi, was in the class Arthoniomycetes. The peculiar niche of Antarctic rocks is here confirmed as a rich reservoir of still unknown fungal biodiversity.

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Microbial communities of Nella Lake, Larsemann Hills, East Antarctica

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Nella Lake is situated in Larsemann Hills (69°23'S, 76°23'E), Prydz Bay, Ingrid Christensen coast, East Antarctica. Bacterial and Yeast isolates were obtained from the sediment core samples cored up to a depth of 90 cm from the lakes. The isolates were orange, yellow, cream and white in colour. Culturable bacterial and yeast diversity was studied using different sub-samples of sediment cores. A total of 200 bacterial and 90 yeast strains were isolated.16S rRNA gene sequence analyses of bacterial strains showed presence of dominant taxa such as Pseudomonas fluorescens, Rhodococcus erythropolis, Arthobacter alpinus, Pseudomonas marginalis, and Edwardsiella tarda. ITS and D1/D2 domains sequence analyses of yeast represented the dominant species as Cryptococcus albidus, Cryptococcus antarcticus, Cryptococcus gilvescens, Rhodotorula glutinis and Leucosporidium sp. Y-36. Besides bacteria and fungi, there are green algae (Cosmarium sp.) and diatoms (Achanthes minutissima, Achanthes exigua, Navicula mutocopsis, Navicula cryprocephala, Diadesmis contenta, Hantzschiia sp.) has also been recorded. Physiological tests such as effect of temperature, pH and salinity (NaCl) on growth of the isolates were studied. All isolates grew at 4 to 22°C. The optimum growth temperature was 15°C for 55.62% isolates and 22°C for 44.38% isolates which confirms them as psychrotolerants. All the isolates can tolerate wide ranges of pH while the optimum is at pH 7 for 55.62% isolates and pH 11 for 44.38% concluding as neutrophiles and alkalitolerants respectively. Among bacterial isolates about 42.14% showed optimum growth at salt concentrations of 3% w/v while 19.66% and 0.562% for 5% and 9 % concentrations of sodium salt respectively. Among the bacteria, all the isolates showed zone of clearances on enzymatic plates at various temperatures except amylase at 4°C. Bacterial isolates of 64.04%, 53.93%, 25.28% and 11.24% showed lipase, protease, cellulase and amylase respectively at 15°C while 57.3%, 50.56%, 7.87% and 0% showed lipase, protease, cellulase and amylase respectively at 4°C. Enzymatic screening of the isolates showed their ability to degrade complex macromolecules such as proteins, carbohydrates and lipids, indicating their probable ecological role. Furthermore, the bacterial strains differ widely in their antibiotic sensitivity characteristics. This adaptation strategy probably helps the bacterial strains to overcome the antagonistic stresses and survive in unique Antarctic lake environment.

When rare things are relatively common: caridean shrimps of the South Orkney area and distinct characteristics of the Antarctic species of Eualus (Crustacea: Decapoda: Caridea)

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Although being relatively poor in species number, Antarctic decapods crustaceans are remarkably important for understanding various distribution patterns of benthic fauna in the Southern Ocean. This study is focused on the composition and distribution of decapods revealed by an extensive survey using an Agassiz trawl and an underwater camera within the South Orkney AntEco cruise on board RRS "James Clark Ross" in March 2016. Only three species of decapods (caridean shrimps) have been recorded on the shelf break and the slope of South Orkney Islands. *Nematocarcinus lanceopes* was the most common and most deep living species. It occurred exclusively deeper than 650 m, while the maximum number of collected specimens and the frequency of occurrence felt over the depth range 909 – 1312 m. *Notocrangon antarcticus* was living mostly shallower than 650 m. These two common species appear to be less abundant in the South Orkney area than in the eastern Weddell Sea where they were studied in the 1980s (Arntz and Gorny, 1991; Gutt et al., 1991). *Eualus amandae* (family Thoridae), a rare shrimp species only recently described from 1500 – 2500 depth in the South Sandwich area (Nye, Copley and Linse, 2013) was recorded for the second time. It occurred mainly between 440 and 880 m throughout the margin of the South Orkney shelf. The present specimens of *E. amandae* (deposited in the Zoological Museum of Oxford University and the Zoological Museum of Moscow University) show some differences from the type series in a relative length of rostrum and the genetic barcode, the mitochondrial COI gene. The phylogenetic reconstruction based on the nuclear histone H3 gene indicates *E. amandae* to constitute a separate clade, which is distinct from the Arctic and North Pacific species of *Eualus* as well as from another high latitude and deep water thorid genus *Lebbeus*. Moreover, *E. amandae* was thought to be different from all other congeners in a unique morphological character, the presence of two vs. one spine on the pleura of the 5th pleomere (Nye et al., 2013). Another Antarctic species *Eualus kinzeri*, described from the eastern Weddell Sea (Tiefenbacher, 1990) was not so far reported to share this character. However our examination of the type series of *E. kinzeri* in the Bavarian State Zoological Collection in Munich revealed that both *E. amandae* and *E. kinzeri* possess two spines on the pleura of the 5th pleomere. Although the latter species remain unstudied with regard to genetic markers, they likely represent a separate, not particularly related to other *Eualus* group that colonized the Antarctic. The causes of a fragmented distribution of the Antarctic *Eualus* (contrasting to a relatively continuous circumantarctic distribution of such species as *N. lanceopes* and *N. antarcticus*) are a puzzling issue.

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Uncovering biodiversity in East Antarctica's nearshore marine habitats: fundamental research to aid monitoring and management

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Studies and assessments of biodiversity underpin efforts to describe both pattern and process in ecological systems and are fundamental to the monitoring of natural and human induced ecological changes. Many Antarctic stations are located in coastal areas and the adjacent nearshore benthic marine ecosystems are hot spots of Antarctic biodiversity. The proximity of highly productive and diverse coastal ecosystems to Antarctic bases makes them vulnerable to human impacts and useful systems in which to monitor natural and human induced ecological change.

The Australian Antarctic Division has a program of continuing work to examine the biodiversity of nearshore marine invertebrates of East Antarctica. Sampling methods range from grabs and cores to video and photoquadrats. Much of ths sampling design has been based around investigating the impacts of stations on marine ecosystems. Using a combination of traditional morphological taxonomy and new genetic approaches such as barcoding, we have identified over 530 species to date from infaunal and epifaunal nearshore habitats (to 30m depth) around Casey and Davis stations. Crustaceans have been found to be very diverse, particularly amphipods and isopods. New species and cryptic speciation are being uncovered. For example, an ostracod previously thought to be a single species has proven to be a complex of up to 9 species, including 5 previously undescribed species and a new genus. Continuing DNA sequencing work is expected to uncover more diversity given that several recent studies have indicated the likelihood of as yet undiscovered intraspecific genetic biodiversity in Antarctic benthic marine invertebrates. Both traditional taxonomy and current and evolving genetic techniques will be key to understanding, protecting and conserving Antarctic marine biodiversity and to fully realising their potential use as early indictors of global issues such as climate change and ocean acidification. Spatially explicit biodiversity data is also essential in identifying biologically distinct areas in need of representation in a protected area network. This biodiversity data will be made available through the appropriate data portals such as the Australian Antarctic Data Centre and the SCAR-MarBIN database.

Connectivity in two congeneric Antarctic shallow-water hoplonemertean species with direct development using a traditional marker and SNPs

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The connectivity and phylogeography of Antarctic benthic organisms has been investigated in just a few species (Riesgo et al. 2015). This is particularly true for shallow-water invertebrates, which will be among the first to feel the effects of climate change. The sympatric Antarctic nemerteans Antarctonemertes valida and A. riesgoae are excellent examples to test the possible effects that climate change may have on shallow-water Antarctic faunas. These congeneric hoplonemerteans are abundant in the shores of the Antarctic Peninsula and the South Shetland Islands, where they brood their eggs in cocoons built by females (Taboada et al. 2003). Because brooders presumably have lower dispersal capacity when compared to non-brooders, we examined the connectivity of populations of these two species across the Antarctic Peninsula and the South Shetland Islands. A total of 362 individuals (177 A. riesgoae and 185 A. valida) were collected from 8 locations spanning ca. 800 km. We sequenced a fragment of ca. 550 bp of the mitochondrial cytochrome c oxidase subunit I gene -COI-. Haplotypic analysis on the COI fragment resulted in a star-like haplotype network for A. valida with a dominant haplotype shared between populations across the study area, indicating that the species went through a bottleneck followed by a demographic expansion. In contrast, A. *riesgoae* showed genetic structure grouping together (1) samples from the southernmost area (Adelaide Is.), (2) samples from the Antarctic Peninsula, and (3) samples from the South Shetland Is. The haplotype networks observed might be explained by differences in ecological behaviour of both species: *A. valida* is normally found in the underside of shallow boulders and algae, while *A. riesgoae* is only found in association to rocks. We thus suggest that the low genetic structure observed in *A. valida* might be explained by passive transport of adults on drifting algae. In contrast, the genetic structure observed in *A. riesgoae* would be explained by the lack of this passive transport. Finally, our results for the COI analysis are compared and discussed with preliminary analysis on single nucleotide polymorphisms (SNPs) generated using ddRADseq on an Illumina HiSeq for a selection of 10-15 individuals per population, thus giving a comprehensive view of the genetic connectivity of both species using a combination of markers with slow (COI) and rapid (SNPs) mutation rates.

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Never two without three: a new member of the genus Antarctonemertes (Hoplonemertea, Nemertea) from Antarctic waters

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Despite the relative low number of described species in the phylum Nemertea in the Southern Ocean (Kajihara et al. 2008), this group of organisms represents an important component in these waters. A few well-known species commonly occur in the shallow Antarctic waters. Amongst these we found the congeneric *Antarctonemertes valida* (Bürger, 1893) and *Antarctonemertes riesgoae* Taboada *et al.*, 2013, two relatively small brooding hoplonemerteans whose females lay eggs inside cocoons (Taboada et al. 2013). Here we document the existence of a third Antarctic member of the genus *Antarctonemertes*, which was originally described as *Tetrastemma unilineatum* Joubin, 1910. Phylogenetic analysis using three genetic markers (COI, 16S and 28S) place the new *Antarctonemertes* in a robustly supported clade –Antarctic *Antarctonemertes*– as sister to the other two congeneric Antarctic species *(A. valida* and *A. riesgoae*). Pairwise COI molecular distances between the three species ranged from 5.2–6.2 % (p-distance), falling within the range of the barcode gap defined by Sundberg et al. (2016) for Nemertea. The new *Antarctonemertes* is similar in shape to its Antarctic congeneric although it is slightly smaller. The most prominent morphological character that distinguishes the new *Antarctonemertes* is the dorsal mid-longitudinal band present along the body, retained even after preservation. As in *A. riesgoae*, the new *Antarctonemertes* also has a cephalic V-shaped white band with the apex pointing backwards. We also report here the presence of a cocoon built by females of the new *Antarctonemertes*, a character shared with its congeneric. Although the three species appear to overlap their distribution, *A. riesgoae* and *A. valida* generally appear in sympatry in the West Antarctica shores while the new *Antarctonemertes* is more frequent in the East Antarctica shores and SubAntarctic Islands. However, further studies should be conducted in still unexplored areas to confirm this.

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Genetic structure between distant Gobionotothen marionensis (Pisces: Nototheniidae) populations in the Southern Ocean.

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Previous morphological studies split *Gobionotothen marionensis* into two species, *G. marionensis* in Prince Edward Islands of the Indian Ocean and *G. angustifrons* in South Georgia and South Sandwich Islands of the Atlantic Ocean. However, a recent phylogenetic study found that the specimens from these oceans represent same species (*G. marionensis*) with geographic variation (Miya *et al*. 2016). The present study assessed genetic structure between the *G. marionensis* populations from Indian and Atlantic Oceans using a mitochondrial DNA (mtDNA) cytochrome subunit 1 (COI) and nuclear DNA recombination activating (RAG) genes. The results obtained from both genes indicated that there is no genetic differentiation between populations from these two oceans, with sequence variance of 6.85% and 0%, respectively, between these oceans. The presence of gene flow in *G. marionensis* distant populations might be due to their long pelagic larval stage. The Antarctic polar front that flows between localities of the two populations may be acting as transport for pelagic larva to both sides of it. On the other side, the highest genetic differentiation was observed among populations in the same ocean (75.52% and 79%, respectively). Given that there is no physical barrier between localities of the same ocean, the results are interesting. Similar results have been observed in other notothenioid species such as *Lepidonotothen larseni* populations found in the Atlantic Ocean sector (Damerau *et al*. 2014). Analyses of the demographic history of *G. marionensis* populations indicated increasing population sizes in both oceans.

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Freshwater diatom biogeography and the genus Luticola: An extreme case of endemism in Antarctica

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Historic views on levels of endemism in the Antarctic region have characterized the region as a frozen desert with little diversity and low endemism. More recent studies however have uncovered an endemism in this region that may be much greater than previously expected in several groups. Assessing levels of endemism in the Antarctic region has become particularly important for microbes, in the light of the ongoing debate regarding the possible cosmopolitan nature of small species.

In order to analyze the degree of endemism of the limno-terrestrial genus *Luticola* in this region, all taxonomical results based on a modern fine-grained taxonomy have been synthesized for *Luticola* in the entire Antarctic region, as well as southern areas of South America. We examined recent and historical taxonomic treatments of freshwater diatoms for the Antarctic region, and compiled data for the number of endemic species and their distributions. Over 200 species of *Luticola* are currently known worldwide. Almost 20% occur in freshwater habitats in the Antarctic region. Of these 43 species, 42 are endemic to the region, with maritime Antarctic localities being the most species and endemic-rich (28, 23, respectively), followed by continental Antarctica (14, 9 respectively) and the sub-Antarctic islands (8, 6, respectively). *Luticola* has one of the highest percentages of endemism in Antarctica of any known diatom genus, in terms of total number of species (=taxon endemism) as well as a percentage of the entire genus (=phylogenetic endemism). These numbers of endemics for *Luticola* are compared with other groups of terrestrial and freshwater organisms, showing that the genus has one of the highest, if not the highest levels of endemicity in Antarctica. The timing of the diversification of *Luticola* has not been established, but the oldest known fossils of the genus date only to the Holocene, suggesting that diversification processes in *Luticola* are rapid, and that single or multiple invasions of the region may have occurred over a very short geologic timescale. Understanding the origin and evolution of endemic species in Antarctica will allow a better understanding of the baseline and impacts during a time of large-scale environmental changes in southern latitudes.

The non-marine diatom flora of the Maritime Antarctic region: an iconographic guide

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A new volume in the series Iconographia Diatomologica was recently published on the freshwater and terrestrial diatom flora of the Maritime Antarctic Region (Zidarova et al. 2016). This region is defined as the zone between the southern limit of the extensive, closed phanerogamic vegetation to the southern limit of the extensive cryptogamic (mainly bryophyte) communities, roughly comprising all landmasses between 70°S northwards to 55°S, including several islands and archipelagos (South Sandwich Islands, South Orkney Islands, South Shetland Islands, Palmer Archipelago), as well as the west coast of the Antarctic Peninsula south to Marguerite Bay.

The new volume provides the first detailed diatom identification guide for the Maritime Antarctic region. A total of 203 taxa found during a large taxonomic and ecological freshwater diatom survey on the South Shetland Islands and James Ross Island are included. Each taxon is discussed on a single page providing the original reference, a morphological description based on LM and SEM observations, a comparison with similar taxa and data on its ecology. Per taxon, an entire plate composed of high quality LM and SEM micrographs is shown, illustrating all morphological details. Confirmed distribution in the Antarctic and sub-Antarctic regions of all these taxa is given as an Appendix at the end of the volume. Nine other taxa, that were very rarely observed in low abundance and for which no sufficient observations were possible at present are also shown. Short morphometric descriptions for them are provided.

The non-marine diatom flora of the Maritime Antarctic Region is mostly characterized by typical aerophilic genera such as *Luticola* (32 taxa), *Pinnularia* (29 taxa), *Muelleria* (16 taxa) and *Humidophila* (12 taxa) whereas typical aquatic genera such as *Nitzschia* (12 taxa), *Navicula* (6 taxa) or *Fragilaria* (1 taxon) are far less diverse. More than 70% of the taxa were previously described as Antarctic endemics, most of them having a restricted distribution to the Maritime Antarctic Region. These data clearly contradict the old-fashioned ideas on Antarctic diatom biogeography stating that the flora in this region was supposed to be dominated by cosmopolitan taxa. The latter, such as *Navicula gregaria*, *Nitzschia homburgiensis* or *Tryblionella debilis*, showing a worldwide distribution constitute only a minority.

The poster presents the new volume of Iconographia Diatomologica and shows some of the typical Antarctic taxa.

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Genetic information at different spatial scales: Southern Ocean islands as study sites

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The importance of understanding and recognizing patterns at different spatial scales is often overlooked in molecular ecological studies, yet when interpreted in concert, provides crucial information to understand how individuals move and disperse within their habitat matrix (landscape genetics). At first, genetic patterns across spatial scales (at the scale of the region, the island, and the population) might seem contradictory (such as e.g., a random genetic structure at the scale of the island, yet a neighbourhood / population size of less than 10 meters as was found in *Azorella selago*). Using genetic information derived for *Azorella* (intermediate and small spatial scale), and various springtail and mite species (large, intermediate and small spatial scale), I will examine these apparent conflicting genetic signals (derived from both sequence and microsatellite data). At large spatial scales, understanding evolutionary patterns in terrestrial species is often confounded by inaccurate taxonomies (using the Amerenothroid mite group as an example), and driven largely by the ability of organisms to disperse within a largely inhospitable matrix. At intermediate spatial scales (i.e., the scale of the island), the history of the islands are important as well as factors such as island orientation with regards to prevailing winds / weather patterns (e.g., *Azorella* with a comparison between Marion and Macquarie islands) or geomorphological features (*Halozetes* and *Pringleophaga* on Marion Island) defining the landscape matrix. At small spatial scales, biotic and abiotic factors determine the genetic neighbourhood size, and dispersal within this neighbourhood (using *Azorella* and *Cryptopygus* as examples). I conclude that a full understanding of the interplay between patterns of dispersal and connectivity across spatial scales is crucial to optimal conservation planning. Identifying priority areas for conservation is essential, and under the current variable climate, these areas act as microrefugia for survival.

The Antarctic Epimeria species flock: a systematic Pandora box revealed by DNA analysis and illustrated by stacking photography.

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Analyses of DNA sequences of Epimeria from the Antarctic Peninsula, East Weddell Sea and Terre Adélie revealed an unexpected genetic diversity within this species flock. Many formerly recognized species were composed of several clades, identified as putative species by DNA-based delimitation methods (bPTP, GMYC, BPP). Careful examination of the specimens revealed previously overlooked morphological differences between the putative species. Moreover, some of them are found in sympatry. Assuming a strict COI molecular clock of 0.018 substitutions/site/My (previously estimated for other amphipods), the divergences between Epimeria species within the complexes were roughly dated between 10.28 and 1.11 Mya. Hence, as these speciation events likely occurred after te mid-Miocene climatic transition, the presence of many closely related (pseudo-)cryptic Epimeria species on the Antarctic shelf could be explained by a scenario of continental shelf refugia. Isolation of populations in refugia during glacial maxima and resulting divergences could have led to allopatric speciations. Following the morphological examinations of all the Epimeria material available, a total of 29 species were described as new, which increases twofold the number of Antarctic Epimeria species known to date. The latter species were used as case study for testing stacking photography as an alternative to line drawings in amphipod taxonomy. It appeared that these large and often very geometric amphipods can be adequately and quickly illustrated by this new technique. As large areas of the Antarctic shelf remain undersampled, the latter taxonomic revision of Antarctic Epimeria is likely non exhaustive.

Preliminary results of Ephausiids and other zooplankton groups around San Pedro Island, South Georgia

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This study present preliminary results of a research survey carried out in this area during April/May 2013 in austral autumn. The South Georgia region is characterised by high productivity of phytoplankton and associated high biomass of zooplankton and numerous predator species.

Biological samples were obtained from 26 oblique tows with a 1m^2 RMT plankton netfrom a maximum depth of 250 m In the catches were identified and quantified including amphipods, euphausiids, mysiids, chaetognaths and copepods. We displayed the results simoultaneous recording of eufausiid larvae and adults and total of plancton using resolution and identification by targetted and regular sampling. Macrozooplankton in net catches consisted mostly of euphausiids, represented by the species *Thysanoessa*spp*., Euphausiafrigida, E. vallentini, E. triacantha and E. superba*(krill), this last one in a relative low abundance. Among the hyperiid amphipods *Themisto audichaudii* was the main species caught. In several areas of high abundance in both northern and southern waters the most conspicuous macrozooplanktonic species showed a general agreement of 200kHz in acoustic records.

Determining prey distribution from stomach-contents of GIS-tracked high-predators of the Southern Ocean

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The distribution of many cephalopod, crustacean and fish species in the Southern Ocean, and adjacent waters, is poorly known, particularly during times of the year when research surveys are rare. To address this challenge put forward recently at SCAR Horizon Scan (Xavier et al. 2016), and following a previous study addressing this issue (Xavier et al. 2006), we analysed tracked seventeen wandering albatrosses *Diomedea exulans* in Bird Island, South Georgia (54˚S; 38˚W) over the austral winter (breeding period) with GPS-loggers, activity recorders and stomach temperature probes (plus at logger retrieval, diet composition was accessed via stomach flushings of the tagged individuals), which combined information provided a novel method to assess where their prey was caught (Pereira et al., *in press*). Wandering albatrosses captured circumpolar and rarer oceanic squid in all water masses of the Southern Ocean (i.e. Antarctic, sub-Antarctic and subtropical waters), complementing much of the knowledge about the cephalopod distribution in the Atlantic sector of the Southern Ocean. This new methodology was able to predict the distributions of a wide number of species, complementing the information gathered from scientific nets and fisheries, and making a contribution to obtain prey ecological information via their predators.

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Kinorhynchs in Antarctica and surrounding area

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Kinorhyncha is an invertebrate phylum which is exclusively comprised of marine meiobenthic species (benthic animal with a body length less than 1mm). To date, about 250 species are known worldwide, from polar to tropical regions and from intertidal to subtidal depths. Followed by harpacticoid copepods and nematodes, they are often the third most dominant taxon in meiobenthos (e.g. Grzelak & Kotwicki, 2012). Since they occur in various types of sediment and their abundance is sensitively affected by the organic enrichment, they are expected to be used as a bioindicator (Dal Zotto et al., 2016). The marine fauna in Antarctica has been extensively investigated since the last century. Although some kinorhynchs have been reported in several studies, most of them are identified only to the phylum-level and mentioned as "Kinorhyncha sp." (e.g. Veit-Köhler et al. 2011). To date, only two species, *Campyloderes* cf. *vanfoeffeni* Zelinka, 1913 and *Polacanthoderes* Sørensen, 2008, have been recognized in the Antarctic area (Zelinka, 1913; Sørensen, 2008), suggesting the faunistic surveys of kinorhynchs in the area have been scarce.

In this presentation, we report the preliminary results on the sample collected during the 42nd Japanese Antarctic Research Expedition in addition to the review on the kinorhynch studies in Antarctica and surrounding area. Kinorhynch individuals were extracted from the sediment sample which had been collected at 900m below sea level off Amundsen Bay in December 2000 and kept frozen at National Institute of Polar Research for 16 years. The light microscopic observation of these individuals detected four species of four genera: *Polacanthoderes* sp., *Campyloderes* cf. *vanfoeffeni*, *Condyloderes* sp. and *Sphenoderes* sp. Of these species, *Polacanthoderes* sp. is an undescribed species, and the second record of the genus in the world. *Condyloderes* sp. and *Sphenoderes* sp. are also possibly undescribed species; however, further materials and observations are required. As we found more number of kinorhynch species than previously recorded from Antarctica in one sediment sample collected at a single locality, a substantial number of kinorhynch species could be expected to be found in further investigations. This study also indicates that the long-term frozen sediment samples are valid and useful for the taxonomic study and identification of Kinorhyncha.

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Genetic insights on the origins and age of the contemporary Antarctic flora

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During the Last Glacial Maximum (LGM; ~22–18 kya), as well as previous Pleistocene and earlier glaciations, thick ice sheets are thought to have covered nearly all currently ice-free land in Antarctica. This led to the view that terrestrial life must have been extremely limited throughout these periods, and that nearly all extant floral and faunal groups must have (re-)colonised the continent post-LGM. However, biogeographic and genetic studies throughout the last decade have revealed evidence that most extant Antarctic terrestrial faunal groups, and at least some microbial groups, survived past glaciations *in situ*, with persistence estimated to have been on hundreds of thousand to multi-million year timescales, and in several separate regions on the continent. However, evidence pertaining to the age and biogeographic structure of the Antarctic flora has been sparse, and low endemism rates based on traditional taxonomic methods remain consistent with most species being recent (post-LGM) arrivals. Combining population genetic and Bayesian inference and dating methods, we assessed the age and origin of several species of Antarctic bryophytes: four bipolar species within the family Polytrichaceae, several species within the genus *Schistidium* (the largest genus of plants in the Antarctic, and also the genus containing most endemic species), the cosmopolitan species *Ceratodon purpureus* and *Bryum argenteum*, and the temperate bank-forming moss *Chorisodontium aciphyllum*, a species also known for its extreme revival abilities. Although some moss populations and species are of seemingly recent (post-LGM) Antarctic origin, others reveal the first clear evidence of long-term (hundred thousand to multi-million year) *in situ* survival of plants in Antarctica, suggesting that, despite the harsh polar climate during glacial periods, the extant Antarctic flora has had a much longer *in situ* presence than previously thought. Focusing on moss species with different distribution patterns (bipolar, cosmopolitan, temperate, endemic) we also identified features that enable and restrict global moss distribution patterns; these features may also be of relevance to understanding the biogeography of other small- and spore-dispersed organisms.

Network analysis of the biotic association between cnidarians and scale worms from the Southern Ocean and surrounding areas

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The analysis of mutualistic and antagonistic ecological networks has become a major topic in ecology in the last decades. The continuous development of new tools of analysis, dedicated software and ad hoc metrics, has enabled a better definition of the ecological and evolutionary characteristics of biological associations, greatly enlarging our knowledge in this research field. In general, terrestrial associations, especially those focusing on pollinators, have dominated the literature for decades and very few examples are available for marine interactions. However, in the last decades, a slowly growing body of ecological evidences started to accumulate, showing that marine symbioses represent a not negligible ecological and evolutionary driver of community organization.

Here we focus on the Antarctic "scale-worms" (Polychaeta, Polynoidae) and their hosts, to produce the first analysis of this marine antagonistic network for the Southern Ocean. This group of polychaetes is known to form associations with a variety of other invertebrates at all latitudes and depths and this analysis is the first of ever focusing on ecological networks in a polar environment. Our results showed a general very high level of specialization in all the considered networks.

These characteristics corroborate the hypothesis that the main ecological driver of specialization might be the intimacy of the association rather than the typology of the interaction itself, as previously stated in literature. Furthermore, the intimacy of the association might be the structural basis of coevolution, with many consequences on the organization of entire communities.

Trematominae and Artedidraconinae: contrasted mitogenome evolution for two Antarctic radiations

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Cellular respiration has been widely studied in Antarctic teleost fishes because of their peculiar adaptations to an extreme environment. In parallel mitochondrial sequence markers have become highly popular for molecular systematics. However, there are few whole mitochondrial genome sequences published, and none available for some of the subfamilies. Here, we present two large mitogenome datasets including most species and multiple sequences for many species of two subfamilies, Trematominae and Artedidraconinae (Duhamel et al. 2014). These include two highly diverse but very different adaptative radiations, with contrasting divergence dates, morphological polymorphism, and habitat dominance. The sampling is based on a well identified, extensive collection resulting from the 2008 CEAMARC survey and the subsequent REVOLTA surveys in Terre Adélie (IPEV), already DNA barcoded and sequenced in previous studies. The mitogenome sequences for these two subfamilies differ in composition, gene order, and relative divergence of mitochondrial markers, with strong, taxon-specific biases like very high C contents in some regions. The gene order change provides a synapomorphy for the subfamily Trematominae and an interesting development in teleost mitogenomes. The complete Artedidraconinae mitogenomes provide a much higher amount of variable sites (approx*30), while previous sequence datasets were plagued by low informativeness (Lecointre et al. 2011). As already established on single mitochondrial genes, intraspecific variability is lower than interspecific variability within each subfamily, however interspecific variability in Artedidraconinae is lower or similar to intraspecific variability in Trematominae. This expanded dataset confirms the unusual evolution of the mitochondrial coded sequences involved in the cellular respiration in Antarctic Nototheniidae, as well as the usefulness of complete mitochondrial genomes for their systematics. The two level multiplexing (Timmermans et al. 2010) and next generation sequencing of long PCR amplicons (following Hinsinger et al. 2015) is efficient to obtain large mitogenomic datasets representative of both inter- and intraspecific variability, key to the understanding of mitochondrial evolution and a step closer to resolving the relationships among these taxa.

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Simply complex? Evolutionary histories of two sea spider complexes

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Understanding factors that shape the origin and adaptation of Southern Ocean biota is of great importance in times of global change. Molecular methods, in particular DNA barcoding of the mitochondrial COI gene, have greatly improved our understanding of these factors by identifying cryptic species and estimating their phylogenetic and biogeographic affinities. However, nuclear data sometimes conflicts with mitochondrial data due to several peculiarities in inheritance mode and ploidy. In most studies, this has not been tested and only mitochondrial gene data are available. Therefore, comparative studies using mitochondrial and nuclear gene data are important when inferring evolutionary histories. Here we report results from studies on the two sea spider complexes *Pallenopsis patagonica* and *Colossendeis megalonyx*. For both, many (19 and up to 20, respectively) highly divergent mitochondrial clades have been identified, indicating cryptic species. Interestingly, the nuclear genetic signatures obtained by sequencing the ITS-marker strongly deviate between the two complexes, although substitution rates are similar. Whereas for *C. megalonyx* only six of the clades are uncovered by nuclear DNA, almost all are supported in *P. patagonica* s.l. One clear result of the direct comparison using the same molecular markers (COI and ITS) for both species complexes is that similar historical processes have led to the divergence of distinct mitochondrial lineages most likely taken place in the same period (Plio-/ Pleistocene). As this period has been characterized by drastic environmental changes between glacial and interglacial cycles an impact of the glacial periods on speciation processes can be assumed. However, the mito-nuclear discordance observed in *C. megalonyx* suggests that hybridization across several mitochondrial clades occurred and led to speciation reversals. Given the limited information on the biology of the species reasons for this distinction are difficult to estimate. One reason might be variations in the reproductive mode (slower build-up of pre- or postzygotic reproductive barriers in *C. megalonyx*), another one differences in dispersal capabilities. Furthermore, we discuss the data also in the light of novel genomic data obtained for both species complexes that add valuable insights into processes driving speciation and adaptation in Antarctic sea spiders.

Genetic diversity of Halicarcinus planatus (*Brachyura, Hymenosomatidae*) in the Southern Ocean

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Climate change directly impacts and shapes the biodiversity. Biological invasions are a crucial component of global change, but also a threat to native biodiversity. Antarctica remains the most pristine and isolated continent surrounded by oceanographic, bathymetric, climatic and geographic barriers. The West Antarctic Peninsula is the most affected by global warming thus enhancing the probabilities of introduction of alien species, their subsequent ecological adaptation and proliferation.

Shallow marine benthic communities around Antarctica exhibit high levels of endemism, gigantism, slow growth, longevity and late maturity. Several families of durophagous predators that are highly abundant and diverse in subantarctic shallow waters are almost completely absent in the Southern Ocean, this is the case of decapods. Nevertheless, many records of non-Antarctic decapods have been reported during the last decades, thus suspecting an ongoing invasion. So far, there are no evidence of expansion in geographic or bathymetric range for any decapod (lithodid) species in the Southern Ocean.

In 2015, a breeding female *Halicarcinus planatus* was reported in Deception Island (South Shetlands, West Antarctic Peninsula) (Aronson et al., 2015). This species is a brachyuran crab with a circum-subantarctic distribution. *Halicarcinus planatus* has a low bathymetric range, a planktonic larval duration of 45-60 days, and tolerates temperatures lower than 0˚C because it is also able to down regulate the [Mg2+] in the haemolymph that increases with the cold.

Larval transportation through the Antarctic Convergence may occur naturally. The increasing maritime traffic associated to human activities in southern summer occurs during the period of planktonic larval occurrence. The West Antarctic Peninsula is experiencing a rise of the sea water temperature. The recent observation of *Halicarcinus planatus* in Antarctica (Deception Island), confirmed the efficiency of the larval transportation and its ability to survive in glacial waters. Moreover, the fact that Deception Island is an active volcano could not be ignored. It is likely that a geothermal activity allows to shelter species that originally inhabits warmer waters.

The present project evaluates the level of genetic diversity of *Halicarcinus planatus* along its Subantarctic distribution, determinate the phylogeographic structure, the geographic scale at which the genetic differentiation operates and the connectivity pattern between remote populations. The phylogenetic relationships are inferred from mitochondrial haplotypes and nuclear introns from the Magellanic Region, Falklands/Malvinas Islands and Kerguelen Islands. We also give an appraisal of the presence of *H. planatus* in the West Antarctic at the end of our first Antarctic expedition.

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Historical DNA Barcoding of trematomid fishes using museum samples

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The Antarctic and the surrounding Southern Ocean contain delicate and unique ecosystems, characterised by cold climate, seasonal photoperiods and remote location. Despite its distance to congested areas, human influences on the ecosystems include direct impacts such as commercial fishing, tourism and research, as well as indirect impacts such as global warming or pollution. With the exception of fishing, the major increase of these impacts occurred within the last 100 years. These drivers may have left imprints on the genetic structure. It has been argued that microevolution, evolution over an ecological timescale (<100 years), might be a yet underappreciated method of species to adapt to rapidly changing environments. Therefore, the adaptive potential of many species might be greatly underestimated or simply yet unknown. Purely ecological approaches often overpredict extinction risk and therefore rapid evolutionary processes should be taken into consideration in parallel. This is especially true when assessing the outcomes of migration into refugia during the Last Glacial Maximum and in in the context of predictive climate change scenarios.

This study focuses on species of the genus *Trematomus*, which are amongst the most abundant members of the Antarctic icefish community. The genus is not exploited commercially and has a circum-continental habitat range. *Trematomus* specimens collected during various research expeditions are preserved in natural history collections around the world.

Historical samples of marine species, however, are commonly preserved in formaldehyde which poses additional challenges. Over time, formaldehyde forms formic acid, which hydrolyses the DNA. Furthermore, formaldehyde causes the creation of crosslinks between DNA and proteins, which complicates/hampers DNA extraction.

We collected tissue from 400 specimens of the genus *Trematomus* from the Natural History Museum London. Specimen were between 20 and 100 years old, fixed in formalin and later transferred to ethanol. Tissue samples were taken from different regions (fin, muscle, liver) and DNA extraction was possible. A 450 bp fragment of the cytochrome c oxidase subunit I (COI) was amplified and sequenced to investigate if unscathed DNA fragments were successfully obtained. We thus evaluate various protocols for the suitability to infer sequence data from historically formalin-fixed samples and, based on results with one marker (COI), identify samples amenable to subsequent sequence-capture approaches, where multiple markers of interest can be analysed simultaneously. Facilitating molecular analyses of museum stored fish holds enormous potential for microevolutionary insights that can benefit current efforts to prioritize conservation units in the Southern Ocean.

A glimpse into the reproductive biology of buttercups in the Kerguelen Islands

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Among the three *Ranunculus* species that are found in the Kerguelen Islands, one is strictly endemic (*R. moseleyi)* to Kerguelen, one is also magellanic (*R. pseudotrullifolius)* whereas the third one *(R. biternatus)* has a much wider distribution extending throughout the circumpolar zone. Both *R. pseudotrullifolius* and *R. biternatus* are found in contrasted habitats *(*aquatic versus terrestrial environments), whereas the halophilous *R. pseudotrullifolius* is only found in coastal areas[1]. The particular ecological (no insect pollinators[2]) and environmental conditions (geographical isolation due to insularity) may have driven the evolution and diversification of the reproductive strategies of these species according to habitats. Moreover, Sub-Antarctic Islands are affected by rapid climate changes, which have resulted over the past decades in Kerguelen in a strong decrease in the number of frost days and rainfalls, and an increase in wind speed, which may already have affected the reproduction of *Ranunculus* populations growing in wet habitats, since they are particularly vulnerable to such changes[3]. We will present original data on the intra- and inter-specific variation of traits defining the reproductive biology syndrome of *Ranunculus* species (pollen to ovule ratio, number of reproductive organs, pollen size, number of seeds produced vs. number of ovules). The contribution of population size and type of habitat (aquatic versus terrestrial), and of biophysical characteristics (substrate conductivity, pH, mean temperature, wind exposure and humidity) to this variation will be discussed. Finally, because a few experiments have suggested that these species may be interfertile, and because several plants with intermediate vegetative morphology between species were found in the field, our data will also be used to discuss the potential occurrence of interspecific gene flow within Kerguelen Islands.

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Comparison of spatial genetic structure and its drivers in Arctic and Antarctic fishes

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Marine populations are genetically structured through historical processes, environmental or physical barriers and life history characteristics. Divergent patterns of demographic history, even among closely-related species sharing climatic changes, raise questions about the influence of species-specific traits on population structure. The Southern Ocean features comparatively high biodiversity, which has been attributed to frequent local extinction-recolonization cycles that have driven benthic, Antarctic organisms into temporary refugia. In contrast, organisms in the Arctic were able to shift latitude in response to changing Pleistocene climate. We therefore hypothesize that Arctic populations were historically less constrained in their distribution than Antarctic fish populations and hence show lower levels of genetic structure.

For assessing the role of lifestyle in influencing demographic history in the Southern Ocean closely related notothenioid fish with benthic (*Trematomus bernacchii*, *T. hansoni*) and semi-pelagic or even cryopelagic (*T. newnesi*) lifestyles were genetically analysed. In the Arctic, polar cod (*Boreogadus saida*), which is often found in association with sea ice, but also throughout the water column to the bottom, can be regarded as semi- or cryopelagic too. The Antarctic species were analysed by six microsatellite and one mitochondrial marker before (Van de Putte et al., 2012) and we extend these analyses with data from nine microsatellite markers in polar cod.

Antarctic species showed significant genetic population structure between High-Antarctic and Peninsular regions and much lower differentiation in pelagic than benthic species. It suggests that the observed patterns are indeed related to ecological traits of Antarctic fish. In the Arctic, we hypothesize genetic structuring inside fjords in Svalbard relative to shelf specimens, which we expect to show low or absent structure as in Antarctic species with a similar lifestyle. Identifying common driving factors for population structure is important in order to enable forecasting, particularly in light of dramatically increasing rates of environmental change. Comparing population genetic patterns and exploring underlying causes from both poles may thus help to shed light on how fish populations survived in the past and may persist in the future.

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New fossil vertebrates for the López de Bertodano Formation (Maastrichtian), of the Seymour Island (=Marambio), Antarctica

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The Seymour (=Marambio) Island, James Ross Archipelago is one of the richest vertebrate bearing locality of Antarctica. Most of the fossil vertebrates there registered become from several Cretaceous levels of the López de Bertodano Formation (Maastrichtian 65,5-68,7 Ma). This formation could be divided in to two informal units: 2-6 (*Rotularia* Units), deposited in a shallow delta/estuary influenced environment and 7-10 (molluscan Units), deposited in shelf environment. During the past forty years paleontological prospection supported by the Instituto Antártico Argentino (IAA) have provided several fossil remains including marine vertebrates and birds. Here we report the results of the last 2017 Antarctic fieldtrip, which provides new material of chondrichthyans (chimaeras and sharks; units 7, 8, 9), actinopterygians (unit 9), mosasaurs (units 7, 8, 9) plesiosaurs, and birds (units 8, 9). Among plesiosaur, remains of long necked non-aristonectine elasmosaurid where collected. The specimen preserves a sub articulated but incomplete postcranium and part of the cranium and mandible. The mandibular symphysis is extremely short comprising only two alveoli. This new plesiosaur material indicates a higher diversity of non aristonectine elasmosaurids than that known for Late Cretaceous marine environments in these latitudes.

The evolution of mitochondrial genomes of notothenioid fish

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Antarctic notothenioid fish have been often considered as bizarre evolutionary experiments. There is much evolutionary and biological interest in the processes that shaped their adaptations via molecular changes. In this study, we focus on the evolutionary pathways that have produced the diversity of gene orders observed in the mitochondrial genomes (mtDNAs) of these fascinating organisms. We concentrated on both Antarctic and non-Antarctic notothenioids, as they are known to differ in the gene order and exhibit translocations of *nad6* and *trnE* genes in different positions with respect to the standard vertebrate gene order. We sequenced the mtDNAs of 11 Antarctic notothenioids and 1 species with sub-Antarctic distribution (Bovichtidae). This information was not yet available for these species. The new sequenced genomes were combined with the 10 notothenioid mtDNAs already available in public databases. A broad set of outgroups, encompassing more than 30 mtDNAs of other Perciform species, completed the final data set. A molecular phylogenetic analysis, based on Bayesian and maximum-likelihood methods, provided a strongly supported notothenioid tree, which was used to map the evolution of gene order in these peculiar fishes. The analysis was completed with the study of the molecular evolution of single mitochondrial genes. In a modern era, when sequencing of large genomes has become a state-of-the-art, this study demonstrates that small compact mitochondrial genomes still embed a large amount of information that advanced analytical approaches can bring to light.

Disentangling the evolutionary history of the diatoms in Antarctica: the Pinnularia borealis species complex as a case study

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Because of their immense diversity, the systematics of protists, and diatoms in particular, is complex and challenging. As species taxonomy has far-reaching consequences for our understanding of diatom evolutionary history, ecology and biogeography, detailed studies into species limits and diversity are needed if we are to advance our understanding of the range dynamics and diversification of diatoms. However, the biogeography and ecology of (pseudo)cryptic diatom species is highly understudied and there are virtually no data available on the timing of lineage splitting within species complexes. This is especially the case for Antarctica for which molecular studies on diatoms are seldom undertaken. In the present study, we used the semiterrestrial diatom morphospecies complex *Pinnularia borealis* as a case study for speciation, evolutionary history and biogeography of terrestrial diatoms, and more generally microscopic eukaryotes, in Antarctica.

During field campaigns on multiple continents, including the entire Antarctic Region, more than 500 samples from (semi)terrestrial habitats were collected. From these, over 900 monoclonal cultures were established for DNA and morphology. Automatic species delimitation based on the cox1 and 28S rDNA genes revealed the presence of at least twelve Antarctic lineages and 93 lineages worldwide. Of all Antarctic lineages, only two were recovered from other continents. A molecular clock analysis on a four marker dataset indicated that the diversification of *P. borealis* started in the late Eocene and strongly increased during the Miocene.

The results indicate a high degree of hidden species diversity in *P. borealis* worldwide and the presence of regional endemics in Antarctica. The topology of the phylogenetic tree and the age of the lineage splitting does not support a radiation of the *P. borealis* species complex in Antarctica. In contrast, it suggests multiple independent colonization events in or out of the Antarctic Region during the past 20 million years. Together with the high levels of genetic diversity, these findings indicate that although the *P. borealis* complex is relatively successful in dispersal, this is not sufficient to prevent speciation. Altogether, our data provide evidence for the moderate endemicity hypothesis for micro-organisms and suggest that, whereas Antarctica is the most remote and hostile continent on the world, it has been reached and successfully colonized multiple times by terrestrial diatoms.

Miocene diatom fossils shed light on the paleoenvironmental and biogeographical history of the Antarctic Continent

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In contrast to the rich marine fossil record that extends to the late Mesozoic, records of pre-Quaternary lacustrine diatom deposits are relatively scarce, particularly from the high latitudes. Such records provide information concerning paleoenvironmental change, as well as new insights concerning the evolution and biogeography of freshwater diatom floras. Here, we report two well-preserved lacustrine diatom assemblages from the Transantarctic Mountains in Continental Antarctica dating back to the Middle Miocene (ca. 14 – 17.5 Ma): Mount Boreas in the Olympus Range in the western Dry Valleys, and the Friis Hills adjacent to the Asgard Range in the southern Dry Valleys.

In total, 17 samples of Mount Boreas and 9 samples of the Friis Hills were investigated. Diverse diatom floras were revealed, represented by at least 131 taxa (38 genera) and 128 taxa (36 genera) from Mount Boreas and the Friis Hills, respectively. Both floras are dominated by small colonial fragilarioid taxa and a large diversity of benthic taxa belonging to amongst others the genera *Eunotia*, *Gomphonema*, *Pinnularia* and *Brachysira*. Detailed counts of the Mount Boreas sediments suggest that the Mount Boreas lake persisted for several thousands of years and underwent progressive natural acidification. Extensive bryophyte growth suggest an initial shallow water phase, followed by deepening and the occurrence of tychoplanktonic taxa including *Aulacoseira*.

Many of the observed Miocene genera and species groups are currently not found in Continental Antarctica, suggesting that the extant Continental Antarctic diatom flora became established after the Mid Miocene cooling event (ca. 14 Ma), when Antarctic glaciation became intensified. In contrast, the Miocene flora shares compositional affinities with the present-day flora of the Arctic region (e.g., high diversity with eunotioid and cymbelloid diatoms), as well as marked biogeographical links with the Gondwanan continents of South America and Australasia, as evidenced by the occurrence of marker genera such as *Veigaludwigia* and *Eunophora*.

Together, these new fossil diatom localities shed a unique light on the evolution of Antarctic lake ecosystems and taxonomic and biogeographic aspects of the Antarctic freshwater flora. Moreover, as the fossil assemblages are extremely well preserved, they provide valuable temporal constraints for time-calibrated molecular phylogenies of modern congeneric diatom taxa.

New insight about Genetic Structure of Adélie Penguin around Antarctica

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Climate changes have affected directly migration rate, survival and breeding behaviour of several seabirds' species. In Antarctica region climate change have modifying sea ice extended, free ice area and intensity of storms and winds. *Pygoscelis adelia* have circumpolar distribution, being found in whole Antarctica continent and in islands from Shetland Archipelago and Scotia Arc. This penguin species are dependent to ice free area to breed and sea ice to forage. Previous genetic population studies with *P. adelia* showed two independent lineages, one from Ross sea (Ross lineages) and another non Ross-sea (Antarctic lineages), supposed that these lineages diverged in Last Maximum glacial (LGM). In this study were analysed 144 individuals of Adélie Penguin through west Antarctica and Ross sea, using mitochondrial DNA (HVR1) and 21 microsatellites. In addition, we compare HVR1 with previous data published (127 individuals) from west and east Antarctica and Scotia Arc. Our data of HVR1 suggest high genetic diversity and low population structure around Antarctica continent and Scotia Arc. Despite Antarctica showed two evolutionary lineages was observed intense gene flown among regions, corroborated meta-population structure. However, the microsatellites data suggest genetic structure more defined, thus it is possible that gene flown of *P. adelia* have been reduced recently. Into this context, evolutionary history of *P. adelia* based in genetic data suggests that, this species was isolated in two distinct refuges, where two independent lineages rise. These lineages expanded and occupy whole Antarctica around 10,000 -15,000 years ago (LGM), followed by intense gene flown among areas. However, recent changes in Antarctica continent can be reduced the migration among colonies, consequently causing high genetic structure between Ross Sea and Antarctica Peninsula. Thus, genetic diversity of Adélie Penguin will be dependent of migrate rate and survival, changes in routes of migration, rest areas and food available will impact directly the meta-population structure. Consequently, it is important monitoring how each population (colonies) have answered to climate change.

Paternity and extra-pair copulation in Gentoo penguin and Chinstrap penguin at Elephant Island

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Recent studies have shown that despite most of the avian species being socially monogamous, they present different reproductive strategies, such as extra-pair paternity (EPP). EPP have been associated to increase of the genetic diversity of offspring and higher assistance to nest for more than one male. Penguins have a monogamous social behavior with biparental care, thus it is expected to find low extra pair paternity and sex ratio near to parity (1:1). However, there are hypothesis that adults can favor one of the sex in response to environmental conditions. In this study, we investigated the genetic mating system and secondary sex ratio of Gentoo Penguins (*Pygoscelis papua*) and Chinstrap Penguins (*Pygoscelis antarticus*) at Elephant island (61°08'S 55°07'W), South Shetlands Archipelago. For this were sampled 160 Gentoo Penguin (40 families, 80 adults and 80 chicks) and 315 Chinstrap penguin (92 families 163 adults and 152 chicks). The parentage was determined based on the analysis of microsatellites markers (8 to Gentoo Penguins, 9 to Chinstrap penguin), using Cervus software. Molecular sexing was done with P2 and P8 in agarose gel (3%). Our outcome showed high EPP in both penguin species. In Gentoo Penguin was detected in 62.4% of all offspring and 55% of the nests had at least one extra-pair young. In Chinstrap Penguin was detected in 63.2% of all offspring and 72.72% of the nests had at least one extra-pair young. In addition, to both species was detected more male than females in nest, showing slight bias to male. Male is considerate sex more expensive to growth, thus have been selected in years with good environments conditions. The EPP yet have been described to others species of penguins (Magellanic ~33%; Marasco et al. pers com,, Adelia ~10%, Pilastro et al. 2001). High rate of EPP never were previously described to one penguin species. In addition, there are not observed genetic difference between nests without EPP and nest with EPP. Thus, genetic paternity of Gentoo and Chinstrap indicate that is social monogamous behaviour, however genetically polygamous.

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Mitochondrial genomes of ostracods from the Southern Ocean

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Ostracods are small, bivalved crustaceans occurring in all aquatic habitats. They also form an important component of marine microbenthos. Phylogenetic research on Macroscaphidae from the Southern Ocean (Nunes Brandao et al. 2010) showed that species from this family with circum-antarctic distribution are in fact a species complex with different morphological and cryptic species and limited geographic distribution. Further molecular studies on this taxonomic group have been hampered by the lack of suitable markers. The small size of ostracods and low amount of DNA makes it also still impossible to apply next-generation sequencing methods (NGS) like RAD seq.

An alternative are mitochondrial genomes, which are currently easy to amplify and sequence at low cost (Hinsinger et al. 2015). Because of their length of thousands of nucleotides, mitogenomes can improve the unravelling of phylogeographic relationships and dating of evolutionary events (see, for example, Keis et al. 2013) and, through comparisons with non-Antarctic taxa, allow to detect cold adaptations as for example in amphipods from Lake Baikal (Naumenko et al. 2017) and Antarctic nototheniids (Mark et al. 2012). Up to now, only few mitogenomes are available for ostracods. Ogoh & Ohmiya (2004, 2007) sequenced mitogenomse of the Japanese, bioluminescent myodocopid ostracod *Vargula hilgendorffi* from several populations, and an incomplete, unpublished mitogenome is available in Genbank from the non-marine ostracod *Cypridopsis vidua* (Genbank accession number KP063117.1). Both species are only very distantly related to ostracods from the Southern Ocean. Here, we will present our first results on the mitogenomes of Macroscaphidae from the Southern Ocean and compare these with mitogenomes of non-marine ostracods from cold Lake Baikal, tropical Lake Tanganyika and the putative ancient asexual ostracod *Darwinula stevensoni* with a General Purpose Genotype (Van Doninck et al. 2002).

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Origin, dispersions and diversification dynamics of Epimeriidae and Iphimediidae (Amphipoda, Crustacea) from the Antarctic shelf

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The physical isolation of the Antarctic shelf and extreme life conditions contribute to its high degree of endemism. The Antarctic shelf fauna would, however, be composed of Gondwanan descendants, but also of more recent colonizers. The peculiar climatic history of this region might have provided environmental prerequisites to the radiation of some lineages, some of which might afterwards colonize the other ocean's shelves. Amphipods from the families Epimeriidae and Iphimediidae are cosmopolitan, but well-represented on the Antarctic shelf. Antarctic epimeriids (represented herein by the genus *Epimeria*) are composed of strictly endemic and presumably more generalist species, while many Antarctic iphimediids appear to be food specialists, with some of them distributed on both sides of the Polar Front. By reconstructing time-calibrated phylogenies based on mitochondrial (COI) and nuclear (28S and H3) markers and including representatives from other oceans, this study aims to investigate, for each of these two families, the origin of the Antarctic component, their propensity towards dispersion in/out of the shelf and the *in situ* diversification patterns. A comparison of observed biogeographic patterns for the two families will give insights into the influence of historical environmental factors on the evolutionary history of organisms with contrasting life history traits. In both phylogenetic reconstructions, all Antarctic and sub-Antarctic (for iphimediids) species formed a clade, sister to a non-Antarctic clade. While the precise timing of origin for the (sub-)Antarctic components could not be inferred in both cases, the (sub-)Antarctic lineages likely arose from late Gondwanan ancestors and hence, did not colonize the Antarctic region after the continent broke apart from the other fragments of Gondwanaland. Moreover, the initial diversification of these two clades occurred during the progressive transition to an Icehouse climate and would therefore be related to cold-waters. A diversification burst within one (or two) iphimediid subclade(s) might have occurred after the mid-Miocene Climate Transition (MMCT). While the Antarctic *Epimeria* lineage appears "locked in the Icehouse", iphimediids historically dispersed at least once from the high Antarctic region to sub-Antarctic islands, after the geographical isolation of Antarctica. However, based on the present taxon sampling, they do not appear to have dispersed further north than sub-Antarctic regions at any point of their evolutionary history.

Contrasting population genetics structure between Gentoo and Chinstrap penguins across the Southern Ocean

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Gentoo and Chinstrap penguin are distributed along the Antarctic Peninsula as well several sub-Antarctic islands. Although the species are sympatric in the Western Antarctic Peninsula (WAP), they show ecological differences, such as the generalist diet of Gentoo penguin compared to more specialist diet of Chinstrap penguin. The WAP has been strongly impacted by climatic change affecting the biodiversity in this region. Chinstrap is mostly decreasing the populations' abundance, whereas the Gentoo is increasing and expanding in WAP. Environmental changes can also affect species distribution and dispersal. Moreover, the Antarctic Polar Front (APF) may act as a barrier between Antarctic and Sub-Antarctic areas. Therefore, we used mtDNA (HVR1) and microsatellites from 14 breeding colonies of Gentoo penguin (*Pygoscelis papua*, n=314) and 12 breeding colonies of Chinstrap penguins (*Pygoscelis antarcticus*, n=238) along the Western Antarctic Peninsula and the South Shetlands Islands (WAP) to the Subantarctic Islands (SAI) to understand the population genetic structure and phylogeographical pattern of both species. Our results showed significant population genetics structure in WAP for Gentoo penguin, however, lack or reduced population structure for Chinstrap penguin as described for the majority of penguins species. Chinstrap penguin also showed an absence or reduced population structure between WAP and Bouvet Island, located 3,600 km away. On the other hand, Gentoo penguin shows strong population genetic structure among all Sub-Antarctic Island and WAP, but also divergent mtDNA clades. Crozet and Marion Islands are basal clades, followed by the Kerguelen Island, to Falkland Islands as well as a more recent divergence between these one and the WAP. APF a significant barrier and an important determinant of genetic differentiation for Gentoo penguin populations, but also differentiation was found between all sub-Antarctic breeding colonies. We detected a signature of expansion for Chinstrap penguin along the entire distribution and the Gentoo penguin in WAP during the last glacial maximum (LGM, about 20 kya), but stability in sub-Antarctic Islands for the colonies of Gentoo penguins. The different ecological characteristics may lead to the different phylogeographical patterns between both species. Ecological and evolutionary responses of those Evolutionarily Significant Units for Gentoo penguins may have led to different strategies to respond to climate changes such as the isolation by distance, local adaptation, and past climate scenarios.

Signals from the South; Humpback Whales Carry Messages of Antarctic Sea-ice Ecosystem Variability

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Southern hemisphere humpback whales (*Megaptera novaeangliae*) are high-fidelity Antarctic krill (*Euphausia superba*) predators that rely on krill summer biomass abundance to fuel the longest migrations known for any mammal on the planet. It is postulated that this species, already adapted to endure metabolic extremes, will be one of the first Antarctic predators to show measurable physiological change in response to fluctuating principal prey availability in a changing climate.

Through long term monitoring of the east coast of Australia migrating breeding stock (E1 as defined by the International Whaling Commission), and team advances in biomarker development, we reveal the synchronous, inter-annual (2008-2013) oscillation population energetic reserves with Southern Ocean environmental variables and climate indices. The two measures of adiposity, namely the adipocyte index (AI) and lipophilic contaminant burdens, indicated that the severe La Niña event of 2010/11 resulted in leaner migrating individuals. Further, bulk stable isotope signatures provide strong indication of population dietary compensation strategies following years indicated as leaner years.

The clear synchronicity of humpback whale dietary and adiposity signals with climate patterns in the Southern Ocean lend strength to this species role as powerful Antarctic sea-ice ecosystem sentinels. The work carries significant potential to reform long-term and circumpolar ecosystem surveillance in the region.

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Investigating spatial concordance between diving predators and prey: King penguins and myctophid fish

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In the Marine environment, the prey distribution is patchy, resulting from interaction between physical processes that influence production, vertical distribution, aggregation and predation impact. Marine predators have to cope with such heterogeneity of prey which is a major constraint on the foraging success. They should choose the habitat that yields the highest reward, as a response to spatial prey availability. Determining how the marine predators use the prey distribution is still a crucial issue. However few at-studies have investigated the foraging movements of predators in relation to real-time sampling of prey abundance through conventional assessments.

During the 2013/14 southern summer, the research cruise MYCTO-3 D offered a unique opportunity to collect simultaneous data about the mesopelagic fish (myctophid) distribution/abundance at the east of Kerguelen plateau (48°45S–50°00S; 68°45–70°58E), Indian Ocean. Myctophid are a major resource of the Southern Ocean still poorly known. Their distribution was evaluated through continuous acoustic method, coupled with scientific trawling. During the same time period, the foraging movements of satellite tracked king penguins (*Aptenodytes patagonicus*) (n=13) were studied in relation to the biotic and abiotic features of the mesopelagic environment. King penguins are deep divers, mesopelagicc foragers, and rely extensively on myctophid fish (Cherel & Ridoux 1991) especially at Kerguelen (Bost et al. 2002).

The objectives of this study were (i) to compare the various independent methods carried out simultaneously in order to provide additional information and cross-validation and (ii) to evaluate whether penguins can be used as bio-indicator of myctophid resources.

The study was able to demonstrate a concordance between the tracking data of marine predators and prey distribution provided by acoustic analysis. We compared the time spent at depth by penguins and prey biomass distributions. The penguins didn't use the areas with the most important biomass of fish. Instead they used the oceanic area where the resource is the most profitable (enough biomass and shallower) in the southern of Polar Front, especially in the branch of cold water of Antarctic Circumpolar Current. Thus, the choice of foraging area for such air-breathing predators was not driven by the total biomass available but by resource available per unit of foraging time. This is of major importance for our knowledge of predator-prey relationships.

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Foraging distribution, habitat preferences and diet of breeding Antarctic fulmarine petrels in East Antarctica

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Knowledge about the currently utilized foraging habitat and diet of Antarctic species is crucial to understand potential impacts of climate-change in the Southern Ocean and to identify overlap with the CCAMLR managed fishery in the Southern Ocean. In comparison to other groups of Antarctic top predators, little information is available for the medium-sized Antarctic fulmarine petrels.

In 2015/16 we investigated the foraging behaviour and diet of southern fulmars (*Fulmarus glacialoides*), Antarctic petrels (*Thalassoica antarctica*) and cape petrels (*Daption capense*) breeding sympatrically on Hop Island (68.82°S, 77.68°E) in the Prydz Bay region (East Antarctica).

Using state-of-the art lightweight GPS loggers, we recorded a total of 277 foraging trips, covering the entire 2015/16 breeding season from incubation to late chick-rearing in all three species, including multiple foraging trips made by several individuals. Blood, feather and egg membranes were collected from the same species, and complemented by prey items obtained in the foraging area during a marine science voyage in the 2015/16 austral summer.

GPS trajectories were separated into foraging locations and commuting legs, using wet/dry data recorded by the GPS loggers and Expectation-Maximization binary Clustering (EMbC; a novel approach based on speed and turning angle to annotate behavioural states). We present the species' foraging distribution during the different breeding stages and identify habitat characteristics (bathymetry, sea ice, chlorophyll a as a predictor of environmental productivity) to determine whether these Southern Ocean predators share foraging 'hot-spots' or if they segregate their foraging activities. Consistency of individuals in their foraging behaviour (e.g. to visit specific areas or show preferences for specific environmental conditions) were also investigated. In addition, stable isotopes were used to explore the dietary overlap between the three seabird species using isotopic niche parameterisation and estimates of resource use through mixing models.

Preliminary results suggest a strong overlap of the foraging locations of all three species at the population level throughout the entire breeding season. Similarly, stable isotope values reflecting the birds' diet during pre-laying, incubation and chick-rearing show a strong overlap among species.

High variability in migration and wintering strategies of brown skuas (*Catharacta antarctica lonnbergi*) in the Indian Ocean

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We studied movements of brown skuas (*Catharacta antarctica lonnbergi*) during the nonbreeding period originating from two populations in the southern Indian Ocean using geolocation. A total of 33 individuals were equipped resulting in 34 annual tracks. Brown skuas varied extensively in their post breeding movements, from true long range migrations to reach distant wintering zones, to short movements in the vicinity of breeding grounds. Overall, they migrated northward to overwinter in different areas in the southern hemisphere, remaining in the Indian Ocean, except two individuals that overwintered in the Benguela Current (Atlantic Ocean). Individuals clearly differed in migratory strategies targeting areas in a continuum from the subantarctic to the tropics. Wintering grounds generally corresponded to productive dynamic upwelling waters or frontal systems. Brown skuas avoided the less productive area of South Subtropical Gyre in the Central Indian Ocean. The inter-individual differences were not sex dependent since there was no evidence that males and females segregated. The migration dates varied between sexes with females leaving earlier and returning later at the breeding sites compared to males. The duration of migration depended on wintering area and sex. Males tended to migrate during shorter periods than females, whatever the wintering area. Isotopic signatures clearly indicated that birds moulted in the wintering area and during migration. The low δ15N values of feathers that grew in mixed subtropical-subantarctic waters suggest that skuas fed on low trophic level prey in these areas. The origin and consequences of such strong inter-individual variation in migratory strategies requires further investigation.

Investigation of the use of very high resolution satellite imagery to detect and monitor four whale species

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We describe and discuss the use of Very High Resolution (VHR) satellite imagery to identify, count and monitor four species of polar baleen whales; humpback (*Megaptera novaeangliae*), southern right (*Eubalaena australis*), gray (*Eschrichtius robustus*) and fin (*Balaenoptera physalus*). We investigate the spectral reflectivity of each species, the ease of identification and the behavioural and environmental factors that could influence their detection. To maximise our chances of testing the technology on whales we targeted four well known locations where each species was known to be present and the environmental conditions (cloudiness and sea-state) were known to be most suitable. We utilized the highest resolution satellite imagery currently available; the WorldView3 satellite at 31cm spatial resolution, to manually identify, count and describe whale like objects.

The ease of use of satellite imagery to detect whales, added to the potentially low cost and wide area coverage could be transformative in the census of whales in the southern ocean, but our findings suggest that it will work better for certain species and in certain environmental conditions.

Initial results agree with previous work that the main limiting factor in detection is sea surface roughness in the image (although this is also a limiting factor in aerial and boat based cetacean survey). In calmer waters the colouration of the whale in relation to its surrounding environment is a key factor in satellite detection along with behavioural factors such as the dive profile, closeness to the surface and size of the animal. Whales displaying courtship or competitive behaviour were difficult to identify with certainty, whereas whales in transit, with a more homogeneous dive pattern gave higher confidence values. Spectral profiles of each species suggest that whales with darker pigmentation – humpbacks and right whales, may not be suitable for spectral classification in clear water, resulting in the fact that automated detection algorithms will be more difficult for these species than whales with a higher spectral contrast with their surrounding environment.

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Squeezed from both ends: Decline in Antarctic fur seals in the South Shetland Islands is driven by both Top-down and Bottom-up processes

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Understanding the relative contributions of different sources of mortality in predator populations is essential to population ecology studies that can improve ecosystem models and management of marine ecosystems. Within the Antarctic bottom-up processes are widely cited for explaining penguin population declines. However, for Antarctic fur seals (Arctocephalus gazella), top-down processes are most often cited as the primary driver for declining pup production of more southerly breeding colonies where distributions overlap with an apex predator, the leopard seal (Hydrurga leptonyx). This has led to an under emphasis of the role of bottom-up drivers for controlling fur seal production within the system. I review the historical data in Antarctic pup production and provide annual pup production estimates from 2002-2016 for Cape Shirreff, Livingston Island. Age-specific natality rates and post-weaning survival estimates are provided as an indicator of bottom-up drivers and I contrast these with pre-weaning mortality and leopard seal predation rates. Fur seal pup production has undergone a dramatic declines in the last decade (12.1% per annum since 2002). Since 1998, natality rate has also declined 14%, largely driven by poor recruitment and an aging population. However, age-specific natality rate has also declined. For the same period predation rate has increased 4% per year. I discuss the relative roles of bottom-up and top-down contributions to the decline in fur seals and how the changing physical environment has led to a trophic cascade and changes in community structure of the coastal marine ecosystem of South Shetland Islands.

Contrasting behaviour between two populations of an ice-obligate predator in East-Antarctica

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Winter is a critical period for capital breeders such as Weddell seals that must optimize resource acquisition and storage to provision breeding in the subsequent spring. However, how Weddell seals find food in the winter months remains poorly documented. We equipped adult Weddell seals during winter with satellite relayed data loggers at two sites in East Antarctica: Dumont D'Urville (n = 12, DDU) and Davis (n = 20). We used binomial generalized mixed effect models (GLMM) to investigate Weddell seals' behavioural response (i.e. "hunting" vs. "transit") to physical aspects of their environment (e.g. ice concentration etc). Weddell seal foraging was concentrated to within 5km of a breathing hole, and they appear to move between holes as local food is depleted. There were regional differences in behaviour so that seals at Davis travelled greater distances (three times more) and spent less time in hunting mode (half the time) than seals at DDU. Despite these differences, hunting dives at both locations were pelagic, concentred in areas of high ice concentration and over areas of complex bathymetry. There was also a seasonal change in diving behaviour from transiting early in winter to more hunting during winter. Our observations suggest that Weddell seal foraging behaviour is plastic and that they respond behaviourally to changes in their environment to maximise food acquisition and storage. Such plasticity is a hallmark of animals that live in unforeseeable environments such as the high Antarctic where resources are unpredictable.

Estimating pregnancy rates from diving behavior: A comparison across the range of Southern elephant seals

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Female southern elephant seals (*Mirounga leonina,* SES) are top predators of the Southern Ocean and adjacent ecosystems, where they play an important ecological role over large spatial scales (millions of km^2) as major consumers of squid and fish in the Southern Ocean (Bradshaw et al. 2003, Daneri & Carlini 2002). Female SES display a characteristic life cycle, returning to land only twice a year to breed during the austral spring (September-November for females) and to molt in the austral summer (January-February for females), spending >80% of their annual cycle at sea (Hindell and Burton 1988, Slip et al. 1994, Slip and Burton 1999). Successful (i.e. full-term and gave birth) and unsuccessful (i.e. did not give birth) pregnancy rates are critical information to understand basic population dynamics, however the cryptic lifestyle of elephant seals makes acquiring those rates difficult. Northern elephant seals (*M. angustirostris,* NES) have an analogous annual cycle in the northern hemisphere, and the striking similarities in their diving behaviour and physiology makes it possible to conduct comparisons across species. Using long-term data on diving behaviour from 223 NES that returned to land to breed (i.e. pregnancy status confirmed), we developed a robust method to predict at-sea pregnancy status by relating day of the trip and daily mean dive duration using a General Additive Mixed Model (GAMM). The dive duration of pregnant females increased until week 19 of pregnancy, when the duration of their dives reaches a plateau and later decreases sharply. The dive duration of non-pregnant NES, on the other hand, increases more rapidly throughout their trip, does not plateau until around week 30, and reaches a higher duration compared to their pregnant counterparts.

These models allow us to predict the pregnancy status of female NES for whom only diving data was collected. We will apply this method to compare the rate of successful pregnancies between SES colonies (Macquarie, Kerguelen, South Georgia, and South Shetland Islands). The South Georgia stock, has not shown the long-term population decline of many other stocks of elephant seals (e.g. Kerguelen and Macquarie), but instead experienced a rapid recovery after the end of the exploitation and is now considered stable (Laws 1994) which may imply that the dynamics of the South Georgia stock are different from those of stocks elsewhere (Kock and Shimadzu 1994). This study will provide important demographic rates for these populations, and will help explain differences in observed trends.

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Hotspots in the distribution of the top predators – seabirds, cetaceans and pinnipeds – in polar marine ecosystems.

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Observations of major hotspots in the at-sea distribution of top predators were tallied during recent years in both polar areas on board icebreaker RV *Polarstern*, Bremerhaven, Germany. They concern cetaceans: fin whale *Balaenoptera physalus*, humpback whale *Megaptera novaeangliae*, Southern right whale *Eubalaena australis*, as well as pinnipeds: crabeater seal *Lobodon carcinophaga*, harp seal *Pagophilus groenlandica*, Antarctic fur seal *Arctocephalus gazella*, and seabirds: grey-headed albatross *Thalassarche chrysostoma*, Southern fulmar *Fulmarus glacialoides,* little auk *Alle alle*, common and Brünnich's guillemots *Uria aalge* and *U. lomvia*, Antarctic prion *Pachyptila desolata* and kittiwake *Rissa tridactyla.* Numbers tallied during a few 30min transect counts (i.e. a few tens nm) concerned can reach thousands of individuals and represent up to 98% of all individuals of the species tallied during the whole expedition. Selected examples of maximal numbers in limited areas are: 1,950 common guillemots out of a total of 1,975 and 133 humpback whales out of a total of 149 (Joiris 2011), 304 fin whales out of 308, 6,945 grey-headed albatrosses out of 6,970 and 76,800 southern fulmars out of 77,000 (Joiris & Dochy 2013), 2,000 crabeaters out of 2,260 (Joiris & D'Hert 2015). Moreover very local concentrations were encountered such as 1,500 little auks during 10min, i.e. less than 2 nm (Joiris et al. 2014). The hotspots were basically observed in autumn, often in areas visited by scientists mainly in summer and sometimes in winter, and located on or around icebergs. They often concern cetaceans, pinnipeds and seabirds at the same location (see higher). They can thus be considered reflecting post breeding and pre-migration gatherings and probably correspond to very high prey (krill) concentrations. Practical consequences are on the one hand that they lead to drastic underestimations of actual densities if undetected. On the other hand, such data should obviously not be included in density calculations.

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Coastal polynyas: A top predator winter oasis in East Antarctica

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Polar marine predators depend upon multiple trophic levels. Understanding their reliance on key physical and biological features is crucial to our knowledge of the structure and function of polar ecosystems. Southern elephant seals (*Mirounga leonina*) are an important consumer of Southern Ocean resources and among the variety of large scale foraging strategies exhibited by this species, some individuals consistently migrate to Antarctic shelf waters. One key physical feature of Antarctic shelf waters is the presence of persistent open water areas known as Antarctic coastal polynyas, which offer access to breathing holes within the winter sea ice cover, especially for southern elephant seals. Antarctic coastal polynyas often harbour high biological productivity in spring leading to an extended period of secondary production. This seasonal bloom persists over time, maintaining ecosystems that may support large populations of feeding seabirds and mammals throughout the ice season. We investigated the seasonal use of polynyas by 23 juvenile males equipped with satellite-linked data recorders between 2004 and 2014 that undertook post-moult trips from Isles Kerguelen to the Antarctic continental shelf during winter. We assessed whether diving and foraging behaviour were affected by rates of sea ice formation in the polynyas and whether specific oceanographic conditions differed between polynyas and surrounding winter sea ice regions within the Antarctic shelf, slope. A total of 18 males visited 9 different polynyas, spending on average 25 ± 20% of their total recorded trip inside polynyas, but up to 75% of a trip. Their foraging activity was significantly higher and dives shallower inside polynyas (296 ± 159m, median ± standard deviation across individuals) compared to outside (350 ± 201m, on the shelf). Inside polynyas and over the shelf, seals performed both pelagic (45 ± 34%) and benthic (55 ± 34%) dives in similar proportions. Foraging activity was higher in cold Antarctic surface water inside polynyas potentially because prey are slowed down by the lower temperatures. The fall transition in the water column stratification (in June) was found to be a key time for the winter foraging ecology of elephant seals, corresponding to the highest foraging activity, the longest dive durations, and the deepest dives of the season inside polynyas. We hypothesize that seals may take advantage of the secondary production resulting from the deepening of the seasonal mixed-layer, entraining the remnant deep chlorophyll maximum into the surface layer and presumably stimulating an autumn bloom.

Monitoring the northernmost colony of Emperor penguin *Aptenodytes forsteri* at Snow Hill Island, Weddell Sea, Antarctica

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Antarctic bird populations have been much studied over the last decades as bioindicators of the nature of variability in the Southern Ocean marine ecosystem. Penguins are a dominant component of the avian biomass of the Antarctic continent and they can be highly sensitive to climate change. They are important consumers at these high latitudes. Most of the studies have been focused on the role of food supply and the extent of sea ice. Currently known that breeding colonies of emperor penguin *Aptenodytes forsteri* are distributed throughout the Antarctic seasonal pack ice zone between 64°S and 78°S from April to December. Even today, new colonies are added to the already known. One of the last colonies of emperors penguins discovered is situated on the south coast of Snow Hill Island, constituting the northernmost colony known in Antarctica, this adds a special interest in regard to their study and research. There is growing concern about the future of some Antarctic species in view of the changes observed in recent years with the extent and thickness of the sea ice pack related to global warming. The Emperor penguin depends on sea-ice pack as a breeding platform during the winter-spring months also it is the molting habitat and the foraging environment. Actual climate models predict a decrease in this Antarctic penguin population as the result of the decline in sea-ice distribution. We conducted aerial census of adult individuals for many consecutive years for the same period of the breeding chronology. We also explored the colony by land, making an estimated counting of the number of chicks when we visited them. Unlike what is observed for other colonies located in the eastern Antarctic, whose populations are decreasing, this colony has increased significantly in the last years. This is particularly striking if we take into account the signs of global warming in this area. The assessment of this penguin population located in the Weddell Sea will contribute to the estimate of total predator biomass in Area 48.

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New censuses in a recent counting colony of Emperor penguin *Aptenodytes forsteri* at Larson Ice Shelf, Weddell Sea, Antarctica

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There is growing concern about the future of some Antarctic species in view of the changes observed in recent years with the extent and thickness of the sea ice pack related to global warming. The Emperor penguin has previously been considered as a sea-ice obligate species. It depends on sea-ice pack as a breeding platform during the winter-spring months also it is the molting habitat and the foraging environment. Actual climate models predict a decrease in this Antarctic penguin population as the result of the decline in sea-ice distribution. During the last hundred years have been discovered new breeding colonies of emperor penguins. Even today, new colonies are added to the already known, reaching a total of 46. Breeding colonies of emperor penguin are distributed in coastal locations around the Antarctic continent between 64°S and 78°S from April to December. Most of these colonies occur on stable fast ice with only two of the total on land. Although many census works have been carried out at few colonies, the total number of breeding pairs and the size of the global population are unknown. Recently, four colonies on ice shelves have been observed and two of them have recently been discovered, being Peninsula Jason´s colony one of the new. The Antarctic Peninsula is one of the places in the world where most signs are observed of global climate change. Recent studies suggest that emperor penguin populations will decline in future decades due to climate change. Current climate models predict that future loss of sea-ice around the Antarctic coastline will negatively impact emperor numbers. We monitored the breeding population of the last three years consecutively. Studies involving regular monitoring allow a determination of the fluctuation in Emperor´s breeding populations and obtaining long-term demographic dataset. The aim of this study is to update the size of the breeding population colony of Emperor penguin at Jason Peninsula.

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Southern elephant seals at Elephant Island, Antarctica –1988-2016: why are their numbers declining?

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In 1997 a pilot study was established within the Brazilian Antarctic Program (PROANTAR) to investigate pinniped occurrence and distribution at Elephant Island (61°05'S; 055°20'W), South Shetlands, Antarctica. Thereafter, the presence, distribution and a description of most activities exhibited by pinnipeds on the island has been monitored, especially those of Southern elephant seals (Mirounga leonina) and Antartartic fur seals (Arctocephalus gazella). Surveys were carried out at Stinker Pt., Elephant Is. during the austral summers of 1998/1999, 2003/2004, 2004/2005, 2005/2006, 2007/2008, 2008/2009, 2009/2010, 2015 and 2016. Daily surveys conducted throughout the study period recorded the temporal and spatial distribution of seals. Our results show similar trends among field seasons from 1988 to 2009. However there has been an increase in the number of AFS and a decline on the number of pups counted. The total number of SES gradually increased from early November to late December, decreasing after that when the number of AFS increased. The maximum number of SES registered was 767 in 1998/1999, 768 in 2003/2004, 692 in 2004/2005, 681 in 2005/2006. The maximum number of pups was 85 in 1998/1999, 149 in 2003/2004, 155 in 2004/2005 and 147 in 2005/2006, corresponding to an increase in numbers. However from 2007-2016 both the total numbers of seals counted and number of pups have decline (857 to 571 and 147 to 76, respectively). Assuming that the number of pups is likely to reflect the number of adult females breeding in the area, the number of breeding individuals at Elephant Island has declined in the past decade. There has been a slight association between low numbers of pups and ice covered breeding beaches. It is important to continue monitoring the occurrence and abundance of pinnipeds at EI in order to enable future comparisons and a more detailed analysis of the present trends reported here in light of potential environmental variability

Habitat preference of southern elephant seals females (*Mirounga leonina*) during breeding season at Peninsula Potter, Isla 25 de Mayo/King George Island, Antarctica.

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In the present study we analysed, using the HAVISTAT 2.0 software, habitat preference of southern elephant seals females during breeding season at the Antarctic Specially Protected Area (ASPA) N132 "Peninsula Potter". Daily census were conducted during 14 (2002 to 2016 except for 2009) breeding seasons and all the data included in the analyses were those obtained at female peak haul-out. The 7 kilometres of coastline in the study area was divided in seven sectors based on the type of substrate; the slope and orientation of the beaches where animals breed. For 11 of the 14 breeding seasons under study around 86 % of the females at Peninsula Potter prefer to breed in a sector of 1.4 kilometres of beaches with sand and gravel substrate and with gentle slope. Thus, during those seasons on land density in that sector was in average 181 females per kilometre of coastline, a number more than 4 times greater than it was previously reported (Carlini et. Al 2006). Additionally, male on land density was also higher at that sector with an average of 18.5 males per kilometre of coastline compared to the 6.7 males for the entire colony. This relative high density situation and the great proportion of males challenging for access to harems could be leading to high levels of harassment and disturbance of the breeding females. Those are probably some of the factors influencing the distribution of the female borne and marked at Peninsula Potter in nearby islands as it was observed and could also explain the seasonal fluctuations in the number of females breeding at peninsula Potter recently reported (Mennucci et. al 2012).

Finally, we also found evidence that during particular seasons some climate anomalies like high precipitation rates and snow accumulation alters the preference of the females for the habitat described. These findings are relevant to conservation efforts and management strategies of protected area since the evidence of an habitat selection of this species had to be considered not only to preserve that habitat in the ASPA but to be aware of potential new areas with those characteristics that may need to be included into protected sites.

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Summer abundance of pack ice seals in the vicinity of Primavera Station, Danco Coast, Western Antarctic Peninsula

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Antarctic pack ice seals are top predators that depend of sea ice to breed, moult, and rest. Therefore, the knowledge of their abundance and trends may be useful to detect changes in the Southern Ocean environment. During 4 consecutive austral summers seasons (January –February) we counted pack ice seals observed in ice floes. Counts were made from zodiac boats between 10 am and 16 pm (local time) in an area of 14 nautical mile^2 in the vicinity of the Argentinean station Primavera. The study area includes three coves (Cierva, Escondida y Santucci Cove) and a series of islands. Climate during summer use to be benevolent providing shelter to seals that hauling out in floes. Except for 2014 season, the most abundant species during the study period (2012-2015) was the leopard seal (*Hydrurga leptonux*) with a mean annual density that range from 0.7 to 1.3 seals per n.m^{-2}. Crabeater seal´s (*Lobodon carcinophaga*) mean annual density range from 0.1 to 3.4 seals per n.m^{-2} while Weddell seals (*Leptonychotes weddelli*) density range from 0.2 to 0.4 seals per n.m^{-2}. A negative trend in the number of leopard seals was observed for the study period ($F = 7.14$ $P = 0.01$, $r^2 = 0.37$) while the numbers of crabeater seals increased ($F = 6.43$ $P = 0.01$, $r^2 = 0.35$). These opposite trends in the abundance of leopard and crabeater seals might reflect competition for resources. Particularly, for animals captured and sampled in this the study area Rogers et al (2014) observed changes in the diet of leopard seals that shifted from eating penguins and seals to a krill based diet. Therefore, it is possible that leopard seals are looking for new areas to moult in order to avoid competition for the same prey with a specialized krill eating species that use to forage in great pods. Considering that crabeater seals are highly mobile species with seasonal migration for foraging, a long time survey could elucidate the trends observed in this short period. Nevertheless, the data presented here is of a great value since represent the first report of seals abundance for the waters surrounding the Antarctic Specially Protected Area N°134 "Punta Cierva".

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Projected climate induced changes to Adélie penguin populations

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There is rapid climatic warming in the Western Antarctic Peninsula (WAP) (Vaughan et al. 2003), with cooling or stable conditions in other sectors of the continent (Cimino et al. 2013). Adélie penguins (*Pygoscelis adeliae*) have been declining in northern sectors of the WAP since the 1970's. The foodweb of the WAP marine ecosystem is trophically short; krill feed on phytoplankton and penguins mainly feed on krill. Therefore, it is often assumed that any climate-driven change in lower trophic levels (phytoplankton) would be reflected in higher trophic levels. A shift towards smaller phytoplankton cells under warmer climates (Montes-Hugo et al. 2009) was the hypothesized explanation for krill declines (Loeb et al. 1997; Atkinson et al. 2004) in the northern WAP. These fundamental changes in the lower trophic levels could be transferred up the short WAP food web, resulting in a decline in Adélie penguin populations through a bottom-up trophic cascade (Ducklow et al. 2007; Schofield et al. 2010) or through competition for krill with other krill predators (Trivelpiece et al. 2011). However, analyses of Adélie penguin foraging dynamics (Oliver et al. 2013; Cimino et al. 2016b), and local (Bernard and Steinberg 2013) and regional (Steinberg et al. 2015) krill surveys suggest that overall krill declines or competition for krill resources may not be the only determinants of Adélie penguin declines in the WAP. A warming climate appears to be acting on Adélie penguin chicks directly through increased precipitation on unprotected chicks leading to higher thermoregulatory costs (Chapman et al. 2011; Cimino et al. 2014) as an additional population stressor Global climate model projections for the WAP show continued warming compared to the rest of Antarctica. We estimated the future changes in Adélie penguin populations for the entire Antarctic continent by merging historic satellite observations with climate model projections (Cimino et al. 2016a). We find that WAP Adélie penguins will be the most vulnerable to climate change while colonies in the Amundsen Sea, Ross Sea, East Antarctica and Enderby Land will be relatively stable. Our analysis suggests that by 2060, 25-60% of Adélie penguin colonies will be in decline due primarily to warming effects that are outside of historic climates.

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Cetaceans as indicators of historical and current changes in the Antarctic ecosystem

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Systematic monitoring of large whales and their environment was carried out for a period of 26 years (1987/88-2013/14) in the Indo-Pacific sector of the Antarctic (70°E-170°W, south of 60°S). The published information on demographic and biological parameter trends from this monitoring was reviewed and interpreted in the context of historical and current changes in the Antarctic ecosystem under two hypotheses: the 'krill surplus' hypothesis in the middle of the past century, and the hypothesis of recovery of krill-eater whale species since the 1980's. The conceptual background followed the schematic diagram of ecosystem perturbation in the Scotia Sea (Trivelpiece et al., 2011). Parameters investigated were the trends in whale's distribution and abundance, recruitment, blubber thickness, fat weight, girth, stomach content weight and age at sexual maturity. Regarding historical changes, the increased krill availability in the middle of the past century (due to the depletion of blue, fin and humpback whales by commercial whaling) could have been translated into better nutritional conditions for some krill predators like the Antarctic minke whale, resulting in a decreasing trend in the age at sexual maturity (ASM) between 1940 and 1970. Whales maturing at younger ages favoured an increase in the recruitment rate and total population size of this species in a similar period. Regarding current changes, the evidence shows a sharp recovery of humpback and fin whales since the 1980's, which coincide with a deterioration of nutritional conditions of Antarctic minke whale (species that once benefited by the 'krill surplus' at the mid of the past century) as revealed by a decrease in energy storage and stomach content weight. This observation is consistent with the stable trend of age at sexual maturity and recruitment for this species, after the 1970's. On the other hand, regional populations of the krill-eater Adelie penguin in similar geographical longitudes have almost doubled in abundance since the 1980's and have been increasing since the earliest counts in the 1960's. Decrease in availability of krill for Antarctic minke whale could have resulted from direct competition with other recovering krill-eater large whale species. To investigate the plausibility of this hypothesis further information on krill biomass trends in the research area is required.

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Searching for Antarctic Seabirds with Landsat

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Breeding colonies of the Antarctic Petrel (*Thalassoica antarctica*) are an appealing target for satellite remote sensing because colonies are often found on isolated nunataks far from inhabited stations, some up to 200km from the shoreline. Indeed, while some 35 Petrel colonies are known to exist, breeding population estimates from known colonies are far smaller than at-sea population estimates suggest. We expect, therefore, that it may be possible to locate and map many of these unknown breeding colonies using satellite imagery. We have developed an algorithm that can detect the largest of the known Antarctic Petrel colonies and the algorithm has been applied in a continent-wide survey using Landsat data. The algorithm is based on earlier studies of *Pygoscelis* spp. penguins which found that satellite remote sensing can detect the unique spectral features of guano-covered surfaces. Petrel colonies are similar in many ways to those of the penguins, but there are some significant differences that affect the accuracy and errors of detection. In terms of similarities, Antarctic Petrel colonies can be very large and they are typically situated on exposed rock outcrops with nests packed closely together. On the other hand, Petrel colonies are found on steep slopes and are therefore subject to more weathering and shadowing than those of the penguins, which nest only in flatter terrain. Furthermore, the Petrel diet typically has a higher proportion of fish-to-krill than the penguin diet, and Petrel guano is thus more likely to be deficient in the chemical constituents (krill carotenoids and chitin) that make penguin guano such a unique and easily detectable target. We report on the theoretical basis of our Petrel detection algorithm, the expected colony detection errors of commission and omission, and the overall results of our continent-wide survey using Landsat data.

Acoustic seasonality and behaviour of Antarctic blue and fin whales off the Maud Rise, eastern Weddell Sea

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Vocalisations of Antarctic blue and fin whales were recorded on the Maud Rise in the Southern Ocean between January and September 2014 using an autonomous acousic recorder (AAR). A random forest model was used to determine the important predictors of blue and fin whale call occurrence (call presence or absence) and rates (calls per hour) between different seasons. Diel call rates of both whale species varied between seasons. Call occurrences and rates of blue whale calls were detected throughout whole period of our study (although peaked in March), suggesting that not all animals migrate to low latitudes but some animals remain in the Antarctic in the austral winter. In contrast, fin whale calls were only detected in January and March; suggesting seasonal presence in the Maud Rise. Month was the most important predictor of blue whale call occurrence; whilst distance to the ice edge and time of the day were the moderately and least important predictors respectively of blue whale call occurrences. Month was the most important predictor of fin whale call occurrence. Blue whale feeding D-calls were only recorded in autumn and were primarily predicted by month; and temperature at the AAR depth and time of day were the least important predictor of D-call rates. Blue whale Z-call rates were most importantly predicted by temperature at AAR depth; followed by months and time of the day as moderately important predictors of Z-call rates. Distance to ice edge was the least important predictor of Z-call rates. Months were the most important predictor of fin whale call rates followed by distance to ice edge as the moderately important predictor and time of the day as the least predictor. Our work verifies the Maud Rise as an important habitat of blue and fin whales whilst identifying factors determining their presence and behaviour in the area.

Drivers of change in Adélie penguin populations: the Ross Sea data set as a catalyst for enquiry

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Adélie penguins *(Pygoscelis adeliae)* are an indicator species used to detect and monitor the effects of environmental change on Antarctic marine ecosystems. Since the early 1980s, New Zealand has conducted an annual census of Adélie penguins in the Ross Sea region, with data submitted to the Commission for the Conservation of Antarctic Marine Living Resources (CCAMLR) Ecosystem Monitoring Programme (CEMP). Annual changes in the abundance and distribution of Adélie penguins in the Ross Sea can be considered in relation to sea ice extent, weather, and other climate parameters in order to distinguish between responses due to natural events and those induced by commercial exploitation. The long-term data set is valuable for characterising Ross Sea ecosystems, developing models of ecosystem resilience under changing environmental conditions, investigating the impacts of fishing and invasive species, and analysis of site-specific environmental relationships and species interactions. Importantly, the data set also provides a baseline for research and monitoring associated with the Ross Sea Marine Protected Area. This presentation will highlight the value of long-term records of top predator abundance and distribution, and discuss the potential for broader utilisation of New Zealand's Ross Sea Adélie penguin census data.

The year-round distribution of the grey-headed albatross *Thalassarche chrysostoma* at sub-Antarctic Marion Island

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The grey-headed albatross *Thalassarche chrysostoma* is an endangered species facing several at-sea threats including climate change and incidental bycatch in fisheries. Therefore increased knowledge of its foraging grounds and distribution has consequences for its conservation.

At sub-Antarctic Marion Island, the larger of the Prince Edward Islands (PEIs), we tracked foraging trips of breeding grey-headed albatrosses during four years between 2012 and 2017 using GPS loggers, and recorded their year-round distribution from 2002 to 2004 and 2012 to 2017, using light-level Geolocation Sensors (GLSs).

When constrained to the breeding site, foraging trips during incubation were significantly more wide-ranging with longer trips, both in distance (5139 ± 2382km, using a 60min sampling interval) and duration (14 ± 3d), extending farther (1674 ± 904km) from the island, compared to foraging trips during brood-guard, when birds remained closer to the island (619 ± 279km) and covered less total distance (1610 ± 842km) in fewer days (4 ± 3d). The core use area during the brood-guard stage was southwest of the island, with little variation among years, and overall 39% was within the PEI MPA. During incubation, however, the core use area, of which only 14% is within the MPA, extended north and both east and west of the island where birds are exposed to high tuna and billfish catches.

Several migration strategies were observed among non-breeding birds; some remained near the island in the breeding home range; others travelled to more distant foraging areas east, west or both east and west of the islands; while some circumnavigated the Southern Ocean one or more times. Core use areas, which overlapped <10% with MPAs overall, were identified in the mid-Atlantic, the south-east Pacific, the South Indian Ocean and near the PEIs. The last two extend farther north into areas of high tuna and billfish catches.

At different spatial and temporal scales, the distribution of grey-headed albatrosses varies. Though it is unrealistic to set aside no-take MPAs on such a large scale, important areas which they utilize can be protected by enforcing the strict application of anti-bird bycatch measures in these locations. This is an essential next step in ensuring their conservation.

On-shore density as potential driver of at-sea foraging behaviour in two sympatric, central-place marine foragers

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Segregation between colonies of central-place foragers is commonplace and presumably due to the distance required to travel to conspecific competitors' foraging area as well as competition avoidance (Furness & Birkhead 1984; Cairns 1989; Wakefield *et al.* 2013). At the same time, individuals from the same colony, and even rookeries within a colony, also display foraging site fidelity (Lowther *et al.* 2011; Thiebot *et al.* 2011; Baylis *et al.* 2012; Arthur *et al.* 2015; Wege *et al.* 2016). Fidelity to foraging sites has long been regarded as conferring long- or short-term benefit to the individual (e.g. Bradshaw *et al.* 2004). However, as populations grow and the number of individuals foraging in an area increases, we would expect foragers to deplete patches and the potential for competition to increase (Furness & Birkhead 1984; Cairns 1989). We hypothesized that forager fidelity to preferred foraging areas in high-density scenarios might not always carry some inherent advantage and even be detrimental. We tested whether on-shore density of two non-territorial marine central-place foragers with differing population dynamics – Subantarctic (SAFS; *Arctocephalus tropicalis*) and Antarctic fur seals (*A. gazella*; AFS) – influenced foraging behaviour in terms of foraging site fidelity and foraging effort. Contrary to the predictions, levels of foraging site fidelity within and between individuals were highest at the high-density rookeries. Females from the high-density AFS rookery had the highest amount of overlap in home rage with each other (summer: 37.2%; winter: 18.6%), followed by high-density SAFS females (summer: 31.7%; winter: 15.2%), and lastly low-density SAFS overlapped the least (summer: 24.8%; winter: 11.3%). Several measures of diving behaviour (a proxy for foraging effort), was also higher at the high-density rookeries; however, differences between rookeries and species were relatively minor. Daily cycles, lunar phases, and seasonal fluctuations overshadowed most of these rookery differences in diving behaviour. In this study, on-shore density did not influence foraging site fidelity or foraging effort. Nevertheless, this study provides a new way of thinking about foraging site fidelity and the local scale at which it might affect foraging behaviour.

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Modelling abundance of Antarctic mosses using presence-absence data

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Climate change and increasing human activity in Antarctica pose threats to the vegetation that occupies the ice free coastal areas of the continent. These pressures may eventually lead to localised extinctions or colonisations of new species, but in these slow growing and low diversity polar communities current impacts may only be apparent as gradual changes in abundance. Nevertheless, it is often cheaper to collect data in presence-absence format, and indeed it may be all that is possible for cryptic species where small samples are necessary for accurate identification while minimising impact. The objective of this study was to examine how presence-absence data for Antarctic mosses could be used to estimate current trends in relative abundances of each species.

To provide a theoretical basis for the study, we simulated presence-absence sampling from communities with a known abundance. These models showed that there were non-linear relationships between the probability of presence and the expected abundance. The expected abundance remained low until the probability of presence exceeded ~60% and then increased sharply. This suggested that models based on probability of presence may exaggerate niche width and place undue emphasis on small marginal populations.

To validate the theoretical models, we collected presence-absence data on mosses from 60 quadrats spanning two sites in the Windmill Islands region of East Antarctica. We modelled probability of presence along a water availability gradient and then estimated abundance using the theoretical model. Results were compared with the cover from photos of the quadrats. As expected, we found that the probability of presence models overestimated the niche width of species and the expected cover of each species. The modelled abundance was a less biased and more accurate representation of the cover of each species.

This study highlights that it is possible to estimate the abundance of species, even if data is only collected in presence-absence format. Care should be taken when using probability of presence models for conservation planning, as they can exaggerate the niche width of species and may lead to conservation resources being wasted on marginal sink populations.

Priority ranking and decision making to prevent the arrival and establishment of exotic species in Antarctica using the Climate Matching Hypothesis

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Invasive species are one of the most important threats to Antarctic terrestrial biodiversity. Prevention is the most cost-effective response, it implies localising the possible propagule sources and the most vulnerable areas to establishment. This can be done using the climate/environmental matching hypothesis which states that species should have higher probabilities of establishing in a new area if the climate and physical environment closely match those of their native range and is associated with establishment success.

We computed Climatic Euclidean Distance (CED) using environmental PCAs to obtain a 10 arc-minutes resolution map describing climate similarity between the world and Antarctica. We found that almost 75% of terrestrial areas are more similar to Antarctic climate than the two most dissimilar Antarctic regions.

Secondly, we searched for Antarctic climatic analogues comparing each cell of the world with those Antarctic locations showing the lowest CED. These areas represent a small proportion of Antarctica (~4%). Among protected areas, the Antarctic Specially Protected Area 124 in Ross Island displayed the highest scores, with corresponding climatic analogues in Greenland.

Finally, we evaluated the risk of invasion for 59 species of insects introduced to Sub Antarctic islands by calculating three indexes. Almost 40% of the species completely occurred in regions that are more similar to Antarctic climate than the two most dissimilar Antarctic regions. Over 70% of the species showed phenotypic plasticity responses to Antarctic climates and 60% showed specialisation to Antarctic-similar environments.

Our results provide a tool for priority ranking and decision making to prevent the arrival and establishment of exotic species in Antarctica.

Acoustic data assimilation in a micronekton model: a method to study species assemblage ?

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SEAPODYM-MTL is a parsimonious model simulating biomass distribution of micronecton (organisms from 2 to 20cm like myctophids, krill...). In the model, micronektonic organisms are divided into 6 functional groups according to their diel vertical migration behavior (Lehodey et al, 2010). Their dynamics is driven by temperature and oceanic currents. Micronekton recruitment is seen as a transfer of energy from primary production (Jennings et al, 2002). The amount of energy allocated to each micronekton group is estimated by acoustic data assimilation (Lehodey et al, 2015). By comparing model predictions and acoustic data, it is possible to estimate mean target strength for each group.

Here we present data assimilation experiments in SEAPODYM-MTL focused on the southern ocean. Parameters are estimated for each interfrontal zone in the southern ocean (such zones are thought to be homogeneous from an acoustic point of view, Behagle et al, 2014). Optimized model predictions are reconstructed for the whole southern ocean based on several model parameterizations. Using these optimized model predictions and acoustic data in each zone, we will be able to estimate mean target strength of the population and compare it to the acoustic characteristics of organisms caught in such a zone. This new approach might be used to study differences of species assemblage in the southern ocean.

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A modelling tool to assess dispersal abilities of Antarctica species

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During environmental changes in Antarctic ecosystems, biota faces three possible outcomes: adaptation, migration or extinction. Successful migration depends on dispersal behaviour which allows individuals to move from natal to reproductive sites or between different reproductive sites. Dispersal is thus an essential key in the ability of Antarctic biota to find refugia and therefore to survive environmental changes. Knowledge of this kind of past and current survival strategies is crucial to predict biota responses to future climate changes (Fraser et al. 2012).

To this end, the regional hydrodynamic model COHERENS (Luyten 2011) is currently implemented with an horizontal resolution of 10 km over a part of Antarctica which covers the Weddell and Scotia seas and surroundings of the Antarctic Peninsula. COHERENS will be coupled to the Louvain-la-neuve ice model (LIM; Vancoppenolle et al. 2009). The Lagrangian particle module of COHERENS will be adapted and used to study the dispersion of several Antarctica species such as the bivalve *Lanternula elliptica* and the fish *Notothenia. rossii* during their egg and/or larval stages. This modelling tool will help understand how dispersal of selected species is influenced by ocean circulation, biological traits and habitat preferences. The tool will also allow to assess the connectivity of populations in the considered geographic area and to estimate the influence of dispersal on species survival during changing environmental conditions (*i.e.* warming of the ocean, increase in fresh water flux)

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Improving the quality of species distribution models at large spatial scale to better future predictions

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The Southern Ocean is one of the regions on Earth that has experienced the fastest climate change over the last 30 years. Environmental consequences such as increase in sea water temperature, shifts in marine front position, seasonal changes in sea-ice extent will impact benthic communities. In this context, determining the factors that drive species distribution is fundamental for conservation issues, as understanding the impact of climate change on species communities is a prerequisite to develop appropriate conservation strategies.

Many works have stressed the need to improve the quality of sampling effort in macroecological and biogeographical studies of the Southern ocean. This idea was supported by the Census of Antarctic Marine Life (CAML), a 5-year project that aimed to improve our knowledge of all levels of marine life in the Southern Ocean. Despite the numerous oceanographic cruises led under the umbrella of the program, gaps still persist in our knowledge of species distribution and diversity in non- and little-explored areas. Species distribution modeling can be used to improve our knowledge of species distribution. Procedures were developed for predicting species distribution over vast areas and quantifying species – environment relationships.

This was applied on *Antarctic echinoids*, which are a common component of benthic communities. Echinoids occur in a large range of habitats from coastal areas to deep sea and *show various ecological traits including nutrition and reproductive strategies. Modeling was performed using occurrence data from* a coherent dataset including over 7100 georeferenced records obtained during 150 years of sampling effort.

Our main aim was to produce robust species distribution models and predict potential shifts in species distribution with regards to environmental changes. We tested the performance of ten different modeling procedures and the effect of the chronological addition of new records on model performance, comparing periods before and after CAML cruises and the consequent increase of sampling effort. Then, we quantified and corrected our models for sampling bias. All analyses were performed with R and incorporated in a GIS.

Modelling present and future distributions of Southern Ocean Lanternfish

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Lanternfish of the family Myctophidae are the most abundant and ecologically important family of pelagic fishes in the Southern Ocean (Murphy et al., 2007, Barrera-Oro, 2002) yet their vulnerability to climate change is largely unknown. To fill this gap, we aim to understand which environmental factors are driving lanternfish distribution patterns throughout the Southern Ocean, and to project these distributions in to the future under multiple climate change scenarios.

Using the software MaxEnt, correlative species distribution models (SDMs) were developed for ten species of lanternfish, including four species known to be important prey items of the King Penguin (*Electrona carlsbergi*, *Protomyctophum tenisoni*, *Krefftichthys andersonni* and *Gymnoscopelus nicholsi*). 3,000 occurrence records were collated and a suite of surface and midwater abiotic factors were used as environmental predictors at approx. 25x25km resolution. Following Boria et al. (2017), SDM settings were adjusted to maximise performance and prevent overfitting. Best performing models were evaluated using the Omission Rate and Area Under the Curve (AUC) scores. The relative importance of each variable was calculated using a jack-knife procedure. Finally, the optimised models were used to project distributions under future ocean conditions (RCP8.5, 2060) simulated by ten climate models.

All SDMs gave high model performance (AUC score 0.82-0.92). Temperature, oxygen, and nutrient concentrations are the most important environmental correlates of these lanternfish distributions. By the year 2060, all but one species is projected to lose a moderate area of current suitable habitat, whilst the severity of predictions is species and climate model dependant. Our results highlight the need for an ensemble approach when projecting future distributions with clear communication of all possible outcomes. The potential ecological consequences of these findings to King Penguin foraging areas is discussed.

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Large-scale historical dataset and their usefulness in modelling species richness: the case of the Ross Sea Mollusca

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In polar areas, where the structure of marine communities and biodiversity could be threatened by climate-driven changes, any information about species distribution is potentially useful and relevant to monitor the current situation and understand future scenarios. Regrettably, part of our knowledge is currently based on historical datasets, which are inhomogeneous and affected by several kinds of biases. On the other hand, they may offer a wide geographical coverage and encompass sampling stations that have never been re-sampled, standing as the unique source of information for a given site and should not be ignored.

In Antarctica, as well as in other areas, molluscs are one of the best-studied taxa. In fact, all past Antarctic expeditions collected samples and, for this reason, this group is a perfect candidate to investigate trends and patterns of marine biodiversity.

Using all the available information, we have compiled the largest dataset about the Ross Sea molluscs that censuses more than 700 sampling events and spans for over a century. This dataset was used to model species richness as function of environmental (e.g. depth, geomorphology, etc.) and sampling-related (i.e. number of sampling events, gear category used) covariates. All the analyses were performed by using generalized linear model (GLM), generalized linear mixed model (GLMM) and extrapolation and rarefaction techniques.

The obtained results clearly indicate that the perceived species richness largely depend on the sampling gear used and that, among the available sampling gears, fine-mesh ones provide the highest number of species and specimens compared to the other ‘standard gears’. Thus, if no corrections for sampling-related issues are adopted in the models, the potential explanatory power of environmental variables does not emerge clearly.

Specifically, to obtain meaningful results, GLMM models have to include the gear category as random intercept and, in the case of GLM models, it is necessary to produce a single model for each gear category.

These outcomes have to be carefully considered whenever historical datasets are included in the analyses of species richness since sampling-related issues may introduce severe biases in the analyses.

Current-correction of southern elephant seal movement trajectories

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During two annual 3-8 month long migrations, southern elephant seals (*Mirounga leonina*, SES) are exposed to the world's strongest oceanic current system: the Antarctic Circumpolar Current. Consequently, their ground-based trajectories are shaped as a function of their own water-related movements and that of the ambient current's flow which can either promote or impede travel. Current-correcting the ground-based trajectories thus allows for a better assessment of where and how marine top predators such as SES migrate. Therefore, a modified method of vector analysis was developed that specifically incorporated information on the diving behaviour to account for when SES were exposed to strong surface or depth-attenuated currents. The resultant method was applied to 45 SES trajectories from South Georgia collected between 2008 and 2009, which revealed that the supposedly intended heading direction significantly differed from the resultant direction of travel described by a seal (Moore's test: $R=28.855$, $p<0.001$). Modelling the water-based paths clearly displayed that currents deflected the trajectories of fast-moving SES, and that the differences between ground- and water-based paths became more pronounced the longer a trajectory. Even when SES were only exposed to strong currents at the surface, their movements were still perceivably deflected. Localised changes in the current's flow led to large inter-individual differences in how strongly trajectories were deflected. Individuals moving north of South Georgia experienced the strongest deflections. However, the difference between ground- and water-based trajectories was largest for benthic diving individuals seeking out fixed bathymetric features around which currents were strong. These individuals counter-acted the deflections and compensated for drift to stay localised. Thus, the degree to which ground- and water-based paths differed strongly depended on the current's strength, an individual's active movement and its compensation ability. Most individuals oriented so that they experienced sideway currents. However four individuals swam against the ambient flow direction and another five individuals drifted downstream for extended periods. This elucidated that during a migration SES are flexible in using several different movement strategies such as compensation, drift and upstream orientation in response to a spatio-temporally varying flow of the ambient current. This visibly large behavioural plasticity could indicate resilience against environmental changes. Additionally, the improved understanding about the water-based movements of SES provided an essential step towards being able to better predict the large-scale movements of these top predators and gauge their reliance on currents, which is particularly important regarding the imminent alterations in the ocean due to climate change.

Modelling species distribution: influences of temporal, spatial, and sampling heterogeneities in data-poor areas. An example from the Kerguelen Plateau

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The field of species and community distribution modelling has undergone a remarkable increase of interest from ecologists during the last decades. Species Distribution Models (SDM) can constitute seminal conservation tools and usually have three main objectives: (i) estimating species realized ecological niches, (ii) interpolating occurrence point data over continuous maps based on correlative connections with environmental descriptors, and (iii) estimating potential shifts in species distribution associated to past and future environmental changes.

Interpolating species distribution over wide expanses of water like the Southern Ocean can constitute a real input to our understanding of marine life in remote and little-investigated areas. However, there are methodological issues caused by data heterogeneities because our knowledge of species distribution relies on diverse sampling campaigns and strategies. Spatial and temporal heterogeneities can impact the performance of modelling procedures, a critical point when considering the growing interest for the approach.

In the present work, we tested the reliability of different modelling procedures using true occurrence data of four common echinoid species of the Kerguelen Plateau with contrasted ecological niches. We used presence-only data compiled from various sampling campaigns led between 1872 and 2015. We tested the impact of spatial bias, record addition, and temporal variation on model performances, assessed the respective prediction performances and proposed a procedure to correct for the different bias. In addition, potential shifts in species distributions were modelled according to IPCC A2 scenario for 2100; they were compared to the magnitude of present changes (2005-2012).

This work provides a synthetic overview of the potential consequences of data heterogeneities for distribution modelling. It proposes a protocol to test and correct for the bias and gives some clues for improvement when using such procedures in conservation issues.

Potential distribution model of *Sanionia uncinata* (Hedw.) Loeske in two Holocene periods at Fildes Peninsula, King George Island

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In Antarctica, specifically in the South Shetland Islands, warmer conditions that occurred after the Last Glacial Maximum (LGM) prompted the phasing out of the ice with the consequently exposure of ice-free areas, favourable to colonizer species. The geomorphology of these ice-free areas shows processes such as glacier fluctuations, isostatic rebounds and marine transgressions, suggesting that the current ice-free areas have undergone a number of changes from the LGM. However, the evolution and spatial extent of those areas suitable for vegetation colonization is still unknown.
In general, a specific combination of ice-free soil and abiotic factors creates suitable conditions for some species to colonize new areas and develop. Among colonizing species adapted to extreme environmental conditions, the moss *Sanionia uncinata* Hedw. Loeske is the most widely distributed throughout the South Shetland Islands. However, at the moment there are no records about its past distribution and population dynamics (mostly related to glacier fluctuation), which resulted in its current distribution.

The aim of this study is to reconstruct the potential distribution of *S. uncinata* in the Fildes Peninsula, King George Island, for the past 15,000 years, using the MAXENT platform to create and to project the past potential distribution of the moss. For the present, topographic variables (elevation, slope and exposure) and temperatures, together with the observed moss distribution, permitted the calibration of the modelled current potential distribution of *S. uncinata*. The resulting potential distribution was validated against the current extent of *S. uncinata*, using a Normalized Difference Vegetation Index (NDVI) map. For the years 11,000 BP and 6,000 BP, extension of ice-free areas and terrain altitude and temperatures, were compiled from literature (Braun et al, 2004; Watcham et al, 2011; Fretwell et al, 2010; Mulvaney et al, 2012; O`Cofaig et al, 2014), to ingest the model and to project it during these past conditions.

The results of the distribution model successfully identified the ranges of abiotic variables that increase the likelihood of current presence of *S. uncinata* in the study area. Nevertheless, some limitations for past dates distribution are identified ought to uncertain in limits of ice-free areas, temperature reconstruction and topography.

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Comparison of methodological approaches for ecoregionalisation: A case study on sub-Antarctic demersal fish

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Understanding the distribution of species and their relationship with the environment is a fundamental goal in ecology that has valuable applications to conservation management. One important application is ecoregionalisation, i.e. delineating spatial management units to assist with planning and evaluating spatial management options, targeting monitoring efforts and managing human activities. Due to the sparseness of biological data, particularly in regions as difficult to access as the Southern Ocean, statistical models that link biological data with environmental data are a promising approach for mapping the distribution of species and identifying patterns of biodiversity. In the Southern Ocean this approach has most often been used to quantify the distribution of single species, yet increasingly conservation efforts must consider biodiversity as a whole or ecosystems more broadly. In recognition of this need, we briefly review the growing number of statistical methods that have been developed to identify and model patterns in the distribution of multi-species assemblages. These methods range from algorithmic distance-based, to machine learning, to GLM methods that incorporate latent variables and differ in their approach to defining assemblages and in how they predict into geographic space. We apply a selection of these methods to a sub-Antarctic demersal fish dataset and compare the resulting ecoregions and their ecological interpretation in light of our knowledge of this region. We discuss the relative advantages and disadvantages of the different approaches from a statistical, ecological and pragmatic viewpoint. Taking into account the role of ecoregionalisation in conservation management, we recommend the methods most appropriate to particular circumstances in describing and capturing the relationships between environment and species distributions in the Southern Ocean.

Ecological relevance of habitat mapping models: A problem of scale

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In 2012 the regional waters surrounding the sub-Antarctic islands of South Georgia and South Sandwich (SGSSI) were designated a IUCN category IV marine protected area (MPA) [1], covering an area of over one million km^2. The MPA is currently entering a period of review, a process which is due for completion in 2018. A detailed assessment of the benthic biogeography of the region, specifically in terms of key management priorities (i.e. the presence of VMEs; endemic species; biodiversity hotspots) is therefore paramount if the importance of the region's benthic habitats is to be reflected in spatial planning policy for the region.

In 2016 we published the results of the first habitat mapping model for the South Georgia region [2] which integrated geophysical and ocean productivity data with a regional oceanographic model. This ambitious synthesis of multi-disciplinary information enabled, for the first time in the Southern Ocean, a broad biotopic characterisation of an entire archipelago's benthic habitats.

Here we present new high-resolution ROV dive video, bathymetry and side-scan sonar data from a range of sites on the South Georgia shelf and slope, collected during the recent MARUM led M134 research cruise to the region. These data are used alongside an extensive regional benthic biodiversity dataset [3] to ground-truth our 2016 habitat mapping model, and assess its application as a proxy for informing on the diversity and distribution of benthic life at South Georgia. We report on the respective influence of small-scale drivers versus large-scale abiotic gradients on the community structure of the region. Fine-scale heterogeneity in the physical environment and the stochastic nature of isolated hard-bottom communities such as glacial dropstones are both identified as key confounding influences on attempts to better constrain ecologically-relevant habitat models for the region. Finally we discuss how our findings may inform on the current MPA review of the region.

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Influence of grouping species by functional traits versus taxonomic relatedness on mapping patterns of seafloor biodiversity.

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Effective management and conservation relies on quantifying and understanding the spatial distribution of biodiversity. Due to the sparseness of Antarctic datasets, mapping the distribution of biodiversity is a difficult task, most commonly approached using species distribution models (SDM), which link biological data with environmental data that has continuous coverage. To date, SDMs in the Antarctic have largely focussed on a few common species or very broad taxonomic groups. However, grouping species by functional traits has gained increasing attention as it is thought to be more closely linked with ecosystem function and resilience. Another advantage is that a functional group approach may be transportable between regions that have different species pools.

Here, we investigate how the grouping of species at different taxonomic and functional levels influences predicted distributional patterns of biodiversity on the George V shelf in East Antarctica. We use a dataset of seafloor images to produce three different datasets: single species, species grouped based on taxonomic relation, and species grouped based on functional role. We use these datasets to map the patterns of diversity emerging from grouping species in different ways. The results provide important insight into congruency and differences in patterns of biodiversity emerging from these approaches and show which one might be more suitable to map biodiversity across regions.

Influence of dispersal processes on the global dynamics of Emperor penguin

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Species endangered by rapid climate change may persist by tracking their optimal habitat; this depends on their dispersal characteristics. The Emperor Penguin (EP) is an Antarctic seabird threatened by future sea ice change, currently under consideration for listing under the US Endangered Species Act (ESA http://www.regulations.gov # FWS-HQ-ES-2016-0072). Indeed, a climate-dependent-demographic model without dispersion projects that many EP colonies will decline by more than 50% from their current size by 2100, resulting in a dramatic global population decline (Jenouvrier et al, 2014). Recent studies have now shown a high degree of genetic homogenization for EP colonies from Adélie Land to the Weddell Sea, suggesting high connectivity in these populations via individual dispersal among colonies (Younger et al., 2015; Cristofari et al., 2016; Li et al., 2014). Here we assess whether or not dispersion could act as an ecological rescue, i.e. reverse the anticipated global population decline projected by a model without dispersion. To do so, we integrate detailed dispersal processes in a metapopulation model - specifically, dispersal stages, dispersal distance, habitat structure, informed dispersal behaviours, and density-dependent dispersion rates. This model predicts species persistence in heterogeneous landscapes and non-stationary environments arising from climate change. For EP, relative to a scenario without dispersion, dispersal can either offset or accelerate climate driven population declines; dispersal may increase the global population by up to 31% or decrease it by 65%, depending on the rate of emigration and distance individuals disperse. Our global sensitivity analysis reveals which aspects of dispersal processes the global population is most sensitive to, which could help prioritize future empirical research as well as conservation and management actions (Aiello-Lammens and Ak¸cakaya, 2016). It shows that the global population size is more sensitive to change in emigration rates, regardless of the magnitude of climate change (i.e. the time period considered) and type of dispersal behaviors (random versus informed). The listing of a foreign species on the ESA such as the EP may increase public attention on species threatened by climate change, motivate the implementation of crucial longitudinal individual-based studies, and highlight the need for a new global conservation paradigm involving international coordination and management. Our general model is flexible such that multiple dispersal scenarios could be implemented for a wide range of species to improve our understanding and predictions of species distribution and persistence under future global change.

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Fast inference of behavioural processes underlying marine predator movement and habitat usage

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Habitat modelling approaches have been used for decades to understand where animals are found, why they are found there and to predict where else they may be located. This approach, however, cannot provide insight into the behavioural processes that underlie species' habitat usage and distributions. Here we present a maximum likelihood-based approach for inferring behavioural processes from satellite-based telemetry data as a function of environmental attributes. Unlike similar Bayesian methods, our approach is computationally fast and allows straightforward model selection. We illustrate our method by inferring the changes between transient and resident movement patterns of southern elephant seals (*Mirounga leonina*) as a function of environmental variables such as distance to sea ice, distance to polynya and temperature at dive bottom. Used in combination with habitat models, our approach provides essential behavioural context for understanding species' habitat preferences and distribution.

Can we predict large surface patches of krill using a dispersal model?

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Many marine species have planktonic forms - either during a larval stage or throughout their lifecycle -that either move passively or are strongly influenced by ocean currents. Understanding these patterns of movement is important for informing marine ecosystem management and for understanding ecological processes generally. Retention of biological particles in a particular area due to ocean currents may be just as important but has received less attention than transport pathways between locations. In a recent study, we demonstrated that patterns of oceanic retention time (calculated from remotely sensed altimetry) in the Indian Sector of the Southern Ocean show a surprisingly high level of correlation with the observed distribution of Antarctic krill (*Euphausia superba*) during summer (Mori et al. 2017). In this presentation we introduce an updated set of outputs at the circumpolar scale. We note that patterns of retention time (from December to March) at this scale are consistent with observations of surface patches of juvenile krill (i.e. Discovery report (Marr 1962) and Japanese ship observations (Suisancho 1980, 1983, 1985, 1986, 2001)).

Formation of these surface patches is one of the well-known conspicuous behavioural characteristics of Antarctic krill, and while sightings and distribution of surface patches is well documented in Marr (1962), there are limited reports on surface patch sightings since Marr's work. This lack of observations is as likely related to a lack of systematic observations as it is to a lack of actual patches. It also seems that the surface patches only occur in certain locations or in narrow streams and are not necessarily evenly distributed across the krill habitat range. We use our results to consider whether these patches might be formed by passive drifting or by active swimming of krill larvae that have recently been released from the ice edge.

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Biotic versus abiotic controls on Southern Ocean coccolithophore biogeography

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Southern Ocean phytoplankton biogeography is important for the biogeochemical cycling of carbon, silicate, and the transport of macronutrients to lower latitudes. With the discovery of the 'Great Calcite Belt', revealing an unexpectedly high prevalence of calcifying phytoplankton in this ocean basin, the relative importance of Southern Ocean coccolithophores for phytoplankton biomass and net primary productivity, the factors controlling their biogeography, and their impact on the carbon cycle need to be revisited. Using a mechanistic regional high-resolution model (ROMS-BEC) for the Southern Ocean (24-78°S) that has been extended to include an explicit representation of coccolithophores, we assess controlling factors of Southern Ocean coccolithophore biogeography over the course of the growing season, with a particular focus on biotic interactions and the relative role of top-down versus bottom-up factors.

In our simulation, coccolithophores are an important member of the Southern Ocean phytoplankton community, contributing ~13% to annually integrated net primary productivity south of 30°S. Coccolithophore biomass is highest in February and March in a latitudinal band between 40-55°S, when diatoms become heavily silicate limited. This region is characterized by a number of divergent fronts with a low Si:Fe ratio of waters supplied to the mixed layer, supporting an increased growth of coccolithophores relative to diatoms. Furthermore, we find top down controls to be a major control on the relative abundance of diatoms and coccolithophores in the Southern Ocean. Consequently, when assessing potential future changes in Southern Ocean coccolithophore abundance, both physical (temperature, light, nutrients) and chemical (ocean acidification) changes, but also biotic interactions need to be considered.

Risk assessments in Antarctic terrestrial ecosystems: new insights using correlative modeling approaches

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Environmental niche modelling can help to predict the distribution of species and to identify potential ecological impacts. The general strengths and limitations of correlative approaches are briefly discussed here together with the associated challenges specific to the Antarctic context. This is illustrated with our findings from recent works. For instance, the existence of non-analogous conditions can lead to underestimated predictions when local records are absent. Furthermore, abiotic effects have a strong effect in shaping the spatial niche of species in Antarctica, thus these techniques can be particularly effective in this region. However, generation and free availability of relevant environmental data is essential for robust predictions to be made. In addition, regional non-climatic factors such the human footprint levels can be incorporated to provide improved risk assessments of biological invasions and faunal disturbances. In turn, mechanistic models based on biophysical and physiological conditions can help inform conservation management decisions where data from known distributions is scarce or the conditions for the species presence are very specific.

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Underwater photogrammetry in ice-covered Antarctic areas: logistic constraints at below zero temperatures and recommendations for video-based long term monitoring programs of the benthos

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SCUBA-based benthic monitoring programs in extreme and logistically challenging underwater environments, such as Antarctica, necessarily have to be efficient, rapid, minimize bottom time and, at the same time, guarantee useful results with the minimum environmental impact.

The PNRA (Italian National Antarctic Research Program) project ICE-LAPSE was funded with the aim of creating a first permanent monitoring station to study and document benthos dynamics in Terra Nova Bay (Ross Sea). In the framework of this project, permanent transects have been fixed in order to record changes in the benthos, through the analysis of video-based time series and of seabed 3D model reconstructions, obtained by means of photogrammetric techniques.

Here we present the results of the elaboration of georeferenced videos depicting the permanent transects deployed in 2015 by the ICE-LAPSE project and of 'historical' videos recorded in 2006 by a NZ expedition in the same area.

Several technological challenges in image elaboration for photogrammetric reconstructions have been faced but, in both cases, 3D models of the seabed were successfully obtained through photogrammetry. Thanks to the details of the models, that enable fine-scale evaluations of spatial patterns with an unprecedented level of detail, it is possible to count invertebrates and estimate shape and volume of large organisms such as sponges.

Taking advantages by the use of geospatial packages of R and GIS software and specific image analysis software, such as those based on chromatic hierarchical segmentation processes (e.g. Seascape and photoQuad), it is possible to obtain a series of quantitative measures that can be used to document the changes occurring in the benthos and hence establish a monitoring program of the communities studied. The availability of photo-mosaics of the Antarctic bottom communities is thus a promising tool in monitoring activities in Antarctic near shore sites. This approach, now part of the proposed monitoring protocols of SCAR-ANTOS, due to its non-destructive nature and relatively low costs, can easily be adopted by other Antarctic research programs in order to establish a network of benthos monitoring stations.

Input sources and retention of biological hotspots along the northern Antarctic Peninsula shelf

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Observations from several multidisciplinary research programs over the last four decades identified a number of localized regions around the northern Antarctic Peninsula (AP) and Bransfield Strait (BS) characterized by high biological production that is in excess of average conditions (e.g. biological hot spots). These regions typically are persistent over several years and appear to be a common feature of the Antarctic shelf environment, in particular in parts of the Southern Ocean where the Antarctic Circumpolar Current (ACC) impinges the shelf break bringing nutrient rich Circumpolar Deep Water (CDW) onto the continental shelf. Ocean circulation and the dynamical processes controlling the CDW intrusions exert a strong influence in the formation of the hot spots regions. The objective of this study is to determine dominant pathways of intrusions of CDW onto the shelf and determine residence times of eight hot spot regions along the north of the South Shetland Islands (SSI) and BS. To accomplish this goal Lagrangian tracking experiments were done using a high-resolution (1.5km) coupled sea ice/ice shelf/ocean circulation model for the Antarctic Peninsula using the Regional Ocean Modeling System (ROMS). The results showed preferred transport pathways along the shelf break in regions characterized by bathymetric depressions. Estimated residence times varied between the hot spots located north of the SSI and inside BS. The longest residence times were observed for the hot spots along the innershelf north of SSI (50-60 days). These time scales were consistent with development times of the local mesozooplankton and may contribute to the local biological processes. The hot spots along the outer shelf were less retentive (5-10 days) and presented similar time scales as the hot spots in the eastern Bransfield Strait. Our results suggest that circulation is important in developing localized areas of high biological production, their formation and maintenance has broad implications for the different components of the food web.

A first approach to calculate BIOCLIM variables and climate zones for Antarctica

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For testing the hypothesis that macroclimatological factors determine the occurrence, biodiversity, and species specificity of both symbiotic partners of Antarctic lecideoid lichens, we present a first approach for the computation of the full set of 19 BIOCLIM variables, as available at http://www.worldclim.org/ for all regions of the world with exception of Antarctica. Annual mean temperature (Bio 1) and annual precipitation (Bio 12) were chosen to define climate zones of the Antarctic continent and adjacent islands as required for ecological niche modeling (ENM). The zones are based on data for the years 2009–2015, which was obtained from the Antarctic Mesoscale Prediction System (AMPS) database of the Ohio State University. The database offers different domains with different horizontal resolutions of which three were analyzed: domain 2 (whole Antarctica, 10km), domain 5 (Dry Valleys, 1km) and domain 6 (Maritime Antarcica, 3km). Despite the (comparatively) short time frame, the data matches quite well to the data derived from meteorological stations. For both temperature and precipitation, two separate zonings were specified; temperature values were divided into 12 zones (named 1 to 12) and precipitation values into five (named A to E). By combining these two partitions, we defined climate zonings where each geographical point can be uniquely assigned to exactly one zone, which allows an immediate explicit interpretation. The soundness of the newly calculated climate zones was tested by comparison with already published data, which used only three zones defined on climate information from the literature. The newly defined climate zones result in a more precise assignment of species distribution to the single habitats. This study provides the basis for a more detailed continental-wide ENM using a comprehensive dataset of lichen specimens, which are located within 21 different climate regions. Above all, the region of McMurdo Dry Valleys (78°S) will be of special interest in future studies, as the climate conditions there are unique even for cold deserts.

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Degrees of Isolation: The Impact of Climate Change on the Dispersal and Population Genetic Structure of Two Antarctic Fish Species

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Understanding the key drivers of larval dispersal and population connectivity in the marine environment is essential for the effective management of natural resources, and for estimating the potential impacts of climate change on the resilience of populations. Small, isolated and fragmented communities will differ fundamentally in their response and resilience to environmental stress, compared with species that are broadly distributed, abundant, and with a frequent exchange of members. Using a 'seascape genetics' approach, combining oceanographic modelling and genetic analyses, we have elucidated the fundamental roles of oceanographic transport and planktonic duration on the connectivity and population genetic structure of two Antarctic fish species with contrasting early life histories, *Champsocephalus gunnari* and *Notothenia rossii* (Young et al., 2015). Here, we extend these analyses to consider the impact of rising sea temperatures on planktonic dispersal and population connectivity of Antarctic fish populations in the Scotia Sea.

Using a theoretical approach, the effect of increased water temperatures on mortality rates and species-specific egg and larval phase durations has been incorporated into the models, and the impact of these climate-related influences on connectivity and population genetic structure has been investigated. Model projections suggest that in a warmer world, populations of *N. rossii* in the Scotia Sea are likely to remain broadly genetically homogeneous, with the exception of the South Sandwich Island population, which is projected to become more isolated. By contrast, rising sea temperatures are projected to increase the isolation of *C. gunnari* populations in the northern and eastern Scotia Sea (Shag Rocks, South Georgia and the South Sandwich Islands). Here we present the key findings of our research and consider the roles of early life history and oceanography in the response of fragmented fish populations to climate change.

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Pristine populations of habitat forming species on the Antarctic continental shelf

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Declines in the abundance of long-lived and habitat forming species of continental shelves have attracted particular attention given their importance to ecosystem structure and function of marine habitats. The study of undisturbed habitats defined as "pristine areas" is essential to create a reference frame of natural habitats without human intervention (Levin and Dayton 2009). Gorgonian species are one of the key taxa structuring benthic communities on the Antarctic continental shelf. Current knowledge on the diversity, distribution and demography of these species is relatively limited in Antarctica. To overcome this lack of information we present first data of pristine and remote populations of gorgonians with the highest abundance and largest size ever recorded at the continental shelf. We assessed the distribution patterns of seven gorgonian species and two morphogroups in front of the Filchner Ronne Ice Shelf (Weddell Sea) by means of quantitative analyses of six video transects (from 251 to 361m depth) recorded by a Remotely Operated Vehicle. The analyses, showed a total of 3140 individuals. Two *Thouarella* species were the most abundant species (n=597 for sp.1 and n=572 for sp.2). We found the highest abundance of gorgonians at the southern part of the study area with maximum values of 6ind/m^2 for *Fannyella rossii* and 10ind/m^2 for *Thouarella* sp.1. Significantly clumped distribution was found for most of the species. Size frequency distribution of all the species was unimodal with many small colonies suggesting high recruitment rates. Only the morphogroup Unbranched showed a very dense patch with 47ind/m^2 and a symmetrical distribution of size frequency with high proportion of large size classes (50-70cm). This study attempts to contribute to the general knowledge of pristine areas of the continental shelf and identify the eastern Weddell Sea as a hotspot for habitat forming species.

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A community ecology analysis of the benthic macrofauna of the South Orkney Islands shelf break

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Both taxonomic and ecological attributes of deep-sea benthic communities in the Southern Ocean remain comparatively poorly known (Brandt et al., 2007), and this ignorance has contributed to the relative controversy that surrounds the recent placement of the South Orkney Islands Southern Shelf Marine Protected Area (SOISS MPA).

To combat this deficiency of knowledge, the British Antarctic Survey (BAS) expedition 'South Orkneys – State of the Antarctic Ecosystem' (So-AntEco) was led between February and March 2016. Focussing on benthic habitats, SO-AntEco aimed to further knowledge of the abundance, diversity, composition and distribution of macrofauna and megafauna. This information will be applied to assess the suitability of the SOISS MPA (in terms of the protection of a representative sample of the biodiversity of the region), and advise CCAMLR with respect to any modifications or refinements that should be made to the current limits of the protected area.

During the So-AntEco research cruise, an Epi-benthic Sledge (EBS) (Brandt and Barthel, 1995, Brenke, 2005) was used to sample benthic macrofauna in the vicinity of the South Orkney Islands. This was deployed a total of 13 times (including both within and outside the limits of the MPA) at depths ranging from approximately 500 to 2000m.

Here, an analysis of the supra-benthic EBS samples (1611 individuals identified at a coarse taxonomic resolution – order to phylum) will be presented in order to identify any large scale ecological trends present. Observed variation in macrofaunal assemblage composition will be linked (using multivariate statistical techniques such as ordination and Generalised Linear Models (GLMs)) to a selection of environmental variables. More specifically, variance in macrofaunal community structure, abundance, diversity, richness and evenness will be will be examined with reference to variance in sampling depth, benthic salinity, temperature and oxygen concentration, seafloor substratum type, and broad-scale bathymetric zone classifications. Further, comparisons will be made between samples collected from within and outside the limits of the MPA.

Such analyses will help further our knowledge of the key factors structuring macrofaunal benthic communities in this particularly poorly-studied region.

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Biogeography and macrophysiology of Antarctic Collembola

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Most of the Antarctic's terrestrial biodiversity exists in the soil, yet soil ecosystems are inadequately represented in regional conservation policy. In line with a global initiative to redress this imbalance, we provide an overview of recent work to demonstrate how key studies can simultaneously inform biogeography and conservation policy. Our focus is on the springtails (Collembola), one of the region's dominant soil arthropod groups. We start with a critical synthesis of information on the diversity, distribution and type localities (an explicit concern of the Protocol on Environmental Protection to the Antarctic Treaty) of the group. Nearly 170 springtail species have been recorded from the Antarctic with 17 type localities listed for the continent and almost 70 for the sub-Antarctic islands. Yet many geographic areas, such as East Antarctica and the Crozet archipelago remain critically undersampled. Although molecular approaches are starting to reveal cryptic speciation and taxonomic complexity, novel molecular techniques to better understand the region's diversity remain underutilized. Indeed, we don't yet have clear indications of the phylogenetic and phylogeographic diversity of the region. From an ecological perspective, the distribution of knowledge is even further skewed. Much is known about a few key species, while most others are completely data deficient. For a growing group of species we can use physiological data, in concert with high-resolution climate data, to build mechanistic distribution models. Thus, mechanistic modelling may have advantages over correlative species distribution modelling for Antarctic species. Correlative distribution models are, nevertheless, proving useful for examining likely threats from extra-regional invaders. We use examples from our work to demonstrate how knowledge deficits for the Collembola, which are concerning given conservation threats from climate change and from biological invasions, may be overcome.

Climatic and environmental constraints on aboveground-belowground linkages and diversity across a latitudinal gradient on the Antarctica Peninsula

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The Antarctic Peninsula is experiencing rapid environmental changes, making it susceptible to alterations in species diversity and distribution, both above- and belowground. However, we lack a firm understanding of soil biodiversity, including linkages with the aboveground community and relationships to changing environmental parameters. This strongly limits our ability to predict the consequences of environmental change for soil communities. To begin determining the nature and strength of aboveground-belowground linkages in influencing soil community biogeography and diversity over a latitudinal gradient of environmental and climatic conditions, we sampled the soil bacteria and invertebrate communities at 10 sites along the Antarctic Peninsula and Scotia Arc (from c. 60-75°S), beneath key aboveground habitats (moss, grass, lichen, algae, and bare soil). Soil chemistry and microclimatic conditions were measured to determine the relationships between soil communities and physical and chemical properties. We observed a significant decrease in soil organic matter and an increase in pH value towards the southern end of the Peninsula, reflecting the greater vegetative influences on the soils in maritime Antarctica as compared to the sandy soils of continental Antarctica to the south. Associated with the broad southern shift in soil organic matter and pH we observed a concurrent shift in belowground community composition, including a decrease in invertebrate species diversity and abundances, and a shift in microbial community composition, particularly in the relative abundance of Acidobacteria and Proteobacteria. Differences in the microbial community across sampling locations was not strictly correlated with latitude, and the mid-latitudes supported more diverse bacterial communities, particularly within lichen, grass, and bare soil associated communities. However, it is notable that one of the southern sites with continental soil characteristics hosted a bacterial biomass comparable to the more maritime Antarctic Peninsula sites, despite the less hospitable environmental characteristics. Within individual sites, the type of vegetation cover significantly altered soil chemical and physical properties, with significant site-vegetation interactions for many soil properties. In association, we also observed significant differences in microbial and invertebrate community composition between habitat types. In particular, soils beneath grass hosted a distinctly different microbial community with the highest number of observed OTUs, with bare ground and moss also being fairly distinct. Ultimately, such knowledge will contribute to a better understanding of potential future belowground responses to global changes in maritime Antarctica.

Testing spatially-based population structure and life history connectivity of *Pleuragramma antarctica* in the Southeast Weddell Sea

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In an effort to expand current understanding of life history connectivity in *Pleuragramma antarctica* in the Weddell Sea, we employed an interdisciplinary approach to investigate population structure by comparing genetics with spatial distributions of size and otolith chemistry. Laser-based inductively coupled plasma-mass spectrometry (ICP-MS) measures trace elements incorporated into the otolith, which reflect oceanographic conditions (Ashford et al. 2007*),* to understand migration patterns and determine the geographic origin of an individual (Campana 1999, Elsdon and Gillanders 2003). Successful validation of otolith nucleus chemistry directly against genetic data from the same fish has demonstrated that nucleus chemistry can be highly effective for examining population structure, even in fully marine species (Ashford et al. 2006).

The present study sets out to examine the life history hypothesis (La Mesa et al. 2015) of population structure shaped by trough systems across the shelf and westward advection along the Antarctic Slope Front and Current System (AFS). The hypothesis predicts shared genetic and chemical signatures between fish collected in the northeastern extreme of Atka Bay off Eastern Antarctica, off the Brunt Ice Shelf, and on either side of the Filchner Trough in the southeastern Weddell Sea under advection from a common origin. While the results from microsatellite-based genetics analysis support this prediction, revealing homogeneity along Eastern Antarctica and across the Weddell Sea (Caccavo et al. In preparation), young, recently hatched fish have been found in the Filchner Trough (Hubold et al. 1984) suggesting local spawning.

Examining standard length (SL) distributions, we found considerable variation among samples collected, indicative of spatial structuring off the Brunt Ice Shelf and in the Filchner Trough, which is consistent with mixing between fish of local origin and advected along the AFS. As a result, we used otolith chemistry to measure whether differences exist between SL modes and between sampling areas within SL mode. Shared otolith nucleus chemistry signatures between fish collected from different sampling areas would support the scenario that one source population supplies fish to the southeastern Weddell Sea, whereas heterogeneity would indicate that fish derive from more than one population, with enough exchange of individuals to retain their genetic homogeneity. Thus, consistent differences in otolith chemistry within SL modes between sampling areas would suggest cross-shelf trough circulation separating populations along the continental shelf. Variation between modes would suggest temporal differences consistent with connectivity along the AFS and mixing with an eastern source population in different proportions in the Weddell Sea.

In this talk, we present the combined data set for the first time. This is a novel use of otolith chemistry in concert with genetic and length data from the same individuals to test a life history hypothesis in a hydrographic framework. The approach can help considerably in understanding what drives spatial and temporal variability in the abundance and distribution of *P. antarctica*, but furthermore, can be seen as a model for multidisciplinary approaches to understanding the spatial structuring of Antarctic fish at the population level.

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Benthic fauna from the deep central basin of Admiralty Bay, King George Island, Antarctica

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Although the benthic communities of Admiralty Bay, King George Island, Antarctica, have been extensively surveyed through long-term sampling programmes, there is still little knowledge of the fauna from its deepest zones. The benthic diversity in the central basin from the proximity of Plaza Point towards the bay's opening to the Bransfield Strait was investigated during the 2009/2010 Austral Summer on board NApOc "Ary Rongel". Three replicate Agassiz trawl (W=60cm, H=40cm, 20mm mesh size) samples were collected at 100, 300, and 500m depth, covering an area of ca. 60m^2 per replicate. Benthic fauna was washed on board with filtered sea water on a 500µm sieve, and sorted into higher taxonomic groups in laboratory. All samples were deposited at the Biological Collection "Prof. Edmundo F. Nonato" (ColBIO) at the Oceanographic Institute (University of São Paulo). Sediment grain-size was examined for each replicate and was mainly composed of silt and clay. A cluster analysis was performed using Bray-Curtis-Index and group average method, using a total of 30 taxonomic groups. Echinoderms (mainly ophiuroids, sea stars and sea cucumbers), polychaetes and crustaceans were the most frequent groups followed by pycnogonids and poriferans. But the most abundant groups were polychaetes (40%), echinoderms (30%), and pycnogonids (15%). Echinoderms (especially ophiuroids) represented 45% of the total faunal abundance at 100m, whereas pycnogonids (35%), echinoderms (29%) and polychaetes (19%) were more abundant in 300m, and polychaetes (60%) in 500m depth. The total benthic community density showed a tendency to be higher in 100 and 500m than in 300m. There was less similarity between replicates in 300m with a highest abundance of ophiuroids and pycnogonids. Potentially, this is a result of aggregation and/or caused by the sheer slope drop at the 300m towards the central basin, which may be more subjected to sediment slides consequent from turnover current impacts within the bay. There has not been a significant difference in diversity of taxonomic groups amongst depths, but this needs further comprehensive investigation with more detailed taxonomic identification.

Population genomics of the marbled rockcod, *Notothenia rossii*, in the Scotia Sea and Kerguelen plateau

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Knowledge of spatial genetic structuring is key to attain sustainable long-term management and conservation goals. While such structuring is commonly observed in fragmented habitats and in sessile species, marine fish populations are often characterized by high connectivity and gene flow. The latter can be enhanced through long pelagic larval phases that enable long-distance via oceanic current systems. Recent advances in molecular ecology show, however, that subtle genetic differentiation and/or local adaptation patterns may persist even in high gene flow systems.

The marbled rockcod, *Notothenia rossii*, is among the most abundant fish species of the Southern Ocean. Following heavy exploitation in the 1960s and 1970s, however, populations collapsed and recovered only slowly subsequent to the closure of the fishery through CCAMLR in 1980. It remains unclear why recovery was slow and if the blatant overexploitation has left imprints on the genomic diversity of marbled rockcod. The species' life history cycle, i.e., marked ontogenetic habitat shifts with larvae being pelagic, juveniles staying in shallow in-shore areas and adults moving to shelf spawning grounds, may furthermore have important consequences for genetic differentiation patterns. Here, we present extensive, updated population genetic data of the marbled rockcod in the Scotia Sea and Kerguelen plateau generated using high-throughput sequencing.

More than 350 specimens from the South Georgia, South Orkney, South Shetland and Kerguelen Islands were used to prepare four genotyping-by-sequencing (GBS) libraries. This reduced representation sequencing method allowed us to characterize thousands of single nucleotide polymorphisms (SNPs) as genetic markers to infer population genetic parameters. We examine genetic differentiation patterns on large and small spatial and temporal scales using ordination and Bayesian clustering methods. Furthermore, the genome-wide markers are screened for putatively adaptive signals and effective population size is assessed. Results are discussed with regard to potential drivers of observed patterns and possible implications under future change scenarios. These insights are valuable in light of ongoing management and protections plans for the Southern Ocean.

A long-lived life in the southern pole: phenology, distribution, and ecophysiology of the winged midge *Parochlus steinenii* across southern South America and the South Shetland Islands

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Antarctic and sub-Antarctic freshwater ecosystems are highly dynamic, and their responses to climate change may be more immediate and evident than in their terrestrial counterparts. Among the freshwater fauna, insects are strongly affected by thermal variation. Studying their natural history and ecophysiology provides valuable tools to predict changes on species distributions and phenological patterns. We focused on the little studied chironomid *Parochlus steinenii* (Diptera: Insecta), which is found in both the maritime Antarctic (MA) and the sub-Antarctic (SA) (Convey and Block 1996). We aimed to 1) contribute to the knowledge of its present distribution and predict upon its future distribution and 2) determine and compare phenological patterns and critical thermal limits across the MA and SA. During the austral summer seasons of 2014-2016, we navigated through the South Shetland Islands, coordinated by the Chilean Antarctic Institute. We searched for specimens at every permanent and non-permanent freshwater habitat encountered, and characterized them following Hahn and Reinhardt 2006. To predict on its present and potential distribution, we created climate layers using data obtained from 1960-2015 from the AWS provided by BAS and AEMET. Distribution and spatial models were obtained with MaxENT, ENMTools PostGIS, QGis, Quantarctica, and R. For phenological patterns and critical thermal limits analyses, we collected live individuals from King George (62˚S) and Navarino Island (55˚S), reared them from egg to adults, and quantified Growing Degree Days (GDD) for each developmental stage. Thermal limits were determined using the Critical Thermal Method. In general, *P. steinenii* MA populations are aggregated and concentrated in freshwater bodies of King George, Livingston and Deception Island, preferring permanent lakes, over non-permanent ponds (chi-square, $p < 0.0001$). In SA, the species is found restricted to High-Andean permanent lakes. Its potential distribution includes the Antarctic Peninsula, extending to Anvers and Ross Islands, where it does not occur at present time (Boyle's Index, 0.98). *P. steinenii* has a merovoltine (3 years) and a univoltine life cycle (1 year) in the MA and SA, respectively, and its thermal range is wide for all life stages, ranging from -3 to 30˚C, thus a possible expansion on its distribution could be hypothesized in a global warming scenario. As more knowledge is gained, we aim towards using *P. steinenii* as an indicator of climate change in MA and SA freshwater ecosystems to generate models that will allow for the prediction and confirmation of changes in its distribution and phenology in the long term.

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The role of gorgonians as engineering species in the diversity and composition of benthic communities

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Biodiversity plays an important role in maintaining and improving ecosystem functioning, thereby increasing ecosystem stability. There is convincing evidence suggesting that autogenic ecosystem engineers like gorgonians enhance biodiversity at the local scale (Idjadi & Edmunds, 2006), primarily through changes produced in the environmental conditions of their surroundings. Their three-dimensional physical structures increase the number of ecological niches available, which in turn seem to favour megafaunal species richness. However, very little empirical data has ever been provided. Gorgonian density and size relationship with the diversity of associated megafauna was explored in two very contrasting regions: the pristine eastern Weddell Sea in Antarctica and Cap de Creus in NW Mediterranean. Monoespecific patches of the gorgonians *Thouarella variabilis* in Antarctica and *Eunicella cavolinii* in the Mediterranean Sea were evaluated using Remotely Operated Video (ROV) images, recorded on the continental shelf at depths below 100 metres. The fauna associated with *T. variabilis* was more diverse than that of *E. cavolinii*, with 108 taxa recorded in the Weddell Sea and 78 in the Mediterranean region. The number of species and diversity rapidly increased with increasing gorgonian densities at both sites, until a maximum was reached. In terms of community structure, there was also a switch in the associated fauna with changes in gorgonian density. In contrast, gorgonian size only showed a positive correlation to species richness and diversity only in the Antarctic region. The results of the present study highlight the role of gorgonians in the diversity and the structuring of benthic communities, indicating their importance when designing management plans to protect the marine benthos. At the same time, this study shows that ecosystem engineers like gorgonians, which act as foundation species, could be used to restore shelf and deep-sea ecosystems that have been altered by human activities.

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Environmental constraints to terrestrial eukaryote distribution in the Prince Charles Mountains (East Antarctica): exploring high throughput sequencing derived biodiversity capability

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Knowledge of the relationship between terrestrial Antarctic biodiversity and environmental constraints is necessary for successful conservation management. The potential impact of environmental change on ecosystems can be revealed by comparisons of biodiversity patterns across large-scale gradients. However, studies to date have been limited by the cryptic nature of many terrestrial Antarctic taxa and the time- consuming nature of morphology-based studies. We used high throughput sequencing (HTS) derived biodiversity information (Czechowski *et al.* 2016a) to elucidate the relationship between soil properties and soil eukaryote biodiversity in the Prince Charles Mountains, East Antarctica.

Initial analyses of 12 samples collected from Mount Menzies, Mawson Escarpment and Lake Terrasovoje revealed trends of increasing soil community richness and diversity with decreasing latitude and altitude, warranting more detailed investigations (Czechowski et al. 2016b). Additionally, distribution of invertebrates detected across 103 soil samples were found to be significantly constrained by the age-related accumulation of soil salts in polar inland areas, in contrast to coastal sites (Czechowski et al. 2016c). In our most recent analyses, overall soil eukaryote distribution derived from analysis of 136 samples was heavily correlated with the presences of organic C, while the influence of spatial variables seemed less pronounced. Our results clearly demonstrate the utility of metagenomic HTS approaches in investigating environmental constraints on the distribution of Antarctic eukaryotes across large spatial scales.

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Island biogeography of glacial microbiota in Antarctica's Taylor Valley and around the world

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Antarctic glaciers are often thought of as large abiotic geological features, but microbes living on and within these glaciers are important components of mass balance, carbon exchange, and hydrological budgets. These microbes arrive on glaciers in the McMurdo Dry Valleys via wind-born sediment, and the predominance of microbial life on a glacier occurs within melted-in pockets of sediment called cryoconite holes - "islands" of liquid water formed as the sediment absorbs solar energy. Since the Dry Valleys experience frequent and strong winds, it is tempting to assume that microbes are transported easily between glaciers and between cryoconite holes, leading to cosmopolitan spatial distributions. However, preliminary work based on limited microscopic observations of algae, diatoms, and mesofauna suggested that different glaciers within the Taylor Valley harbor distinct microbial communities, even though the vast majority (i.e. almost all) of Antarctic cryoconite microbes have yet to be described. Here, we present a thorough biogeographic investigation of the Canada, Commonwealth and Taylor glaciers at scales from several centimeters to several kilometers, using DNA sequence data spanning all 3 domains of life. We found that glaciers in the Taylor Valley each harbor distinct bacteria, eukarya, and archaea, but the structure and ecological function of these communities varies significantly within glaciers as well. Within glaciers, geographic space was a strong determinant of microbial community structure, indicating that dispersal is limited between distant cryoconite holes, but proximate holes are more connected. However, between glaciers in the Taylor Valley, community dissimilarity was more strongly related to biogeochemical differences among the glacial environments. At the largest scale, we compared the microbial communities of our Antarctic cryoconite holes to cryoconite from glaciers in the Himalayas, Alaska Range, and from Greenland. This global analysis showed that cryoconite communities are more similar to each other than they are to non-cryoconite communities, but each region included in our analysis was distinct, likely because the cryosphere is not contiguous, and has its own "islands" around the globe.

Spatial and temporal variations in the macroalgal community of Potter Cove (Antarctica) over two decades

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Climate warming has been associated to retreating of ice fronts and increased melt water run-off in the Western Antarctic Peninsula (Cook et al. 2005). One effect of glacial retreat along the WAP is the opening of newly ice-free areas (NIFAs, Rückamp et al. 2011). Furthermore, it increases the sediment inflow and diminishes the light penetration into the water column (Schloss et al. 2012). At Potter Cove (62º 14' S, 58º 38' W), a big fjord at King George Island/Isla 25 de Mayo a deeper knowledge of the macroalgal community spatial and temporal variation has been achieved during the last two decades. Video surveys of macroalgal extension within the cove were repeatedly performed in 1993/4, 2008 and 2013. In 1994 the sublittoral macroalgal vegetation was restricted to the outer part of the cove whereas the inner cove was devoid of macroalgae (Klöser et al. 1996). The extension of macroalgal occurrence into the inner part could be proofed during the last two surveys (Quartino et al. 2013). The increase of macroalgal extension into the inner cove is related to the NIFAs, with new hard substrate for benthic colonization. Furthermore, at sites more distant to the retreating glacier more complex communities were identified, whereas less mature communities (lower richness and lower presence of perennial species) occurred in sites with the highest sediment inflow (closer to the glacial run-off). Macroalgal communities in the NIFAs did not significantly change in structure and spatial distribution between 2008 and 2013. The expansion of the macroalgal community into the inner Potter Cove could lead to higher macroalgae primary production. On the other hand, increased turbidity is leading to a narrowing of the vertical distribution of the macroalgae (Deregibus et al. 2016, Jerosch et al. 2017). Certainly, the benthic communities have undergone profound changes within the last decades with multiple factors interacting in synergistic or antagonistic ways. Repeated surveys are necessary to follow the changes and to validate and improve the models.

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Fifty shades of poo – Determination of penguin species in satellite imagery using guano colour

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In recent years methods were developed to use satellite images to analyze the size and population density of penguin colonies in Antarctica. Particularly for newly detected and inaccessible colonies it is of high importance to determine the respective penguin species. So far, the available data hardly allow any differentiation exclusively based on remote sensing. A possible parameter for the identification could be the spectral signature of the guano which is clearly visible in satellite images.

The aim of the study was the applicability of the guano colour to determine the particular penguin species expecting detectable variation in their excrements due to differences in food composition. Thus, the results could be used as basic groundtruthing for the analysis of satellite imagery. The observed colony is located on Ardley Island adjacent to King George Island and is home of three penguin species: *Pygoscelis adeliae*, *P. papua* and *P. antarctica*. Only the first two species were studied, as P. antarctica only breeds in small numbers there. For the classification of colour differences of the guano we used high resolution remote sensing data and surface photography. The latter was carried out by using digital photocamera with an internal flashlight. A closed box with an open bottom was used to eliminate the unpredictable sunlight. The colour intensity is defined as the average value of the RGB channels of each image. Additionally, the photographed guano was sampled in order to reveal the characteristics that determine the guano colour.

First results of the study indicate differences in the guano colour of *P. adeliae* and *P. papua* in certain periods of the breeding season presumably caused by a change in food composition and availability. The evaluation of data on fish and krill distribution will contribute to interpret any changes in guano colour.

Moraine ecology and genetic diversity: A comparison of moss colonization after glaciers retreat in Southern Patagonia and Antarctica

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In recent decades, glaciers are increasingly in the focus of worldwide research interest, especially in connection with the global glacier recession and associated melt occurring since the 20th century. Many of the Fuego-Patagonian glaciers are experiencing major wasting in comparison with worldwide average rates (Pellicciotti et al., 2014). The spatial variability of the disappearance of glaciers in Patagonia and Antarctica varies due to different ice dynamic processes, latitude and altitude, topography and partially decreasing snow precipitation process that has been occurring since the Little Ice Age (Davies & Glasser, 2012). Mosses are a part of the flora in Patagonia and Antarctica. They are currently used as model to monitoring responses to climate change (Ochyra et al. 2008), where the distribution of them and their limits can be altered with variation in climate and it is possible to establish relationships among the historic periods of glaciations. All these species reach here the limits of their distribution and the margins indicate which the limit of the adaptation to the abiotic conditions and climatic oscillation are. Thus, currently they represent limits of survival and colonization, where mosses are very successful in the places where they used to be, from wetter areas and channel banks to dry moraine detritus and crevices of rocks, on flat or sloped surfaces. Furthermore, some moss species are very sensitive to the smallest edaphic and microclimatic differences, expressed in the dominance of one species and the structure of the communities. The 3-year long German-Chilean project network GABY-VASA aims to strengthen existing research cooperation oriented to decipher the impact of the changes in the cryosphere and biosphere in the past and the future. We are using (cp)DNA trnT-trnF sequence for the analysis of the genetic diversity and phylogeography of different moss species and how this distribution could be linked to changes in glaciers and the surroundings moraines in southern Patagonia and Antarctica. Sampling sites include surveys at Grey Glacier (Southern Patagonia Icefield) and Schiaparelli Glacier (Darwin Range in Tierra del Fuego), and compared with patterns gathered at Hanna Point in Livingston Island, Antarctica.

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Local and regional scale heterogeneity drive bacterial community diversity and composition in a polar desert

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The simplified trophic structure of soil in the McMurdo Dry Valleys (MDV) is ideal for studying microbial community-environment interactions. Considered one of the coldest, driest, and most oligotrophic deserts on Earth, the MDV are a microbe-dominated ecosystem. Consequently, MDV microbial communities appear to be primarily shaped by physiochemical factors, particularly small-scale spatial variations in moisture, salinity, pH, and carbon availability. In addition, frequent freeze-thaw cycles cause expansion and contraction of permafrost layers and physically sort rocks and soil particles to create patterned ground formations in the shape of polygons that represent gradients of pH and conductivity. This study sought to explore the relationships between edaphic gradients on bacterial community structure and composition as they vary across regional, landscape, and local scales. We sampled radial transects of eight polygons within each of three lake basins of the Taylor Valley and conducted 16S rRNA gene and soil chemistry analyses. The relationships between bacterial community structure and edaphic characteristics were highly variable and contextual, ranging in magnitude and direction across regional, landscape, and local scales. Significant differences in pH and conductivity were found between the three lake basins. While landscape soils were generally dominated by *Acidobacteria*, *Actinobacteria*, *Bacteroidetes*, *Cyanobacteria*, *Firmicutes*, *Gemmatimonadetes*, *Planctomycetes*, *Proteobacteria*, and *Deinococcus-Thermus*, each lake basin hosted distinctive communities. No significant differences were found between the polygons within each basin, however environmental factors and bacterial communities did vary along the radial transects of the polygons. These patterns were particularly prominent in the Fryxell lake basin where *Acidobacteria*, *Bacteroidetes* and *Proteobacteria* declined along the transects while *Deinococcus-Thermus* and *Gemmatimonadetes* increased. Conductivity, pH, and distance from the polygon trough in sum explained 28.95% of the bacterial community variation. Correlations between conductivity and community phyla composition were strongest within the Fryxell basin, perhaps because it had the greatest range and on average, highest soil conductivities. Similarly, the strongest correlations of major phyla abundance to pH were found within the Hoare basin, which had the highest average pH values. Thus, as in other environments, conductivity and pH appear to be master variables responsible for structuring microbial communities in the MDV. These data, however, further suggest a hierarchical control of these parameters, with conductivity acting as a dominant driver of community composition at high concentrations and pH driving community composition at lower soil conductivities. The tipping-point at which conductivity becomes most influential will be discussed in the context of a threshold-dependent model.

Antarctic vegetation assessment methodologies, recommendations for ANTOS sampling

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Continental Antarctic ecosystem responses to climate change are still uncertain, due to a paucity of available biodiversity data across the continent. In order to sufficiently understand and appropriately respond to the impacts of climate change on the Antarctic continent, evidence of climate change impacts on Antarctic ecosystems across continental scales needs to be provided to scientists, environmental managers and decision-makers. This requires a concerted effort of integration of long term studies and data across Antarctica, with international collaborative research efforts to establish the current state and diversity of Antarctic ecosystems and determine future change in ecosystem structure, functioning or services.

The Antarctic Near-shore and Terrestrial Observing System (ANTOS) Expert Group are establishing a monitoring network which aims to use consistent methodologies to identify change in the environment at biologically relevant scales across Antarctica. A tiered measurement system has been suggested, with three primary tiers for terrestrial measurements. A vital component of the ANTOS is the assessment of biodiversity at 5-year intervals. However, species identification will be difficult in some regions using current nzTABS methodologies, due to the cryptic nature of some bryophyte species.

Here, we present a repeatable sampling methodology for long-term monitoring of continental Antarctic vegetation, as a potential addition to the methodology protocol for the ANTOS. Long-term Antarctic vegetation monitoring programs must assess both broad-scale vegetation community distributions and fine-scale species distributions in order to detect changes in vegetation health, extent and species composition in these communities of small, slow-growing plants. To comply with Antarctic Treaty principles, methods using photography and micro-sampling techniques have been devised to be minimally destructive to the fragile, unique continental Antarctic ecosystem. In order to ensure that sampling can be undertaken every five years, the sampling methodology was designed to require minimal field time to assess vegetation distribution and species composition in Antarctic communities.

These methodologies are fast and effective, and can be implemented within the existing nzTABS protocol, at the tiered levels of the ANTOS. If implemented across the continent, this would help to provide valuable data on vegetation biodiversity and change across the region.

Morphological variation in Adélie penguin: geographic and environmental correlates

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Environmental and geographic factors may play an important role in morphological variation between individuals of the same species. Despite this, there are few studies evaluating these components in seabird species, and there are no studies in Adélie penguins (*Pygoscelis adeliae*). For this reason, phenotipic traits among three Antarctic islands populations of *P. adeliae* separated by >300km were studied: Ardley (62°13'S, 58°56'W), Biscoe (65°26'S, 65°30'W) and Lagotellerie (67°53'S, 67°24'W). An analysis of 10 morphological characters revealed significant differences between localities in 8 of these measures. To understand patterns driving the variation, with linear mixed model analyses we examined these differences in relation to environmental (chlorophyll and sea surface temperature) and geographic (latitude and longitude) parameters. As it was also found in South Australian little penguin (*Eudyptula minor*) colonies, morphological variation in Adélie penguins were correlated to environmental and geographic parameters. And, similar to gentoo penguins (*Pygoscelis papua*), *P. adelie* showed geographical morphological variation, decreasing in size toward southern latitudes. In most characters, birds of northern breeding colonies surrounded by hotter sea surface temperatures were larger than the southern colonies surrounded by lower temperature. These results suggest that significant differences in body size among populations of the same species are due to geographic distances and ecotypic differentiation. In addition, it seems that *Pygoscelis* penguins do not follow the Bergmann's rule, since two out of the three species of this genus show patterns opposite to it.

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Changes in circumpolar spatial distribution of baleen whales in the Antarctic from 1980s to 2000s

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The circumpolar spatial distribution of baleen whales (blue, fin, sei, Antarctic minke, humpback and southern right) was estimated using two sets of circumpolar sighting survey data conducted by the International Whaling Commission (IWC). The first set was conducted in 1980s while the second was conducted in 1990s and early 2000s. Generalized additive models (GAMs) were used for the estimation. Geographical features (bathymetry and distance to upper slope) and climatological data at the surface (water temperature, sea surface height, salinity, and chlorophyll, silicate, nitrate and oxygen concentrations) as well as longitude and latitude, were used as explanatory variables in the models. Multiple collinearly among the variables was tested by using variance inflation factors (VIFs) prior to inclusion in any modelling. The relationships between the spatial distribution of baleen whales and spatial/environmental variables were complex, as indicated in the shapes of the functional forms of the GAMs. The results indicated that suitable environmental conditions differ for different regions of the Antarctic for the same species. Predicted spatial distribution of blue, fin and humpback whales showed expansion between the years covered by the first and second circumpolar surveys, respectively. Antarctic minke whales were distributed throughout the survey areas of the two surveys but their regions of high density appeared to be reduced from the first to the second. The spatial distribution of sei whales appeared to be constant between the first and the second, but it was difficult to come to a firm conclusion because of the small number of sightings. The spatial distribution of southern right whales expanded from the first to the second though the conclusion was doubtful because of the small sample size in the first. The changes in the spatial distributions of these species between two circumpolar surveys apparently corresponds to changes in the reported point estimates of their abundance, but the cause of the changes should be investigated using different modelling frameworks such as ecosystem models which can take account of species interactions.

Does timing matter? Detecting breeding pair numbers of penguins by UAV at different dates of a breeding season

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Unmanned aerial vehicles (UAV) have become increasingly used for wildlife monitoring worldwide and in the Antarctic as well. By application of this technology, penguin colonies can be mapped fast and with a much lower level of disturbance compared to traditional field methods. Particularly the quality of breeding pair censuses of large and remote colonies can be improved by UAV mapping.

While the processing of orthophotomosaics from hundreds or thousands of single images taken during such a flight campaign is almost a standard procedure today, the analysis of this data is not yet standardized and highly subjective. The presented study aims to develop a robust method to analyze such data objectively and efficiently.

Previous experiences have shown that it is much more efficient and objective to count the total number of all penguin individuals, than trying to distinguish incubating penguins, sitting on their nests, from other individuals like their mates or resting non-breeders. For obtaining breeding pair numbers from the total individual counts a preliminary mean ratio of the two parameters was found by groundtruthing in a pre-study. However, penguins are known to show circadian and intraseasonal rhythms, leading to a varying number of non-incubating individuals present in the colony. Since UAV operations are highly weather dependent (particularly wind and ceiling) the timing of image acquisition can rarely be exactly scheduled. Thus, it is necessary to know the range of the individuals/nests ratio and how it is dependent on time of day and season.

To examine the stability of the found ratio in dependence of time and date of data acquisition we installed time lapse cameras that observed parts of a colony of *Pygoscelid* penguins at Ardley Island (South Shetland Islands) over the course of three months (November 2016 – January 2017). Images were taken in an interval of 1 hour. The obtained results show regular patterns in the presence of non-incubating penguins over the course of a day as well as over the progress of the breeding season. For interpreting this, data of the breeding phenology will be compared with these results. The relevance of the found changes in penguin presence at the colony to the referred ratio will be discussed against the background of deriving penguin breeding pair numbers from UAV orthophotomosaics.

Diversity and distribution of polychaetes from the central basin of Admiralty Bay and adjacent areas of Bransfield Strait, Antarctica)

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Polychaetes are one of the most abundant marine invertebrate groups from unconsolidated sediments' macrofauna. Commonly found in shallow and deep waters, polychaetes exhibit great variability and flexibility of life strategies and considerable diversity in marine environments worldwide. Despite the studies already conducted in Admiralty Bay, King George Island, Antarctica, there is still little information on the macrofaunal community including polychaetes from its deepest zones. Their composition, diversity, and density were described here in relation to depth distribution within the bay, and its adjacent slope towards the Bransfield Strait. Sediment samples were collected using a box-corer in five different depths from 100 to 1100m in December 2008 on board NApOc "Ary Rongel". All sediment samples were sieved over a 0.3mm mesh size, stored in 4% formaldehyde solution, and conserved in 70% alcohol. Polychaetes from the first 2cm were counted in laboratory, identified and deposited at the Biological Collection "Prof. Edmundo F. Nonato" (ColBIO) from the Oceanographic Institute (University of São Paulo). A total of 677 specimens was recorded and 47 species identified, belonging to 25 families. The most abundant families were Syllidae (*Brania rhopalophora*, *Exogone heterosetosa*, *Exogone minuscula*), Paraonidae (*Aricidea* spp., *Levinsenia* spp.), Cirratulidae (*Chaetozone setosa*, *Tharyx* cf. *cincinnatus*) and Maldanidae (*Maldane sarsi antarctica*). There was a higher density and diversity of polychaetes within Admiralty Bay (between 100-500m) than in the Bransfield Strait (700-1100m). These differences have been probably related to the sheer slope drop subject to slides influenced by the Antarctic Circumpolar Current in the Bransfield Strait. The sediment from the strait was basically formed by silt and clay, but it showed a higher content of very fine sand than that found in the central basin of Admiralty Bay. Although the composition of polychaete species was similar to those previously recorded for the area, the dominance of families/species was different from that in the shallow zones.

A different view – the suitability of Sentinel-2 imagery for detecting penguin colonies

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Sentinel-2 is an earth observation mission developed and operated by the European Space Agency (ESA). The mission includes two satellites each carrying a 12-band multi-spectral sensor system.

In the initial setup the coverage of this system was restricted to 56° South latitude. Hence, it could not be used for science and environmental monitoring in the Antarctic. This missing opportunity was discussed during the SCAR OSC 2016 in Kuala Lumpur by the Action Group on 'Development of a satellite-based, Antarctic-wide, remote sensing approach to monitor bird and animal populations' and the Expert Group on Marine Birds and Mammals. Following the emphasized interest of Antarctic researchers during this discussions SCAR addressed a request to the European Space Agency (ESA) to consider the extension of the coverage of Sentinel-2 satellite over the area of Antarctica. The Directorate of Earth Observation Programmes of the ESA responded positive and extended the Sentinel-2 observations to a monthly coverage for the austral summer season of 2016/17.

Thus, it was possible to use the imagery of this platform for detecting Antarctic wildlife for the first time. We compared the results of monitoring penguin colonies by multispectral Sentinel-2 imagery with the results gained traditionally by high resolution imagery from other platforms and the medium resolution imagery of Landsat-8. The comparison considers the quality of the results (spatial and spectral resolution, detection quality) as well as the availability (spatial and temporal coverage, costs) of the data.

Weddell Sea benthic communities under the influence of different ice regimes

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Ice in its different forms affects benthic communities in Polar Regions directly and indirectly. In order to recognize effects of ice on benthic communities we analyzed benthos in four regions of the Weddell Sea: a) the southeastern Weddell Sea shelf (SEWSS); b) the Filchner-Rønne Outflow System (FROS); c) the Larsen A/B embayments; and d) the tip of the Antarctic Peninsula. These regions differ considerably in their ice regimes: The SEWSS is a typical high Antarctic habitat, influenced by seasonal sea ice coverage; the FROS is influenced by seasonal ice on its eastern edge, but under heavy year round ice conditions on its western edge; the Larsen A/B embayments were covered for hundreds of years by thick ice shelves, which recently disintegrated providing large areas for recolonization by benthos; and the shelf around the tip of the Antarctic Peninsula which can be considered as being unaffected by ice. Benthos in these four regions revealed distinct differences in abundance, biomass, and production values. Highest abundance values were found at the tip of the Antarctic Peninsula and along the SEWSS (2,767 and 2,535ind.m^{-2}, respectively), whereas the lowest abundance corresponded to the Larsen A/B region (682ind.m^{-2}). In terms of both, biomass and production, the southeastern Weddell Sea region showed the highest values (3,944.2g wet weight.m^{-2} and 10.3g C.$y^{-1}m^{-2}$, respectively), whereas the lowest values were found at Larsen A/B (71.08g.m^{-2} and 1.62g C.y^{-1}.m^{-2}) and FROS regions (71.08g.m^{-2} and 1.62 g C.y^{-1}.m^{-2}). A PERMANOVA showed the differences among regions to be significant in all three terms: abundance (Pseudo F=7.10; p=0.001), biomass (Pseudo F=6.01; p=0.001), and production (Pseudo F=6.28; p=0.001). These differences were mainly caused by sponges, ophiuroids and polychaetes. This study also shows pronounced differences in the structure, composition of the benthic communities in the four regions. We hypothesize that these differences are primarily due to the different sea-ice regimes in the regions.

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Large-scale distribution of coccolithophores and Parmales in the surface waters of the Atlantic Ocean

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Coccolithophores and Parmales are important functional groups of calcified and siliceous marine nanophytoplankton. Large-scale biogeographic distributions of the two groups were investigated based on 71 samples that were collected in the Atlantic Ocean (60.3°S-26.0°N). Since the large-scale distribution of nanoplankton, especially of the microscopic Parmales, has been rarely reported in the Atlantic Ocean, this study provides species-level information on these organisms, which could be of great value to biogeochemical research and help modelers to more accurately predict future climate change. Surface seawaters (1–2 l) were vacuum filtered through 0.6μm pore-size polycarbonate filters under low pressure. Each membrane with filtered particles was then transferred to a plastic petri-dish and preserved at -20°C until analysis. Qualitative and quantitative analyses for coccolithophores and Parmales were performed at 4000× magnification using a tabletop scanning electron microscope (TM3000, Hitachi). Species-level taxonomy was based on the morphological characteristics of coccoliths and coccospheres for coccolithophores, and plate configurations for Parmales. For statistical stability, at least 500 coccoliths, coccospheres and Parmales were counted in each sample. For low abundance, a minimum of 500 random selected areas were checked. A total of 48 taxa of coccolithophores and 8 taxa of Parmales were recorded, with *Emiliania huxleyi*, *Tetraparma pelagica* and *Triparma strigata* as the predominant forms. The highest abundances of coccolithophores (376×10^3 cells l^{-1}) and Parmales (624×10^3 cells l^{-1}) were observed in waters northeast of the Falkland Islands and the South Georgia Island, in close association with the Subantarctic Front and Polar Front, respectively. Three major biogeographic assemblages, i.e., the Falkland Shelf Assemblage, the Southern Ocean Assemblage and the Atlantic Ocean Assemblage, were revealed in cluster analysis. Additionally, Canonical correspondence analysis (CCA), a constrained ordination of the unimodal method, was used to estimate how much of the variation in the species distribution (response variables) could be attributed to changes in the environments (explanatory variables). CCA results indicated that temperature significantly affects the latitudinal patterns of the two algal groups. High abundances of Parmales were closely coupled with those of *E. huxleyi* in waters of the Southern Ocean with low temperature (<10°C). However, the number of coccolithophore species, along with the Shannon-Weaver diversity, significantly increased with elevated temperature, suggesting more diverse assemblages in tropical waters.

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Vulnerability of marine benthic algae to climate change in Potter Cove Ecosystem: a local case of study

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Coastal marine ecosystems are complex, dynamic and with a great biodiversity. The Western Antarctic Peninsula (WAP), including coastal islands and tidewater glaciers, is a hotspot of global warming and glacier mass loss. In this region the coastal ecosystems are changing very quickly. One local case of study is Potter Cove (King George Island/Isla 25 de Mayo), a small fjord of Maxwell Bay, where the visible melting of Fourcade Glacier has exposed new hard bottom ice-free areas available for benthic algae colonization. This small- scale system has been deeply studied during the last 25 years. Moreover, since 2010 several phycological studies were performed with the aim to detect temporal and spatial changes in the distribution of the subtidal and intertidal algae assemblages related to the new climate change scenario. Two types of studies were performed: ecological studies to analyse the spatial and temporal distribution of the algal assemblages in both, subtidal and intertidal habitats; and ecophysiological studies to detect the physiological responses of the algae to increasing melting/low light conditions in the Cove. The main results revealed a conspicuous subtidal macroalgal community developed even in close proximity to the retreating glacier where the sediment load was high. Some species as the red alga *Palmaria decipiens,* were also abundant in the most disturbed sites. *Gigartina skottsbergii* and *H. grandifolius* were adapted to rough abiotic conditions but the red one *G. skottsbergii* seemed to be more sensitive to the external stress. The vertical distribution of the subtidal species in the inner part of the cove did not fit with the typical macroalgal distribution. Instead, intertidal algal communities were mainly structured by the vertical stress gradient. The changes in temperature between seasons and years have a great influence in the structure of the intertidal algae community. Finally, integrating ecological and environmental data, a habitat distribution model was performed. This information improve the understanding of the spatial distribution and the prediction of the possible changes in the community of Antarctic macroalgae in Potter Cove in the light of global warming

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Drivers of biodiversity in Antarctic terrestrial ecosystems

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Antarctica is the coldest, highest, driest, windiest continent on Earth, a huge desert with lots of water, but almost all of it locked away as ice. Despite this harsh environment, terrestrial biodiversity thrives in ice-free areas around the coast and on mountain tops (nunataks) that represent island communities in a sea of ice (Convey *et al.*, 2014). Climate change is altering this landscape with obvious consequences for biodiversity but we lack understanding of the drivers of such change. In addition the components of climate change; increased carbon dioxide, changing temperature, wind and precipitation patterns and the impacts of ozone depletion manifest differently across the continent (Robinson & Erickson, 2015). As an example the Antarctic Peninsula experienced some of the most rapid warming on the planet at the end of the last century (Turner *et al.*, 2016) but across East Antarctica there is evidence of cooling in many coastal areas (Turner *et al.*, 2014, Turner *et al.*, 2016). In order to predict how biodiversity will change in coming decades we need to better understand the environmental drivers of biodiversity and the scales at which they operate as well as their temporal variability. Here we will attempt to synthesise current knowledge based on examples from both East Antarctica and the maritime region.

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Biogeography and macroevolution in the Arctic and Antarctic lacustrine microbiomes

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Despite similar contemporary environmental conditions, the Arctic and Antarctic regions have a different tectonic, glacial and paleoclimatic history. Combined with interhemispheric differences in spatial configuration of landmasses, these past events exerted strong constraints on the present-day patterns in the diversity and distribution of polar plants and animals. In contrast, little is known about the diversity and biogeography of microorganisms in polar lake and terrestrial habitats, though they play a considerable role in nearly all the ecosystem functions in these habitats. We performed a continental-scale inventory of benthic microbial mats in 223 (sub)Arctic and (sub)Antarctic lakes to study bipolar differences in the community structure and biodiversity of bacteria and eukaryotes by using high-throughput amplicon sequencing (Illumina MiSeq), of parts of the 16S (V1-V3) and 18S (V4) small subunit ribosomal RNA genes. Distinct biogeographic zones in both eukaryotes and bacteria emerged, with a clear differentiation between the Northern and Southern hemisphere communities. The Antarctic food-webs appeared to be less complex and truncated, with particular functional groups being absent (e.g. Annelida) while others were comparably diverse (e.g. ciliates) as their Arctic counterparts. Moreover, local OTU-richness of both eukaryotes and bacteria was significantly lower in Antarctica compared with the Arctic and decreased with increasing latitude in the Southern Hemisphere. Generalized linear models revealed that this interhemispheric diversity-asymmetry in bacteria diversity could be significantly explained by environmental properties of the lakes and differences in energy availability, while in eukaryotes, the lack of connectivity appeared to put additional constraints on OTU-richness. Also at the higher taxonomic level interhemispheric difference in diversity patterns emerged; the Arctic communities appeared to be more diverse in all eukaryotic groups (except Cercozoa) based on OTUs clustered at sequence similarities ranging between 90 and 97%. Although diversity unique to Antarctica was consistently much lower at these different OTU-clustering similarities, each OTU harboured a markedly higher amount of sequence diversity compared to those unique to the Northern hemisphere. Combined, for eukaryotes this suggests the survival of diverse and complex lacustrine food webs in glacial refugia during ice ages, probably facilitated by high dispersal rates between well-connected Northern hemisphere landmasses. In Antarctica, on the other hand, glacial-interglacial cycles and the isolation of the continent resulted in regional extinction events in some groups and selective survival or possibly radiations in others. Conversely, most bacterial groups did not exhibit these interhemispheric differences, which might indicate better dispersal and/or lower extinction rates.

Multi-domain evidence for fine-scale bioregionalisation patterns in the Antarctic lacustrine microbiome

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The geological, climatic and glacial history of Antarctica has highly influenced its terrestrial biodiversity and resulted in disjunct distributions of taxa, impoverished communities and clear bioregionalisation patterns. The Antarctic Realm is traditionally subdivided into three regions: Continental, Maritime and Sub-Antarctica. Recent meta-analyses, mainly based on the inventory of multicellular, macroscopic organisms, further allowed the recognition of more fine-scaled biogeographic entities, namely the Antarctic Conservation Biogeographic Regions (ACBRs). Although the Antarctic is dominated by microbial communities, it is unclear whether these subdivisions effectively hold true for bacteria and single-celled microeukaryotes. Such region-wide studies were mainly hampered by the absence of methods that enabled to characterize entire microbial communities with a consistent taxonomic resolution and at a relatively low cost. Here we used a large scale high-throughput sequencing approach to target the V1-V3 and V4 variable regions of the 16S (Bacteria) and 18S rRNA genes (Eukarya) in 138 lakes from 8 ACBRs and 2 Sub-Antarctic islands, in combination with morphology-based enumerations of diatom morphospecies in 453 lakes (7 ACBRs and 6 Sub-Antarctic islands or archipelagos. Clear biogeographic and macroecological patterns in both eukaryotes and bacteria emerged, including a significant latitudinal diversity gradient. In the diatoms, the incidence of endemism appeared to be high and increased with latitude, which could be significantly explained by variation in summer-winter temperature, time since deglaciation, and isolation from the nearest continent other than Antarctica. In Bacteria, biogeographical patterns were present, with a clear separation between Sub-Antarctica and the continent, but also between Continental and Maritime Antarctica. Nevertheless, also on smaller geographical scales did lakes in close proximity show higher similarities in bacterial community composition, although in particular electric conductivity was an important forcing environmental variable. In microeukaryotes were biogeographical patterns more pronounced, with much less OTUs shared between different regions. Multivariate analyses revealed that these patterns could be significantly explained by a combination of differences in environmental properties and historical factors (including the time of deglaciation and the amount of isolation), with the relative importance of both sets of predictors being different between Bacteria and the main Eukaryotic phyla. Historical factors being more important in the latter. Our results confirm that microbes exhibit patterns congruent to those found in multicellular organisms, which urges the application of effective conservation measures to prevent the admixing and homogenization of microbial communities in the Antarctic Realm.

Oceanographic and topographic conditions structure benthic meiofauna communities in Weddell Sea, Bransfield Strait and Drake Passage (Antarctic)

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The marine environment of the tip of the Antarctic Peninsula is characterised by three oceanographically distinct regions for which we linked continental-slope meiofaunal patterns and environmental drivers on a large scale. Samples for meiofauna communities and sediment analyses were collected with a multicorer, water-column data were derived from water samples and CTD recordings [1]. Meiofauna communities including individuals from 19 higher taxa were compared to a set of 16 environmental variables. We detected significant differences between the communities of Weddell Sea and those of Bransfield Strait and Drake Passage. The amount of phytopigments in the sediment, their freshness and the silt and clay content were driving factors for this separation. The highest meiofauna abundances were found at slopes in the Weddell Sea. Food banks may facilitate high standing stocks. There, the highest ever recorded copepod percentages for the Antarctic were related to the highest phytopigment contents while nematodes [2] were extremely abundant even in deeper sediment layers at stations with fresh organic material. For Bransfield Strait and Drake Passage a sampling scheme of slopes and adjacent troughs was applied. The two regions were divided into three geographical “areas” with the two “habitat” types investigated for each area. Multivariate non-parametric permutational analysis of variance (PERMANOVA) showed that Bransfield Strait and Drake Passage slope and trough meiofauna communities significantly differed between and within regions. The responsible environmental drivers were 7 out of 11 water-column and sediment-bound factors. Environmental characteristics of the benthic habitat are dependent on large-scale oceanographic conditions and are thus sensitive to changes in water temperature, salinity, sea-ice cover and the related primary production.

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Distribution of bacterial communities in microbial mats ecosystems in a latitudinal gradient at both polar regions

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Polar Regions are arguably key in planetary homeostasis. They also harbour a remarkably diverse range of freshwater bodies and probably the last pristine ecosystems on Earth. Low temperature (<5°C) not only controls which organisms exist (i.e. biodiversity), but is likely to have affected how life evolved on Earth.

Microbial mat systems are widespread in freshwater environments of Cryosphere and they often dominate the total biomass and productivity in these ecosystems Microbial mats are though the most important C and N sources on non-marine ecosystems in Antarctica. However, the knowledge about the elements conforming the community and the interaction among them is still quite limited. and requires further attention. This is an important gap in our knowledge because microbes are central to life on the planet —they perform processes no other living organisms can do – and we have little idea about how they respond to environmental cues, or how they may respond to future global ecosystem changes.

Ecosystem processes are sensitive to climate variability (natural or anthropogenic, spatial or temporal) and community composition. In that purpose, we sampled different lakes and ponds at different locations in the Canadian High Arctic (Ward Hunt Island, Ellesmere Island, Cornwallis Island/Resolute Bay and subarctic Hudson Bay) and thus in Antarctica (, Patuxent Range, Duffek Massif, Shackelton Mountains, Dry Valleys, Alexander Island and South Shetland Islands) covering either almost both latitudinal gradients from 55º to 84º.

Bacterial diversity was investigated *in vivo* along the latitudinal gradients of polar freshwater ecosystems and then analysed by high throughput tools —by using Illumina MiSeq Next Generation Sequencing technology. A set of environmental variables was extracted from MERRA dataset (re-analysed satellite data by NASA) and then correlated to community's composition by a multivariate approach.

The high-throughput results pointed out the ecological and taxonomical differences in communities' composition. Apparently, there were not any single environmental variable explaining such differences, but a selection of sub- sets of variables may act as proper proxies to those differences attending to the bacterial fraction.

New insights on biodiversity and organisms interactions in such communities will advance our knowledge about microbial ecology and possible effects of environmental change endangered polar landscapes.

Kelp rafting as a mechanism for dispersal of non- native marine species in the Southern Ocean

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Floating rafts of kelp are a major and highly visible feature of the waters surrounding the Falkland Islands and in the sub-Antarctic. It has been shown that these rafts are a mechanism of dispersal for epiflora and fauna, which can be carried great distances (Helmuth et al., 1994; Nikula et al., 2012). Smith (2002) suggests that there may be up to 70 million kelp rafts in the Southern Ocean north of the Polar Front (PF) at any one time. No study has yet examined the waters south of the PF, even though kelp rafts are often observed in this region (authors, personal observations). Here we present preliminary data on the distribution of floating kelp rafts and their infauna from sites south of the PF in the Scotia Sea and Antarctic Peninsula. We report the first record of *Macrocysis pyrifera* close to Signy (South Orkney Islands). The sample of *M. pyrifera* appeared to be fresh with no decay and new growth clearly visible at the tips. This poses an interesting question as to its origin as there are no reports of this species south of South Georgia (Griffiths and Waller, 2016). We hypothesise that floating kelp rafts may act as a mechanism of long distance transport of temperate and subantarctic marine invertebrate species across the PF. These preliminary results have importance implications for the colonisation of shallow water and intertidal habitats in the Southern Ocean in a warming environment

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Using stable isotope tracers to understand the role of mesopelagic fish in Antarctic and Southern Ocean marine food webs

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Mesopelagic fish play a key role in oceanic ecosystems and global ocean biogeochemical cycles by partitioning energy throughout the water column during diel vertical migration. In the Southern Ocean (SO), their high biomass, abundance and calorific content ensures their importance to higher trophic level squid, predatory fish, birds and mammals. Very little is known about the bio-physical determinants controlling the spatial and temporal distribution of mesopelagic fish in the open ocean regions. Here, we combine natural abundance stable isotope tracers and survey data to address key gaps in our knowledge about mesopelagic fish ecology in a large-scale region of particular ecological importance, the Kerguelen Plateau and nearby continent (hereafter 'Kerguelen Axis') in the Indian Ocean Sector of the SO. The Kerguelen Axis region contains highly productive shelves and frontal zones which support the production of large numbers of birds and mammals during the breeding season and high value finfish fisheries. A better understanding of the trophic dynamics of the Kerguelen Axis region is therefore required to evaluate the system's responses to environmental change, and for conservation and management purposes.

The trophic niches of key mesopelagic fish assemblages were investigated using bulk and amino acid compound stable isotope tracers and stomach content analysis. To investigate spatial variation in trophic interactions, fish were collected along a series of transects from the Antarctic continent to the BANZARE Bank and waters to the west and east of the Kerguelen Plateau in January to February 2016. Mesopelagic fish were sampled using an IYGPT net equipped with a MIDOC multiple-opening cod-end device. Depth stratified net hauls (from the surface to 1000 m) were undertaken concurrently with active acoustics at 36 stations.

Amino acid compound stable isotope tracers were used to examine the dynamics of the food web baseline across the Kerguelen Axis region. To capture most of the variability in the nutrient sources and environmental features present in the Kerguelen Axis region, a sub-sample of fish were analysed across a wide spatial range. Specifically, samples from dominant fish species were analysed from four zones: (1) near the Antarctic continent, (2) BANZARE Bank, and (3) east and 4 west of the Kerguelen Plateau.

The consolidated dietary data on mesopelagic fish and their zooplankton prey will be used to determine factors that differentiate fish assemblages in the region, something that is currently unknown, and to improve our understanding of the structure and function of mesopelagic components of food webs.

Diversity and biogeography of microorganisms in microbial mats of Antarctic lakes

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The BelSPO project CCAMBIO aims to study the biogeographical distribution of microorganisms (bacteria, cyanobacteria, microeukaryotes) in lacustrine microbial mats using a combination of techniques including microscopic observations, strain isolation and genetic characterisation, and molecular diversity assessments using High Throughput Sequencing of environmental DNA. The samples were collected in different Antarctic and sub-Antarctic biogeographical regions.

Preliminary multivariate analysis of >130 samples revealed strong bioregionalisation patterns in microbial eukaryotes, which are in agreement with the classical subdivision of the Antarctic Realm into Maritime Antarctica, Continental Antarctica and the Sub-Antarctic Islands generally observed in plants and animals. The biogeographic structuring was less strong between the continent and Maritime Antarctica in prokaryotes suggesting more regular dispersal events between these two regions. The Sub-Antarctic assemblages harboured more complex foodwebs, with arthropods, nematods, rotifers, flatworms and annelids as main metazoan groups. Lakes on the continent, however, were characterised by fewer metazoan groups and a greater importance of microbial herbivores and secondary consumers, including a relative high diversity of ciliates and tardigrades. A first study of the biogeography of cyanobacteria was performed on samples from microbial mats collected in 13 Antarctic lakes with different ecological features and situated in 4 distinct ACBRs. Biogeographic patterns appeared unrelated to geographic location but rather linked to lake physicochemical composition, mainly conductivity and DOC. Most OTUs (77.0%) were related to cyanobacterial lineages (defined at ≥ 99.0% sequence similarity) restricted to the cold biosphere. 21,4% were associated to lineages currently restricted to Antarctic biotopes. The results suggest a constant dispersal of cyanobacterial propagules at the regional, intracontinental level, resulting in communities mostly arranged according to environmental gradients. At the global level, on the other hand, barriers to dispersal appear to exist for some cyanobacterial lineages, especially those making up the rare fraction of the communities.

In the coming months, the molecular diversity data will be deposited into the "Microbial Antarctic Resource System (MARS)" presently developed into the webportal 'biodiversity.aq'. Better knowledge of the diversity and distribution of microorganisms will contribute to a better assessment of their resilience and local/regional responses to global change.

Trophic status of subsurface oceanic and coastal waters surrounding South Orkney Islands: A view from planktonic protists

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For the purpose of contributing to the understanding of productivity fluctuations within the first levels of the trophic web, the main goal of the study was to analyze the planktonic protist community structure at different spatial scales covering from oceanic to coastal waters around South Orkney Islands. A total of 36 samples were collected in February-March 2014 by means of Niskin bottles (10 m depth) in Scotia Bay (Laurie Island) and in the oceanic sector located at 60-64°S, 40-48°W (including the northern sector of the South Orkney Islands southern shelf MPA). Sample analyses included chlorophyll concentration and density of the main taxonomic groups of nano- and microplanktonic protists. Crustacean larvae were considered as well.

Results for open waters revealed that average chlorophyll values were extremely low (0.14 µgChl L^{-1}). Flagellates (>5µm) contributed with 99% of total abundance (mean: 1.3 x 10^6 ind. L^{-1}), followed by diatoms (5 x10^3 ind. L^{-1}), dinoflagellates (3 x10^2 ind. L^{-1}) and naked ciliates (2 x10^2 ind. L^{-1}). Silicoflagellates, loricate ciliates and crustacean larvae reached densities comparatively lower. Highest abundances of flagellates (2.6 x 10^6) were found at isolated sites along the ocean-slope transition (62°S, 46°W) and in the proximity of Coronation Island (in coincidence with the sole chlorophyll peak found in the area: < 1µgChl L^{-1}). Crustacean larvae showed up in 34% of the stations, mostly in the western sector; a single peak was detected in slope waters at the only site where dinoflagellates were absent. When excluding flagellate abundance from the analysis, a patch of simultaneous increase of other groups was observed in shelf waters SW of Laurie Island, resulting in the highest abundances of diatoms, dinoflagellates, silicoflagellates, and loricate ciliates within the area investigated. A comparison between open waters against the coastal waters of Scotia Bay revealed that average values of chlorophyll and diatom abundance were over twenty times lower in the former environment. Conversely, dinoflagellates and naked ciliates of open waters showed densities around 90 and 380 times higher, respectively. These findings suggest that while coastal waters show mesotrophic conditions in summer, the surrounding open waters rather resemble a typical oligotrophic status with average chlorophyll values even lower than those of Scotia Bay in winter. Relationships between each group and sea water temperature will be assessed.

Macroalgal-mesograzer mutualism on the Western Antarctic Peninsula

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Macroalgae dominate the hard benthos along the Western Antarctic Peninsula to depths of up to 40 m or more. Most of the macroalgae are chemically defended from a variety of macro- and mesograzers but harbor very high densities of amphipod mesograzers. The amphipods benefit from living on the large, chemically-defended macroalgae because they gain refuge from fish which are their primary predators. Most amphipod species do not consume most of the macroalgal species, but are of benefit to the macroalgae by keeping them relatively clean of epiphytic microalgae and filamentous macroalgae. Consequently this represents a mutualistic interaction between the macroalgae that structure the community and the most abundant animals living within it. However, one amphipod species does consume some of the chemically defended red algal species it is most commonly found on and is able to sequester algal metabolites for its own use as defenses against fish. This is the first known incidence of defensive metabolite sequestration in marine arthropods and represents a “cheater” in the community-level mutualism.

The importance of amphipods in the selective benthic feeding of the sister species *Notothenia rossii* and *N. coriiceps* (Pisces, Nototheniidae) in West Antarctica

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The feeding selectivity of the congeners *Notothenia rossii* Richardson, 1844 (NOR) and *N. coriiceps* Richardson, 1844 (NOC) was studied at Potter Cove, South Shetland Islands, in January-March of 2016, by means of a comparative analysis of the benthic organisms found in the fish diets with those collected along a depth gradient in rocky bottom with macroalgae (Ivlev index). Among the algae associated epifauna and in line with its high abundance and high energetic value, benthic amphipods, mainly the pontogeneiid *Gondogeneia antarctica* (Chevreux, 1906) and the lysianassid *Cheirimedon femoratus* Pfeffer, 1888 constituted the most important and frequent prey for the two nototheniids (IRI index). MacroalMacroagae were the second important food source, represented byrepresented by *Palmaria decipiens* (Reinsch) R.W.Ricker, 1987 and *Desmarestia* sp. asas dominant species. Although NOR and NOC are both benthic feeders with broadly similar diets, a statistical test between their prey (by weight) indicated a significant difference. Likewise, the diet was significantly affected by ontogeny (fish sizes) (fish sizes) and depths in both species. NOC fed more intensively on a wider diversity of benthic organisms such as algae and some algal-associated groups like gastropods and bivalves; whereas NOR fed on a higher proportion of amphipods than algae. Nevertheless, and despite their distinct morphology and ecological habits, the feeding selectivity tested with the more general Ivlev index for the primary food items, algae and amphipods, and other benthic groups similar in NOR and NOC. No substantial distinction for preference or rejection of any particular prey species between the two nototheniid species was found. Present results are compared with studies carried out at Potter Cove in the 1990s about feeding selectivity in NOC on epifauna and macroalgae. The abundance and vertical distribution of macroalgae in the sampling site in the outer cove did not change significantly over a period of two decades and probably were not greatly influenced by the retreating calving front of a glacier in the inner cove. Nevertheless, the differences in the feeding selectivity, of NOC on amphipods, observed nearly three decades later, which could apply also for the ecologically similar NOR, may be explained by variations in the assemblage of the algal-associated epifauna during this period. We hypothesize on factors that may have produced these changes in Potter Cove.

Sea-ice dynamics and food web organisation in a species rich Antarctic ecosystem: implications for biodiversity conservation and management

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The Ross Sea is considered the most pristine marine ecosystem on Earth. The absence of direct anthropogenic pressure, in association with long-term environmental stability, resulted in high levels of biodiversity, mainly represented by benthic invertebrate consumers. In turn, marked seasonality in light and sea-ice coverage control biological productivity in the region. This forced benthos to adapt to pulsed resource inputs and to prolonged periods of resource shortage. Disentangling mechanisms underlying species' ability to adapt will improve our understanding of biodiversity organisation in the Ross Sea ecosystem and our ability to predict how variations in sea-ice dynamics and resource supply will affect species composition, food web organisation, and biodiversity loss within the Ross Sea ecosystem.

We described benthic food web organization and heavy metals contamination levels in five locations across a gradient of seasonal sea-ice persistence (i.e. from early to late seasonal sea-ice break up) in medium deep waters (80-500m depth) at Terra Nova Bay, Ross Sea. By mean of stable isotope analyses of numerous taxa and basal resources, we described both feeding and competition links subtending to species coexistence and nutrient flux across trophic levels. Species' trophic niche varied across locations, with implication for food web structure. Inputs of sympagic algae to benthic consumers increased were sea-ice break up occurred earlier. Niche overlap between species, intraguild predation and food chain length all decreased where consumption of sympagic algae was higher. The coupling of energy pathways within the food web was higher were sea-ice break up occurred later and sympagic inputs to benthos was reduced. Contamination levels of species varied with both species diet and trophic level, the observed pattern being strongly dependent on the considered metal.

The study of the food web clarified the relationship between seasonal sea-ice persistence and nutrient and contaminant transfer within the ecosystem. Biodiversity organization at Terra Nova Bay seemed to be highly adapted to the seasonal sea-ice dynamics and release of sympagic production. Food web reorganization following pulsed input of resources could be a key factor allowing for the high biodiversity level in the Ross Sea. Rapid environmental modifications associated to climate change and to potential anthropic activities impacting the Ross Sea food web could represent an unprecedented ecological change which could have profound implications for food web stability and biodiversity persistence, with a high risk of species extinction and modifications in nutrient and contaminant transfer across trophic levels as a consequence.

Krill surf the trophic wave: Modelling seasonal changes in the pelagic zooplankton food web

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High latitude zooplankton communities are characterized by extreme seasonality marked by changes from high to low/no primary productivity and open water to ice covered conditions. Adaptations to survive the seasonal environment include horizontal and vertical migrations, reductions in metabolic rate and seasonal changes in diet. The latter may take the form of intraguild predation (IGP) where competitors for a resource also have a predator/prey relationship. Here we model IGP between krill and micro- and mesozooplankton and phytoplankton as a time dependent functional response to the seasonal change in primary production. The result is a predatory release on smaller zooplankton in summer which translates to energy available for krill in winter. This energy propagates up the food web during winter a phenomenon which we call a trophic wave.

Species-specific effects of passive warming in an Antarctic moss system

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In many ice-free regions of Antarctica, mosses are a dominant terrestrial vegetation, and over 100 Antarctic moss species have been described. In this research we investigated the impacts of passive warming by Open Top Chambers (OTCs) in moss-dominated ecosystems on Fildes Peninsula, King George Island, Antarctica, a region of increased climate warming. We compared leaf morphology, photochemical measurements, sexual reproductive effort, and invertebrate communities between OTC and control moss communities for two moss species, *Polytrichastrum alpinum* and *Sanonia uncinata*, that make up over 65% of the vegetative cover in the area. We found distinct reproductive shifts in *P. alpinum* under passive warming compared to those without warming: warmed mosses invested more towards primary productivity and gametangial development. On the other hand, *S. uncinata* was never reproductive during the experiment. Moss communities under warming also had substantially larger invertebrate communities than those in control moss communities, and invertebrate communities were significantly affected by moss species and moss reproductive effort. Our results suggest that warming will substantially change the reproductive output of moss systems and change moss ecosystems from the bottom up, but to understand these effects we must understand the complex, mechanistic role that dominant moss species play in the Antarctic system.

New insight for Antarctic marine benthic food web: a case study in a rapid warming glacial cove in King George Island

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We report a food web characteristic of shallow-water benthic communities in Marian Cove (MC), a typical Antarctic fjord in King George Island (KGI). The KGI is maritime Antarctic and it belongs to WAP where warming and deglaciation on land is proceeding fast. Rapid retreating of tidewater glaciers has been reported in MC (~1.7km for the last 60yrs), and a recent survey revealed a striking phenomenon, massive benthic diatom blooming on the shallow sea floor. This phenomenon was distinct from the previous reporting on benthic diatom blooms in the water column due to its large scale on benthic substrates, in particular with its presence as being attached to a variety of common megabenthic fauna, mostly filter feeders such as ascidians, demosponges, bryozoans, tube-dwelling polychaetes, and bivalves etc. Aiming at finding whether the benthic diatoms are actually consumed as the primary food source by these filter feeders, we analyzed $\delta^{13}C$ and $\delta^{15}N$ ratios of various common filter feeders along with their potential food sources (benthic diatom mass, macroalgae, and surface sediment deposit etc.). We also analyzed other fauna at higher trophic levels to get a better understanding on trophic structure in the fjord benthic communities. The isotopic values of the most filter feeders analyzed were very close to the values of benthic diatoms, demonstrating that the benthic diatoms were utilized as the primary food source by the associated filter feeders. Analysis also showed that even some deposit feeders (the polychaete *Flabelligera* sp.) and omnivores/browsers (*Sterechinus* sp. etc.) seemed to rely in part on benthic diatoms. Trophic levels determined from the $\delta^{15}N$ values indicated that the benthic food web in this glacial cove supported up to 4 trophic levels with starfish and isopods at the apex. Thus, our study showed that the benthic diatoms are primary food items for herbivorous consumers in the rapid warming fjord. Other findings from this study also contributed to enhance our knowledge on the trophic ecology of Antarctic fjords. Further studies are, however, necessary to understand driving forces or underlying mechanisms for massive blooming of these benthic diatoms. Elucidating whether the benthic diatom blooming is related to the climate-induced processes (e.g. introduction of trace elements along with ice-melt water) would provide a new prospect for future scenario in the fjord ecosystem.

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The food web of Potter Cove (Isla 25 de Mayo/King George Is.): complexity, structure and function

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The study of food web structure and complexity is central to better understand ecosystem functioning. A food-web approach includes both species and energy flows among them, providing a natural framework for characterizing species' ecological roles and the mechanisms through which biodiversity influences ecosystem dynamics. Here we present for the first time a high-resolution food web for the Potter Cove marine ecosystem (Isla 25 de Mayo/King George Is.). We studied eleven food web properties to analyze network complexity, structure and topology. We found a linkage density of 3.4, a connectance of 0.04 and 45% of omnivory, as well as a path length of 1.8 and a clustering coefficient of 0.08. Comparison of food web properties with other marine food webs revealed a particular combination of characteristics for Potter Cove ecological network: middle size (S = 91), low linkage density and connectance (not being an artifact of resolution or assembly procedure), low omnivory percentage, short path length and low clustering coefficient. Furthermore, relating the structure of the web to its dynamics, we found that the degree distribution (in- and out-links) fit the best to an exponential model. For two of the three more connected functional groups, competition overlap graphs (only considering predator species) reflect high trophic interaction between demersal fish and niche specialization according to feeding strategies in amphipods. On the other hand, it can be inferred from the prey overlap graph (only considering prey species) that multiple energy pathways of carbon flux exist across benthic and pelagic habitats in Potter Cove ecosystem. Although alternative food sources might add robustness to the web, network properties results (low linkage density, connectance and omnivory, and short path length) points to fragility and potential trophic cascade effects. Our results suggest that species with a high number of links (e.g. *Notothenia coriiceps*, *Ophionotus victoriae*, *Gondogeneia antarctica*) could be considered keystones for the robustness of Potter Cove ecosystem.

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Increased sea ice cover disrupts food web structure in Antarctic coastal benthic ecosystem

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Antarctica currently undergoes strong and contrasted impacts linked to climate change. While the West Antarctic Peninsula is one of the most rapidly warming regions in the world, resulting in sea ice cover decrease, the sea ice cover of East Antarctica unexpectedly tends to increase. Here, we studied shallow (0-20 m) benthic food web structure on the coasts of Petrels Island (Adélie Land, East Antarctica) during an event of unusually high spatial and temporal (two successive austral summers without seasonal break-up) sea ice cover. Using time-tested integrative trophic markers (stable isotope ratios of carbon, nitrogen and sulfur) and state-of-the-art data analysis tools (Bayesian ecological models), we studied the structure of the food web associated to benthic macroinvertebrates communities. In total, 28 taxa spanning most present animal groups (sponges, sea anemones, nemerteans, nematods, sipunculids, sessile and mobile polychaetes, gastropods, bivalves, pycnogonids, crustaceans, sea stars, sea urchins, brittle stars and sea cucumbers) and functional guilds (grazers, deposit feeders, filter feeders, predators, scavengers) were investigated.

Our results indicate that the absence of seasonal sea ice breakup deeply influences coastal benthic food webs. We recorded marked differences from literature data, both in terms of horizontal (i.e. primary producers and resources supporting animal populations) and vertical (i.e. trophic level of the studied consumers) structure of the food web. Overall, sympagic algae dominated the diet of many key consumers, and the trophic levels of invertebrates were low, suggesting omnivore consumers relied less on predation and/or scavenging than in normal environmental conditions. Surprisingly, few animals seemed to feed on the extremely abundant benthic biofilm, whose exceptional development was also presumably linked with the peculiar sea ice conditions. Comparison of data obtained in the austral summers of 2013-2014 (first year without seasonal breakup) and 2014-2015 (second year without seasonal breakup) clearly showed that the observed trends were linked to actual temporal changes in invertebrate feeding habits rather than with other potential ecological drivers. Our results provide insights about how Antarctic benthic consumers, which have evolved in an extremely stable environment, might adapt their feeding habits in response to sudden changes in environmental conditions and trophic resource availability. They also show that local and/or global trends of sea ice increase in Antarctica have the potential to cause drastic changes in food web structure and therefore impact benthic communities.

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Krill vs salps at the regional scale: the effect of habitat overlap between *Euphausia superba* and *Salpa thompsoni* on ecosystem energy flow in East Antarctica

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Through fluctuations in abundances of *Salpa thompsoni* (salps) and *Euphausia superba* (Antarctic krill), the Indian Sector of the Southern Ocean may experience a substantial change in energy flow to higher trophic levels. By how much might these lower trophic level dynamics alter energy flow, and how do we measure this? To quantify the extent of potential change, we must first i) determine what environmental conditions favour high salp abundances in the region, (ii) identify the potential for niche overlap between Antarctic krill and salps and (iii) quantify and compare ecosystem energy input from Antarctic krill and salps. We present an up-to-date nutritional profile of Antarctic krill and *S. thompsoni* populations in the region, which suggests that, under high salp abundance scenarios, higher trophic level species may be faced with a food source with <50% of the energy content of Antarctic krill. We also use stable isotope and gut content analysis to identify potential niche overlap, including competition for diatom species between Antarctic krill and salps. Results from statistical modelling elucidate the role of the Antarctic Circumpolar Current and sea-ice extent in the location and magnitude of recent *S. thompsoni* blooms. Results from this work provide much needed quantitative estimates of the ecosystem input from *S. thompsoni*, which may be a major determinant of the future structure and functioning of the Southern Ocean ecosystem.

Influence of different water masses on the shaping of the coastal Antarctic micro-eukaryotic community

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The phytoplankton community of the coastal western Antarctic Peninsula is rapidly changing due to shifts in the marine environment resulting from climate change. Often suggested is a shift from a classical, diatom-dominated ecosystem to one dominated by small flagellates, primarily cryptophytes. These shifts are considered to be related to different watermasses, for example more saline, nutrient-rich water from the open ocean or fresher, nutrient-poor glacial melt water. Yet the shift in phytoplankton community composition is classically investigated using a crude pigment fingerprinting technique (HPLC and CHEMTAX) which can distinguish between cryptophytes, haptophytes and diatoms but lacks the ability to resolve the community to greater taxonomic depths.

In our research we explore which “species” within the major phytoplankton groups are responsible for the aforementioned trends. We suspect that these trends are driven by only a few species which potentially holds great consequences for the food web build on these primary producers. As such, we combine two methods of community analysis: pigment fingerprinting and high-throughput 18S sequencing. We obtained greater taxonomic depth while ensuring compatibility with the long-term data sets. Moreover, we exploited Ryder Bay, location a long-term data set (RaTS), as a natural laboratory to minimize the temporal variability. As such, we sampled three different stations and depths (2, 15 and 75m) on 20 events over two summer seasons (2012-2014). These stations offered a gradient in influence of the difference water masses (sea ice or glacial melt, and mCDW) while phytoplankton communities were in the same stage of succession.

Initial analysis (CCA) on abundances of the CHEMTAX-derived phytoplankton groups (at 2 and 15m) confirm a preference of cryptophytes for positive sea water temperatures, and haptophytes for high salinity and density when compared to diatoms. Moreover, flagellates in general were associated with more unstable and nutrient rich water columns. We observed linear relationships between CHEMTAX-derived relative abundances and 18S sequence counts of members of the major groups. Partitioning of the CHEMTAX derived abundances results using the annotated sequences on MED (Minimum Entropy Decomposition) nodes showed different preferences for watermasses (including glacial melt) of members within each of the major phytoplankton groups. For example, the two most dominant members of the haptophytes showed contrasting temperature preferences. Thus, while HPLC-CHEMTAX is successful in capturing major dynamics, sequencing allows to identify the underlying dynamics in the less abundant components of these groups. These results refine our understanding of the phytoplankton community dynamics and implications thereof.

Soil food webs in carbon-limited soil rapidly respond to elevated carbon in a field microcosm experiment in Taylor Valley, Antarctica

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The McMurdo Dry Valleys soils are an extreme cold desert habitat: low temperature, low moisture, low organic matter, high pH, and high salinity. Their food webs are composed of basal levels of cyanobacterial mats, bacteria, archaea, fungi, and higher levels of protozoan and metazoan consumers (i.e., two mite, one springtail, two rotifer, two tardigrade, and four nematode species). Much of the metazoan biodiversity occurs in wetted stream and lake margins where cyanobacterial mats provide carbon (C). However, wet soil is ~5% of total habitat and >95% is dry soil. A single endemic nematode species, *Scottnema lindsayae*, dominates dry soils. With low contemporary primary production, these soils are extremely C limited (15 to 35µmol g^{-1} soil). Yet, climate-driven increases in biotic and hydrological connectivity across the landscape are expected to alter C and nutrient dynamics, which could lead to increased available C, altering dry soil habitats and ultimately the distribution and abundance of *S. lindsayae* and its influence on ecosystem structure and functioning.

We asked: Will elevated C affect the dry soil food webs? We hypothesized that soil food webs would incorporate an influx of C, but incorporation in higher trophic levels would take several active seasons to reach significance due to low temperatures that limit feeding, metabolism, and growth. To test our hypothesis we established a field-based microcosm experiment to trace the flow of increased C through the soil food web near Many Glaciers Pond in Taylor Valley, Antarctica. Briefly, 19.6mg of ^{13}C-enriched mannitol (99.9 atom %) was added to 50g of fresh, unsterilized soil for each of 48 microcosms. In November 2014, microcosms in 50mL falcon tubes were established in the field. Half of the microcosms were collected after one summer (January 2015), the remaining were collected after the second summer.

Here we present the metazoan results from the first year of our experiment. Results showed the metazoan community consisted of one nematode species, *S. lindsayae.* Population density of *S. lindsayae* was 1003±274 individuals kg^{-1} dry soil, comparable to nearby field data. Two months after C addition, *S. lindsayae* had incorporated mannitol-C in significant amounts. Nematode biomass from all samples was significantly enriched in ^{13}C vs. control samples. Overall, $\delta^{13}C$ was 21,760.07±3488.52‰ and total nematode-C was 15.07 to 24.08% (95% CI) mannitol-derived. This research reveals that Dry Valley food webs can rapidly respond to increased available C and incorporate this significantly into higher trophic level biomass (e.g., *S. lindsayae*).

Macromolecular composition in Antarctic microalgal communities

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Marine microalgae form the base of the marine food web and as such, are the primary source of macromolecules (including lipids, proteins and carbohydrates) in the marine environment providing the nutrients and energy for higher trophic levels. Antarctica, with its vast circumpolar ocean, is a highly dynamic environment, where marine organisms are exposed to seasonal shifts in environmental conditions from deeply mixed waters in summer to frozen ice sheets in winter (Gleitz & Thomas 1992). Yet Southern Ocean and Antarctic microalgae support one of the most biologically productive ecosystems on Earth (Busalacchi 2004). This is because Antarctic microalgae have evolved adaptations to survive and thrive under highly dynamic and often extreme environmental conditions. This changeable environment strongly influences phenotypic traits such as, photosynthetic performance and macromolecular composition, traits that underpin nutrient cycling, grazability and thus, energy transfer through trophic levels. Here we assessed community composition, photosynthetic performance and macromolecular composition (lipids, carbohydrates and proteins) of microalgal cells sampled from the coastal waters and sea ice, around Prydz Bay, Antarctica, as well as the microalgal community from a hypersaline lake in the Vestfold Hills. Community diversity was greatest in samples from the coastal waters comprising of diatoms, dinoflagellates, silica flagellates and haptophytes. In contrast, the sea ice was dominated by diatoms, while the hypersaline lake contained only one chlorophyte species, *Dunaliella sp*. The photosynthetic efficiency and photoprotective capacity of the microalgal communities differed significantly between locations and chl *a*-specific gross productivity was four-fold greater in the coastal community than the sea ice. Single-cell macromolecular profiles performed on the most dominant species from each location revealed that at the community level, the sea ice had a greater amount of saturated and unsaturated fatty acids, while the hypersaline lake had almost double the carbohydrate content of the sea ice and coastal communities. Within each community there were species-specific differences in macromolecular composition with coastal species varying in carbohydrate content while sea ice species showed differences in lipid and protein content. These findings demonstrate that variability in nutritional quality of the base of the food web is largely dependent on environmental condition and community composition. Furthermore, the high lipid content in the sea ice diatoms emphasises the importance of sea ice assemblages for the Antarctic marine food web, providing a concentrated source of energy for Antarctic keystone grazers such as krill.

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A new method based on isotopic trophospecies to reconstruct food web of Terra Nova Bay, Ross Sea

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Ross Sea, the largest protected marine area in the world, is considered a pristine ecosystem and biodiversity hotspot. Here, biodiversity is strongly influenced by key environmental drivers associated with climate change, such as temperature and sea-ice coverage [1]. Thus, it is expected that warming and changes in sea-ice dynamics will be directly reflected on the architecture of biodiversity [2]. Yet the current lack of knowledge of it impairs predictions on impacts of climate modification. The study of food webs is important to understand how climate change pressures could affect mechanisms that regulate Antarctic ecosystem key processes such as productivity, stability, vulnerability to biodiversity loss and circulation of contaminants [3-4]. Antarctic food web is still difficult to reconstruct on a taxonomical basis. While morphological and genetic approaches remain essential, in Antarctica there are many cryptic species not yet well defined, whose trophic role is still unknown. Since ecosystem processes, as the transfer of energy and matter, depend firstly on individual foraging choices within the community, the trophospecies (*sensu* 5) could be effective to reconstruct Antarctic networks, overcoming the low resolution obtained on a taxonomical basis at the whole food web level. Several samples of basal resources, invertebrates and fish were collected at two sites differing in the seasonal timing of the Ross Sea ice break-up: Adelie Cove, with short seasonal sea-ice persistence, and Tethys Bay, with longer seasonal sea ice persistence. Accordingly, differences in basal resource inputs are hypothesised between sites [1-2] Each single sample was classified taxonomically and analyzed isotopically. Then the data were used for the food web reconstruction according to two methods: a traditional “taxonomic” method and an innovative "isotopic-unit” method. The latter is based on the "trophospecies concept”, in which groups of individuals that share the same position along food chains and resources axis (based on $\delta^{15}N$ and $\delta^{13}C$ values respectively) are expressed in isotopic-units. These sets of individuals are represented in the isotopic bidimensional space by squares having a $\delta^{13}C$ and $\delta^{15}N$ ranges equal to 1‰. The emerging output of mixing models was a grid where each isotopic-unit can be a resource and/or a consumer. Food web metrics were then calculated and compared between methods. Robustness of the comparison of food web metrics highlights the effectiveness of the trophic-functional method as a promising simplified and time-saving approach to develop reliable description of trophic pathways and biodiversity architecture in Antarctica.

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Benthic food web structure of Andvord Bay (Antarctica) revealed by fatty acids and stable isotopes

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The food web structure of marine communities is fundamental to understanding organism interactions as well as nutrient cycling and energy flow. Traditionally, bulk stable isotopes (^{13}C and ^{15}N) have been used to determine both primary carbon sources and relative trophic position for marine food webs. Similarly, fatty acids can be traced from prey to consumer to understand trophic linkages and the dietary composition of fauna. The combination of fatty acid and stable isotope techniques has proven particularly powerful in determining the trophic structure of benthic communities. This study aims to expand previous stable-isotope work (Honig and Grange, unpub. data) conducted in Andvord Bay, a glaciomarine fjord with a rich benthic community, by incorporating fatty acid analyses along a fjord-to-shelf gradient into analyses of the benthic food web. Samples of megafaunal tissue and various food sources including macroalage, ice algae, phytoplankton, zooplankton and surficial sediments were analyzed for their fatty acid and bulk stable isotopic compositions. Comparison of the resulting profiles revealed trophic relationships and diets of megafauna both in Andvord Bay and on the adjacent open shelf. While results remain in the early stages of analysis, these data suggest differences between fjord and shelf food sources utilized by benthos. These data will also be used to assess inter-annual variability in fjord and shelf benthic food-web structure and to provide a baseline to evaluate climate related changes in the future.

Biological diversity in Antarctic microbial mats subjected to a trophic gradient

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Microbial mats represent the most abundant and diverse ecosystems of non-marine polar zones. They are complex communities that develop close relationship leading to the formation of dynamic, and sometimes very structured, communities. In addition to representing the largest non-marine biomass fraction in many of these polar ecosystems, they are able to form soils and allow the installation of more complex communities by the contribution of nutrients and structuring of the soils, becoming crucial in maintaining further developments. A great diversity of microorganisms, such as diatoms, green algae, bacteria, viruses, tardigrades, ciliates, nematodes and rotifers, among others, contribute to the development of these micro-ecosystems. Although in recent years polar microbial mats have been investigated by different groups and much has been published on the matter, the differences resulting from growing under different trophic conditions are unknown.

Here we present a comparative study of the structure, trophic relationships and prokaryotic and eukaryotic community of cyanobacterial microbial mats along the Antarctic Peninsula, associated to a trophic gradient established from oligotrophic (not influenced by animals) to eutrophic conditions (influenced by animals). Different optical and electronic microscopy techniques have been used, as well as metagenomic analysis, stable isotopes to establish the trophic structure and the interactions among different groups within the microbial mat. Results show that eutrophic systems, being subjected to a greater degree of disturbances, are less complex and can be more sensitive to alterations (climatic, infections or other ecological imbalances), giving them a role as bioindicators of perturbation effects in polar regions.

The methanogenic potential of Antarctic wetlands: effect of temperature increase on microbial community structure and activity.

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Methane is a powerful greenhouse gas produced under anoxic conditions in natural ecosystems such as lake sediments, wetlands or peatlands, through organic matter degradation by methanogenic Archaea in combination with bacterial hydrolyzers and fermenters. The optimal temperature for methane production is usually mesophilic, but increasing attention is paid to the methanogenic potential of cold environments such as Arctic tundra and thawing permafrost, where active methanogens have been reported. In the context of climate change, high-latitude ecosystems are being more strongly affected by global warming: methane emissions are expected to increase as a result of enhanced microbial activity and enhanced release of available organic matter. However, little is known about the methanogenic potential of Antarctic ecosystems, the microbial key players of the process and their response to temperature changes.

In this study, 41 soil and sediment samples were collected from coastal wetlands among seven islands from the South Shetland and the Antarctic Peninsula during the 2013 summer expedition of the Chilean Antarctic expedition (INACH ECA 49). The extensive sampling provided a high range of pH, temperature, organic matter and nutrient content, resulting in diverse potential niches for methanogens development. The targeted methanogenic activity could be found in most samples under controlled incubation conditions at close-to-natural temperature (5°C), with highly variable levels, usually higher in superficial than deep sections. The effect of incubation temperature on methanogenic activity was evaluated between 5°C and 37°C, resulting in optimal conditions between 20-30°C. Different levels of tolerance to low/high temperatures could be observed according to the sample origin and physicochemical characteristics.

Microbial communities were analyzed by qPCR of four different methanogenic families and Illumina MiSeq sequencing of bacterial and archaeal 16S rRNA genes, leading to the identification of discriminant genera explaining the sample segregation, such as *Methanocorpusculum*, *Gelidibacter* and *Flavobacterium*, previously described as psychrophiles. Nitrite, ammonium and phosphate concentrations were the strongest driving forces of the community at 5°C. The temperature shift from 5 to 37°C had a stronger influence on microbial community composition than the geographic origin, resulting in a decrease of microbial abundance and diversity, and significant population shifts at the phylum level. The most remote sampling sites (O'Higgins station, Antarctic Peninsula) displayed a clearly distinct community and methanogenic activity profile in response to temperature change.
This study evidenced the methanogenic potential of Antarctic wetlands, identified the key players of methane production and demonstrated the effect of temperature increase on both microbial community structure and activity.

Structure and function of natural microbial community in a harbour of an Arctic glacial fjord (Kongsfjorden, Svalbard)

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The Kongsfjorden Fjord, located in Svalbard Islands (Norway), is an important marine ecosystem widely investigated by the international scientific community. This area is considered the most representative than other open fjords in the Arctic and it is affected by the inflow of Atlantic waters as well as by glacier melt water runoff (Hop et al., 2002). Prokaryotic communities play a key role in relevant processes such as carbon fluxes, energy transfers and nutrient regeneration and can be viewed both as sentinels and amplifiers of global change. In this context, further research is needed to quantify the role of these microorganisms in the flux of organic matter in the Arctic marine food web. In this study the main principal chemical-physical parameters, bacterial abundance (DAPI, CFU and MPN count) and structure (16S rRNA clone libraries) and extracellular activity were analyzed at 3 sites in Ny-Ålesund harbour (Svalbard islands), 2 for seawater and 1 for sediment samplings. The metabolic function of the microbial community was studied through isolation of psychrophilic heterotrophic bacteria and measurements of potential enzymatic activity rates on organic polymers (leucine aminopeptidase_LAP, beta-glucosidase-GLU and alkaline phosphatase-AP) by fluorogenic substrates.
Data of microbial abundance obtained revealed as general uniformity between (seawater) samples in study; values, generally larger of a logarithmic order, were observed against the sediment sample.
Phylogenetic analysis of community structure reveals as Gamma-Proteobacteria and Alpha_proteobacteria were the most abundant groups. Many of analyzed sequences were affiliated to clones identified in cold areas, in ports, in biofilm covering, antifouling paint and in oil contaminated facility.

Phylogenetic analysis of thirty-five isolated bacterial strains revealed the affiliation of sequences to *Pseudoalteromonas* sp. isolated in Kongsfjorden, *Psychrobacter immobilis*, *Vibrio* sp., *Sulfitobacter* sp. identified in Arctic and Antarctic waters)seawater, *Leucobacter komagatae*, *Flavobacterium frigidarium* and *Polaribacter* sp. These results highlight different signs of human settlement in sampling sites.

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Molecular and physiological characterization of five psychrotrophic hydrocarbon-degrading *Alcanivorax* sp. strains isolated from Antarctic coastal seawater (Terra Nova Bay, Ross Sea)

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Study of Antarctic bacteria, especially hydrocarbon-degrading strains (Yakimov *et al*., 2004, Gentile *et al*., 2003; Gentile *et al*., 2006), stands as an extremely interesting ecological challenge, especially if aimed to an environmental monitoring, maintaining the preservation of these unique ecosystems. This study is based on the isolation (from Antarctic coastal waters) and characterization (by physiological and molecular methodology) of five psychrotrophic strains related to obligate hydrocarbonoclastic bacterium *Alcanivorax* sp. In particular for each strain in study, complete *16S rDNA*, *alk-B* and *P450* genes sequencing were performed. Moreover, analysis of BIOLOG microplates (to test ability to oxidize different carbon sources), API 20E, oxidase and catalase (to evaluate biochemical isolates profile), mobility and Gram staining were carried out. Temperature range for growth was determined by incubating each strain in ONR7a amended with 1% (w/v) of acetate at different experimental temperatures (4, 15, 20, and 25°C). Growth ability in hydrocarbon mixture was evaluated by inoculation of strains in ONR7a amended with 1% (w/v) of crude oil and incubation at 4 and 25°C. Biosurfactant production tests (drop collapsing and oil spreading) and emulsification activity test (E_{24}) were also performed. Complete *16S rDNA*, *AlkB* and *P450* genes sequencing of isolates showed a high similarity to the same genes of others *Alcanivorax* species. Metabolic prophyles (BIOLOG) showed no particular differences compared to *Alcanivorax borkumensis* wild type. Growth analysis both with acetate and tetradecane demonstrated a great versatility of isolates to develop at temperatures from 5 to 25°C, while no growth in Marine Agar medium was observed. Biodegradative tests of strains reflected their capability to grow at different temperatures. At 4°C, for almost all strains, a beginning of biodegradation processes at the end of the lag phase (from 4 to 10 days) was observed; at a temperature of 25°C, hydrocarbon degradative efficiency was evident in the early days. All strains showed biosurfactant production and emulsification activity. Isolation and characterization of Antarctic hydrocarbon-degrading bacterial strains acquires a particular importance both from a biotechnological that environmental point of view, since it may be conceivable the application of these microorganisms for the recovery of contaminated polar areas.

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The hidden life of Antarctic rocks

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Rocks represent the last refuge for life in some of the most extreme environments on Earth, such as the Antarctic. Microbial communities that inhabit rocks are known as endolithic. These organisms are able to colonize cracks, fissures and pores of rocks as well as alter them, directly and indirectly, through physical and chemical interactions. On a global scale, these interactions affect the element cycles of the biosphere(Wierzchos et al. 2012)(Horath and Bachofen 2009)(Warscheid and Braams 2000).
Our work aims at characterizing the functional diversity of microbes inhabiting Antarctic rocks, focusing on bacterial systems involved in metal homeostasis. Also, we intend to determine bacterial capacity to produce pigments and to know whether pigment production depends on metal tolerance.
In order to discover new functions involved in metal homeostasis in Antarctic endolithic bacteria, and taking into consideration that earlier studies demonstrated a general recalcitrance to cultivation for endolithic we employ complementary approaches(Lorenz and Eck 2005)(Cowan et al. 2005)(Martiny et al. 2011).
We have already identified culturable bacteria present in two samples of different Antarctic rocks. Rocks have been identified as basaltic andesites. As expected, number of colony forming units was several orders of magnitude below of that obtained from other environmental samples (water, ice, sediment, mats). Most of the strains belong to Actinobacteria and were taxonomically related to *Arthrobacter* and *Mucilaginibacter* and in less extent to *Rhodococcus*, *Hymenobacter*, *Frigobacterium* and *Cryobacterium*. Interestingly, many isolates showed low identity (96% or less) with available public sequences, which may be a reflection of the apparent novelty of the microorganisms colonizing this niche. Furthermore, we detected isolates able to grow and to produce enzymatic functions involved in metal homeostasis at 4°C. We identified many isolates resistant to Cu(II) 1mM, Mn(II) 3mM, some isolates resistant to Ni(II) and Zn(II) 1mM, Ag(I) 50µM and Co(II) 200µM. Interestingly most of the isolates were pigmented and almost all pigments were identified as carotenoids. We are currently optimizing the methodology for the construction of a functional metagenomic library and for the analysis of metagenomic DNA. These methodologies will be used for the evaluation of the richness and diversity of microbial endolithic communities as well as for the identification of selected functions such as metal resistance and pigment production.
Despite its relevance, our understanding of these environments is just at the beginnings. Generation of knowledge on bacterial endolithic communities present in Polar environments will certainly contribute to fields such as ecology, biogeochemistry, biotechnology, bioremediation, climate change and astrobiology.

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Fungal diversity in Antarctic cryptoendolithic communities by NGS

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Endolithic life is one of the most spectacular adaptation of microbes to environmental constraints of the Antarctic desert and the predominant life-form in Continental Antarctica (Nienow et al., 1993). The endolithic microbial communities host among the most resistant and adapted organisms known to date (Onofri et al., 2008; 2012), evolved over a timescale of evolutionary significance in complete genetic and geographic isolation. The biodiversity of these microbial communities and its variation with the environmental pressure remain still unknown. Sandstone is the best substrate for cryptoendolithic microbial communities supplying protective niches to prokaryotic and eukaryotic microbes and allowing the spreading at higher altitudes and longer sea distances (Zucconi et al., 2016). This study focuses on fungal diversity of these communities and its variation along gradients of environmental extremes due to altitude and sea distances. Thirty sandstone samples were collected during the XXVI (2010-2011) Italian Antarctic Expedition from 12 different localities in the Victoria Land, ranging from 1000-3100m asl and 29-96km sea distance. The ITS amplicon sequencing of environmental DNA was obtained by Illumina MiSeq; taxonomy, alpha and beta diversity were analyzed by QIIME software 1.7 and are here presented. Ascomycota, Basidiomycota and Mucoromycotina were found in all samples with a large predominance of ascomycetous lichens in the Class Lecanoromycetes. The Class Capnodiales, to which most of Antarctic black fungi belong, was recorded with a much lower frequency of total diversity.

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Metabolic changes underpinning the life phase transitions of snow algae in Antarctica

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Snow algae communities consist mainly of green algal species of the *Chlamydomonas* and *Chloromonas* genera. They have a bi-phasic life cycle consisting of an active reproductive motile stage seen as green patches in the snow and a dormant encystment phase during which the cells accumulate the red keto-carotenoid astaxanthin as a photoprotectant, giving rise to red snow patches. We measured the metabolic composition of snow algae in both green and red phases, from samples taken in the field at various locations in Antarctica (compared to laboratory grown samples) during the 2014/15 austral summer season. We also tested for evidence of spatial variation in the metabolic composition of each algal patch.

Our data showed that the metabolic composition of the cells was the same (when expressed on a per cell/dry weight basis) from four geologically distinct but spatially close locations in the vicinity of Ryder Bay. However, our data also show a high degree of patchiness in the snow melt between the locations where snow algae communities occurred, from mean values of 0.5g dry algae per L of snow melt at Lagoon Island to 3.25g dry algae per L of snow melt at Léonie Island. There was a corresponding site variation in the chlorophyll and lipid content of the snow melt between Lagoon Island and Léonie Island. Our lipidomic data showed that the snow algae were rich in 16:4, 16:1, 16:0, 18:1 fatty acids and that Fourier transform-infrared spectrometry (FT-IR) and gas chromatography-mass spectrometry (GC-MS) were able to detect detailed changes in lipid, carbohydrate and protein chemistry in the cells during encystment. This provides the means to study environmental factors important in the green-red transition that characterises the life cycle of these snow algae.

Biogeographic patterns and genomic adaptation of benthic cyanobacteria in Antarctic lakes

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Cyanobacteria are a major component of Antarctic lacustrine ecosystems, usually forming conspicuous complex benthic communities known as microbial mats (Singh & Elster 2007; Vincent & Quesada 2012). Despite their importance as the dominant phototrophs, a comprehensive understanding of the ecology, function and biogeography of Antarctic cyanobacteria is far from being achieved. The present study assessed (a) the biogeographic patterns of benthic cyanobacterial communities in 13 Antarctic lakes and (b) the genomic make-up of the strain *Phormidesmis priestleyi* ULC007, which belongs to a widely distributed Antarctic lineage. Community-level profiling using 454 pyrosequencing of the 16S rRNA revealed communities largely dominated by phylotypes ascribed to the order Pseudanabaenales. Biogeographic patterns were unrelated to geographic location and highly connected to lake physicochemical composition, mainly conductivity and DOC content. The vast majority of phylotypes (79 OTUs, 77.0%) were related to cyanobacterial lineages (defined at ≥ 99.0% sequence similarity) restricted to the cold biosphere (i.e. polar and alpine biotopes). These results suggest that cyanobacteria are widely distributed within Antarctica, resulting in communities mostly arranged according to environmental gradients. At the global level, on the other hand, barriers to dispersal appear to exist for some cyanobacterial lineages, resulting in a high degree of endemism within the Antarctic continent. In order to gain further insights on the functional diversity and adaptation of Antarctic cyanobacteria, the genome of *P. priestleyi* ULC007 was sequenced. This strain was isolated from Lake Bruehwiler in the Larsemann Hills (Taton et al. 2006; Lara et al. 2017) and, according to our pyrosequencing analysis, appears restricted to Antarctic lakes with low TOC content. Duplication patterns of genes involved in stress response (e.g. *dnaI*, *dnaK*, *recF*, *cspA*) and circadian clock (e.g. *kaiA/B/C*, *cikA*, *pex*, *sasA*) were investigated and compared with other publicly available genomes. Preliminary analysis grouped *P. priestleyi* ULC007 with other extremophilic strains, giving further support to the role of gene duplication in the adaptation to extreme environmental conditions. Additional analyses on evolutionary mechanisms (e.g. horizontal gene transfer, genome rearrangements) are being carried out and characterisation of other genomes is in progress, including cyanobacterial strains isolated from hypersaline Antarctic lakes. This will provide a better understanding of the survival strategies developed by mat-forming cyanobacteria in harsh conditions, contributing to the better understanding of the ecological and biogeographic ranges of Antarctic cyanobacteria and potential impacts of environmental changes.

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Influence of hydrothermal activity in microbial diversity in deep-sea marine sediments at Bransfield Strait, Antarctic Península

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The undersea trough of Bransfield Strait It was formed by rifting and hosts a chain of submerged seamounts of volcanic origin. Ongoing rifting has caused recent earthquakes and volcanism. Hydrothermal sites in the Bransfield Strait potentially provide a stepping stone between chemosynthetic communities in the Atlantic, Indian, and Pacific Oceans (Rogers et al., 2012) as well as providing an interesting site to explore how deep Southern Ocean microbial communities respond to reducing environments. The aim of this project was to describe and compare microbial communities of deep-sea sediments influenced by hydrothermal activity with off-vents areas of the Bransfield Strait. Sediment samples were collected at three different volcanic edificies: Hook Ridge (1090mbsl), The Axe (520 mbsl) and Three Sisters (1188mbsl) and at Bridgeman Island (Subaerial volcano, 707mbsl). Only Hook Ridge (HR6) was reported to be hydrothermally active sediments from the off-vent site, however the microbial functional or taxonomical diversity has never been studied before. Genomic DNA was extracted from 0.25 g of surface sediment in quadruplicate using a PowerSoil DNA Kit (MoBio, Carlsbad, CA, USA) and then amplified with barcoded primers U519F and U809R that corresponds to the V4 regions of E. coli 16S rRNA gene (Caporaso et al., 2012). Amplicons were sequenced in Illumina MiSeq 2500 and resulted in 1,619,488 sequences of varied length (280-300 bp). High quality and non-chimerical sequences were clustered into OTUs by setting a 97% of similarity and classified using the SILVA 128 database (Yilmaz et al., 2014). Based on average relative abundance, Chloroflexi (30.4%), Proteobacteria (15.1%), Atribacteria (9.9%), Aminicenantes (6.9%) were the four major bacterial phyla in Hook Ridge (HR6). The Axe, Three Sisters and Bridgeman showed similar microbial composition profiles and relative abundance dominated by *Proteobacteria* (39.5%), *Actinobacteria* (16.4%), *Planctomycetes* (10.8%), *Verrucomicrobia* (6.2%),*Chloroflexi* (6.1%),and *Bacteroidetes* (5.6%). Twelve Archaeal phyla were founded, including *Woesearchaeota* (65.9%), *Thaumarchaeota* (25.2%), *Euryarchaeota* (5.7%) and new groups recently described such as *Altisarchaeales* (1.3%), *Diapherotrites* (1.1%), Hadesarchaea (0.9%), *Lokiarchaeota* (0.6%), *Aenigmarchaeota* (0.4%) and *Parvarchaeota* (0.2%) were founded only in HR6. Our results provided first insights showed an specific microbial community composition at Hook Ridge, influenced by the hydrothermal activity.

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Biocrust biogeography in the McMurdo Dry Valleys and two cold deserts in China and the USA

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Biological soil crusts, or biocrusts, are communities of bacteria, fungi, algae, lichens, and mosses that perform essential ecological functions in cold deserts, including nutrient cycling, soil stabilization, and water dynamics alteration (Belnap 2003). These functions are particularly important in Antarctica's McMurdo Dry Valleys, where extreme temperature, nutrient, and moisture conditions exclude higher plants (Convey et al. 2014). Previous studies have examined biocrust coverage and the distributions of their algae and bryophytes in the Dry Valleys (Colesie et al. 2013, Makhalanyane et al. 2015), but the bacterial communities of Antarctic biocrusts are poorly understood, as is the global-scale biogeography of bacteria and fungi in cold desert biocrusts. Understanding the distribution and diversity of these communities in Antarctica is useful because of their promise as model systems in ecology, and because their richness correlates with nitrogen and carbon cycling (Bowker et al. 2014). Comparing biocrusts within the McMurdo Dry Valleys and across other cold deserts will also help to identify potential community assembly processes and build a predictive understanding of cold desert biocrust diversity.

To better understand the diversity and distribution of Antarctic biocrusts in relation to other cold deserts, we collected 36 biocrust samples from three different cold deserts on three continents: Antarctica's McMurdo Dry Valleys including Miers, Taylor, and Garwood; the USA's Great Basin Desert; and China's Junggar Basin. We determined taxonomic diversity and composition by extracting genomic DNA from each sample and sequencing the V4 and V9 regions of the 16s and 18s rRNA genes on an Illumina HiSeq 2500. To assess functional diversity, we performed shotgun metagenomic analyses on a subset of 18 samples. We also measured soil physicochemical characteristics at each sampling location. Our preliminary results show that Antarctic biocrusts are less diverse (mean Shannon index = 4.04 ± 0.18) than US and China communities (mean Shannon = 5.38 ± 0.04 and 5.67 ± 0.02, respectively). Community co-occurrence networks describing species interactions also show that Antarctic biocrust communities are dramatically less complex (number of nodes = 144, number of edges = 602) than in the US and China (nodes = 792, edges = 14643, and nodes = 967, edges = 21135, respectively). Compared to the other cold deserts, the bacterial communities of Dry Valleys biocrusts were dominated by *Deinococcus,* Chloroflexi, and Actinobacteria. Our findings suggest that the Dry Valleys' extreme environmental conditions exclude otherwise cosmopolitan taxa, reducing community complexity and likely function in Antarctic biocrusts.

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Establishment and evolution of microbial communities during ecosystem development

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Natural and anthropogenic activities lead permanently to the exposition of new terrain for soil development. In this context, different chronosequences of ecosystem development like glacier forefields, sand dunes, volcanoes and restoration sites emerged, which are interesting aspects to study the development of nutrient cycling processes as well as the driving functional microbial communities. Although most initial ecosystems are characterized by nutrient shortage, especially nitrogen (N), microbial N demands are covered by aerial N deposition, leading to a highly active heterotrophic community of mineralizing microbes feeding on ancient and allochthonous carbon (C). In contrast to other terrestrial habitats, Antarctic ecosystems lack this continuous N deposition (except in areas in proximity of bird colonies), which makes them an ideal playground to study the establishment of nutrient turnover processes and their microbial key players without aerial N input. To overcome spatial heterogeneity, different soil chronosequences of the maritime Antarctic defined by different deglaciation schemes (directly as uncovered substrate or indirectly as raised Palaeobeaches) along succession gradients are investigated. Using barcoded highthroughput sequencing targeting bacterial 16S rRNA genes and fungal ITS regions, the establishment and evolution of microbial communities during ecosystem development could be followed. Microbial communities differed significantly between different soil chronosequences and development stages. Furthermore, clear succession trends for bacteria and fungi were observed. Detailed results on microbial diversity pattern will be presented at the conference.

Microbial mat assemblages within aquatic habitats in the Wright Valley, Southern Victoria Land

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A goal of our current research is to develop methods to identify variables that control local biodiversity within Antarctic landscapes. In continental Antarctica, habitats that contain liquid water are important foci of biodiversity, but our understanding of what determines how organisms are distributed within the diverse array of mostly small, ephemeral and isolated water bodies is limited. To address this we set out to test the degree of linkage between measureable habitat characteristics and community assemblage. Our study is focussed on the Wright Valley, one of the McMurdo Dry Valleys of Southern Victoria Land, which contains a variety of aquatic habitats, from rivers and ponds to large lakes, representing gradients of irradiance, duration of freezing and salinity. However, to a large extent they are all visibly dominated by cyanobacteria-based microbial mats often sharing organisms across diverse habitats. We have assembled an extensive dataset of physical and chemical descriptions of habitats and microbial community composition, based on bacterial metabarcoding (16S rRNA gene), for the Wright Valley. We pay particular attention to cyanobacteria, which are dominant habitat formers and primary producers. A clear distinction occurs between deep lake communities and those from seasonally frozen habitats, with a lower overall diversity and different dominant species. Within pond systems, a mix of geographic and environmental parameters appear to be the key drivers in structuring community assemblages..We discuss the need to consider the ephemeral nature, over a range of timescales, and local connectivity as well as habitat characteristics in developing an understanding of the processes that maintain diversity in aquatic habitats of the McMurdo Dry Valleys.

Perennially-ice covered Lake Joyce is a refugium with diverse niches for distinct benthic and planktonic microbial assemblages, Antarctica

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Lake Joyce is perennially-ice covered meromictic lake located in Pearce Valley; and one of the least studied lakes in the McMurdo Dry Valleys (MDV), Antarctica. Taylor Glacier forms the south-east shore of the lake and experienced considerable increase in water levels of the last decades. The lake's major ion chemistry is characterised by fresh, hyperoxic waters overlying an anoxic NaCl brine. The water that is supersaturated with calcite particularly in the upper, oxic part of the water column, leading to the formation of three-dimensional microbial structure with internal calcite skeletons. Lake Joyce is also the only MDV lake with an endemic phytobenthic copepod population (*Diacyclops joycei*), and therefore might represent a refugium during the last glacial maxima. However, the majority of the biodiversity is microbial with rich benthic microbial mats and phyloplankton. We carried out the first high throughput 16S rRNA gene and 18S rRNA gene metabarcoding sequencing of three distinct microbial ecosystems in Lake Joyce such as benthic microbial mats, three-dimensional mat structures and plankton assemblages. Our analysis showed that planktonic communities were distinct from any of the benthic communities and showed a strong structuring along the water column, especially from oxic to anoxic water layers. The phototrophic primary production was dominated by microbial eukaryotic algae in the water column. In comparison benthic microbial mat communities were dominated by cyanobacteria and also shifted to some extend by lake depth likely driven by irradiance, however greatest shift in community structure of the benthos were associated with some of the three-dimensional microbial structures. In summary, these findings suggest that benthic and planktonic ecosystems provide diverse and distinct niches and refugia in perennially Antarctic lakes that support diverse taxonomic and functional microbial assemblages as demonstrated for Lake Joyce.

A sub-ice marine ecosystem beneath the Ross Ice Shelf, Antarctica

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The Ross Ice Shelf, Antarctica, covers an area of the Ross Sea which is considered strained for the nutrients required to sustain complex life as a result of perpetual darkness and low geothermal activity. Hot water drilling at the Whillans Ice Stream grounding zone, along the Siple Coast of the Ross Ice Shelf in Western Antarctica, has resulted in the discovery of a community of microorganisms, vertebrates, and invertebrates. This is a region of particular interest with respect to the biodiversity of microbial organisms and nutrient flux in recently explored subglacial lakes beneath the Whillans Ice Stream that drain into the Ross Sea. Current data suggests that the presence of these microbes in the subglacial lakes may be the result of past marine incursions into the lakes. The drainage from these lakes in turn provides the grounding zone with nutrients generated from relict organic matter in lake sediments, water, and ice. An analysis of microbial 16S rDNA and rRNA in the grounding zone revealed similarities in this community to the chemosynthetic organisms found within subglacial Lake Whillans. Culturing of isolates from the Whillans ice stream grounding zone water column has also identified bacteria that share similar genetic backgrounds to microbial genera obtained in subglacial Lake Whillans. The genomes of several closely related Lake Whillans and grounding zone isolates are currently being sequenced to aid in this comparison. Our work seeks to further elucidate the role of microbes within the sub-ice sheet environment through analysis of the *Abyssorchomene rossi* amphipod gut microbiome. Characterization of the microbial gut communities of amphipods obtained in the grounding zone is providing new information about the relationship between macroscopic and microscopic life in this unique environment. Stable isotope analysis of amphipod 13C content places the amphipods between herbivory and scavengry trophic levels, indicating the consumption of microbes as a potential primary food source. Our bacterial community data from the water column, amphipod gut communities, and 13C isotopic analysis indicates that chemotrophic microbial mats may serve as an alternative source of biomass for heterotrophs. Additionally, these findings suggest that the Whillans grounding zone represents a microbial community that is influenced by both subglacial inputs and the marine environment.

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Shifts in bacterial diversity in a biopiled bioremediation process for hydrocarbon-contaminated Antarctic soil at Carlini Station (Arg.)

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Hydrocarbon contamination represents a world-wide problem, even to be found in remote areas, as the Antarctic continent. Bioremediation is considered as an appropriate tool to recover soil matrixes from pollution. In this sense, biostimulation –involving the optimization of key variables, such as the levels of Nitrogen (N) and Phosphorus (P) - has proved to be one of the cheapest and simplest methods to apply in cold environments. Nevertheless, this contaminants removal strategy is not carried out by the entire microbial flora, because only certain groups prevail over the others, leading the remediation process. For these reasons, the understanding of changes in microbial communities of soils under bioremediation is crucial to achieve optimum results. In this work, we compared how the bacterial community in hydrocarbon-contaminated Antarctic soil shifted throughout an entire "in-situ" biostimulation process, comparing two biopiles systems: a biostimulated system (BS), which included the addition of N and P up to a previously optimized level (Martinez Alvarez et al 2015); and a community control (CC) with no addition of nutrients. Soils was disposed over high-density polyethylene (HDPE) geomembranes and mixed on alternate days for aeration. Samples were taken every 10 days, for an entire treatment period of 50 days (5 samplings for each biopile) during 2013/2014 Argentinian summer campaign in Carlini Station.. Afterwards, we performed amplicon sequencing by Hi-seq for the v3-v4 hypervariable region of the 16S ribosomal DNA. Resulting sequences were processed using Qiime, including a quality control check for dismissal of non-suitable sequences. All sequences (above 300,000 per sample) were analysed with the use of a proper pipeline for bacterial communities' studies, resulting in the assignation of bacterial genera for each sequence read. The results showed that in the CC biopile, the bacterial community remained almost unchanged throughout the entire experimental period, while in the BS system (where 75% of hydrocarbon removal was detected) several changes occurred through time. One of the most important changes in BS was a rapid increase in *Pseudomonas sp.* during the first 30 days, with a subsequent fall by the end of the experiment that was accompanied by the rise in the number of *Rhodococcus sp*. These results evidenced the relevance of microbial community shifts in bioremediation processes and proved that the understanding of those changes may be a key step to assure the success of biostimulation schemes.

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Functional symbiosis improve salt tolerance in crops: A promising partnership for global food security

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Climatic variations are widely indicated as a major driver for global food security. Considering the current models of climate change, decrease in soil water availability will be a conspicuous constraint for both native plant communities as well as several crops worldwide. Hence, lands under osmotic stress (due to salinity and/or drought) are expected to increase during this century, decreasing food production, especially in those areas where a drastic decrease in precipitation has been predicted, or is already occurring at high rates. In this context plant root-associated fungi appear as a new strategy to improve ecophysiological performance and yield of crops under abiotic stress. Thus, use of fungal endophytes from ecosystems currently subjected to severe salt conditions could improve the ecophysiological performance and quantum yield of crops exposed to salinity. In this study, in both controlled conditions and field, we evaluated how the inoculation of fungal endophytes isolated from Antarctic plants can improve the net photosynthesis, water use efficiency and production of fresh biomass in cultivars of tomato, lettuce and quinoa, grown under different salt conditions. In addition, we assessed if the presence of biochemical mechanisms and gene expression related with salt tolerance are improved in presence of fungal endophytes. Overall, those individuals with presence of endophytes showed higher net photosynthesis and maintained higher water use efficiency in salt conditions, which was correlated with greater fresh and dry biomass production as well as greater root system development. In addition, presence of fungal endophytes was correlated with a higher proline concentration, lower peroxidation of lipids and up/down-regulation of ion homeostasis. Our results suggest that presence of fungal endophytes could minimize the negative effect of salt by improving osmotic tolerance through biochemical mechanisms and improving nutritional status. Thus, root-endophytes might be a successful biotechnological tool to maintain high levels of ecophysiological performance and productivity in zones under drought, acting as potential solution to maintain the global food security.

Functional resilience of Antarctic microbiome to climate-Induced changes

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The functions and productivity of McMurdo Dry Valleys ecosystems rely on microbial processes, which are limited by the availability of water and severe weather conditions. For the next coming years, climate models predict an increase of the temperature in the Dry Valleys[1]. Such event will have direct consequences on temperature regimes and water-ice dynamics across the region. The increased availability of water and the alteration of chemical properties of the soil (e.g. conductivity, nutrients concentration) will likely result in a structural and functional response of the terrestrial microbiome[2,3]. Structural alterations could involve the loss of endemic dry-adapted oligotrophic microorganisms whereas functional responses might include a significant stimulation of primary production[2]. Facing a regime of change, it becomes relevant to understand to what extent microbial communities are able to retain their structure and function to maintain ecosystem service. Work of this type will help us to understand the fragility and resilience of polar ecosystems.

During 2016/2017 Antarctic summer, our team conducted environmental surveys in three locations in the Wright Valley. The locations included: Lake Brownworth, a system where water level has been constant due to the presence of an outflow, Lake Vanda, a system where the water level has been dynamic over the past 20 years, and several ponds located in the labyrinth in the Upper Wright Valley. Using a "space-for-time" substitution approach[4], four wetness gradients were established at each one of these locations. Proxies such as conductivity, ATP levels, pH and water activity were used to help defining the gradient. Controlled attributes such as light, temperature, soil texture, and presence of water tracks were taken in consideration in order to decrease as much heterogeneity as possible during sampling. Along each gradient, five samples were obtained to assess the functional and structural elements of microbial communities. Structural elements included looking at the genetic diversity and richness of microbial communities (rRNA and rDNA) along the wetness gradients. Functional elements included looking at the functions performed by each community, firstly by predicting the metagenomic functional content from 16S rRNA gene datasets and secondly through shotgun metagenome sequencing in the most relevant samples. Metagenomic datasets were complemented with transcriptomic datasets targeting specific expressed functional genes that are related to key microbial processes and ecosystem services.

A synthesis of the microbial processes along wetness gradient and the level of functional redundancy present in communities from both stable and dynamic systems will be presented. The capacity of microbial communities to engage with future environmental change system will also be discussed.

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Structure and function of the core microbiome associated with the natural product producing Antarctic ascidian, Synoicum adareanum.

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Ascidians are conspicuous members of Antarctic subtidal benthos where they have sedentary filter feeding lifestyles in which they are continuously exposed to and filter the gamut of marine microbes in their surroundings. Molecular approaches targeting several low to mid-latitude ascidian species have indicated that persistent and specific host-microbe relationships occur, though in many cases, the nature of the associations has not been elucidated. Microbial symbioses with Antarctic marine invertebrates, in general, have been little studied, including relationships amongst the Ascidiacea. This study addresses a significant gap in biodiversity knowledge in Antarctic marine ecosystems by targeting the nature of polar ascidian symbioses and the services that the microbial symbionts provide. Here, we present the results of efforts in which we have characterized the microbiome diversity, metabolome, and metagenome-encoded functional capacity of the palmerolide-producing Antarctic ascidian, *Synoicum adareanum,* collected in the waters off the Antarctic Peninsula.

Surveys of the microbiomes of fifteen individuals identified a consistent (core) set of partners in this marine symbiosis. Only four SSU rRNA gene phylotypes were found to co-occur across the fifteen individuals surveyed upon comparisons of ~5000 454 gene tag sequences per individual. Interestingly, each ascidian colony surveyed also contained a rare, individual-specific set of phylotypes that were unique to each colony, suggesting that the depth of diversity covered in the rare microbiosphere of ascidians is potentially vast. Secondly, metabolome analysis by ESITOF MS of microbe-enriched fractions supports the co-occurrence of palmerolide and host-associated microbes. We have hypothesized that palmerolide is the product of a combined non-ribosomal peptide synthase-polyketide synthase (NRPS-PKS) microbial biosynthetic pathway, and have subsequently mined a microbiome-metagenomic data set to investigate biosynthetic gene encoded capacity for biosynthesis. This effort turned up several biosynthetic gene clusters, and a candidate scaffold for palmerolide biosynthesis.

This study attempts to bridge significant gaps in understanding linkages between climate-ocean-biological systems at high latitude, in particular how host-microbiome systems will respond, adapt, and tolerate invasions (macro or micro-organism). Invasive characteristics of ascidians in fact, may be intimately tied to their microbiomes, and specificity therein; thus in addition to ascidians being recognized as vulnerable marine ecosystem indicator taxa in the Southern Ocean, understanding their ecology with respect to microbiome diversity and function may help inform their potential sensitivity to changes in oceanic conditions.

Succession of microbial photoautotrophs along a soil chronosequence in maritime Antarctica

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The Antarctic Peninsula has experienced extensive regional warming since the 1950's, which is reflected in accelerated rates of glacier retreat and ice shelf collapse in the region (Cook et al. 2005). As a glacier retreats, it exposes new terrestrial habitats for the colonization of pioneering organisms. The study of plant succession in glacier forefields is at the core of ecology (Matthews 1992), but very little is known regarding the primordial stages in which soil biomass and processes are dominated by microorganisms. Microbial phototrophs, such as cyanobacteria and green algae, are usually the first colonizers on exposed glacial deposits (Hodkinson et al. 2003; Kaštovská et al. 2005). Here we investigate the structure of soil microalgal communities along the Meseta chronosequence (Fildes Peninsula, King George Island, maritime Antarctica), consisting of twelve sites encompassing 6,200 years of deglaciation (Boy et al. 2016). A total of 333,776 16S rRNA gene sequences were obtained by 454 pyrosequencing, which were clustered into 195 OTUs at 97.5% similarity. OTUs were assigned to Cyanobacteria (131 OTUs), Chlorophyta (35 OTUs), Stramenopiles (12 OTUs), Streptophyta (7 OTUs) and Rhodophyta (1 OTU). Total, cyanobacterial and plastid richness followed a polynomial distribution along the chronosequence (R^2 = 0.72, p = 0.006). Community structure changed from a cyanobacteria- to a plastid-dominated state at about 4,500 years BP, which was mirrored by exponential shifts in cyanobacteria and plastid relative abundances (R^2 = 0.95, p < 0.001). Earlier communities (<4,500 years BP) were dominated by cyanobacterial OTUs related to *Nodularia*, *Phormidium*/*Phormidesmis*, *Pseudanabaena* and *Chamaesiphon*. Later communities (>4,500 years BP), on the other hand, were dominated by green algal OTUs related to *Prasiolopsis*, *Stichococcus* and *Elliptochloris*. These results show a consistent successional pattern of microbial photoautotrophs and emphasize the essential role of cyanobacteria as pioneers in recently deglaciated soils, where they contribute to the stabilization of the soil matrix and organic matter accumulation.

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Cyanobacterial Diversity from equator to pole: A metagenomic comparison of Malaysia and Antarctica

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Cyanobacteria are the most ancient and widespread group of photosynthetic prokaryotes, which had a major role in the evolution of the plant kingdom and Earth's atmosphere. They are primary producers that live in a wide variety of habitats, and are able to thrive in harsh environments. In this study, metagenomic approach was used to determine the diversity of cyanobacteria in soil samples. Selected areas of Antarctica (Browning Peninsula, Dee Island, Greenwich Island and Reeve Hills) represent the South Pole, whereas, Pinang River Basin tributaries (Air Itam River, Air Terjun River, Dondang River, Jelutong River and Pinang River) represent the tropical region. DNA was extracted using Mo-Bio Powersoil DNA kit and the genomic DNA was sent for sequencing using illumina, Miseq platform with targeted V3 and V4 region. The reads were then processed using Qiime with at least 97% similarity. *Phormidium* sp., *Leptolyngbya* sp. and *Pseudanabaena* sp. were dominant in all tropical and Antarctic samples based on the hit counts. But the diversity of cyanobacterial species in tropical exceeded the diversity in Antartic. Thus, based on the diversity showed tropical might be the best thriving place for cyanobacteria as they are known for less harsh environment instead of Antarctic.

Exploring Antarctic Microbiomes as Source of Bioactive Molecules

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Microorganisms represent an extremely rich reservoir of potentially valuable natural small molecules on the planet, such as polyketides, nonribossomal peptides and alkaloids, between other classes of compounds. Among microorganisms, Bacteria are the most prolific producers, including Cyanobacteria, which have proved an extremely rich source of secondary metabolites together with Actinobacteria, Firmicutes and Myxobacteria. One of the strategies employed to uncover new secondary metabolites, relies on the study of microorganisms inhabiting extreme environments, as is expected that a large part of them are still unknown and possess unique adaptations to their habitats, including the production of unique chemical entities with unprecedented biological activities. Here, we present our results on the diversity and chemodiversity of microorganisms and microbiome obtained from environmental samples collected in a hyper-arid desert, the McMurdo Dry Valleys at Antarctica. Samples were obtained from a rock with endolithic colonization and from a soil transect with decreasing water availability. The 16S rRNA was amplified and sequenced through 454 pyrosequencing technology to allow an analysis of the microbiome biodiversity. The sequences will be analysed through PICRUST to predict the functional profiling of the microbial communities. Until now, two endolithic cyanobacterial strains with high similarity to *Leptolyngbya antarctica* were obtained. In order to isolate secondary metabolites produced by these strains, a large-scale cultivation was performed followed by organic extraction. Bioassays (Antimicrobial, Enzymatic and Cytotoxic) were performed and the promising results obtained allowed us to conduct the isolation process. It was found that these strains possess the diterpenoid dehydroabietic acid, a secondary metabolite from the Terpene family, reported by the first time to be present in Cyanobacteria (Costa, M.S. et al, 2016). From the soil samples, a diversity of Firmicutes species with high similarity to *Paenisporosarcina macmurdoensis* and *Sporosarcina antarctica* were obtained as well as two fungi species, with high similarity to Penicillium citrinum and Dicyma pulvinata. Future work will include a screening of the bioactivity of the compounds produced from these late identified species following a bioactivity-guided approach in order to isolate the compounds responsible by the activities. An overview of the whole experimental approach and of the most promising bioactivities is conveyed.

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Global Metagenomic Analysis of Cold Desert Bacteria

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Some bacterial taxa when stimulated by water additions will break dormancy, grow, and become dominant members of the community and contribute significant pulses of CO2 associated with the rewetting event. These pulses of activity are associated with high levels of bacterial productivity in soils. (Aanderud et al. 2011) I am examining the bacteria taxa that resuscitate and become metabolically active following two forms of water stress (soil drying-rewetting and freeze-thaw cycles) and I am capturing and measuring the CO2 emanating from those soils. Specifically, I am using target metagenomics, which uses a specific gene pool within bacteria that is associated with a function of an ecological process, in this case active (16S mRNA communities) bacteria and all bacteria (16S rRNA communities) during drying-rewetting and freeze-thaw cycles. I am measuring an array of community dynamics (i.e., evenness, richness, diversity, relative abundance of taxa, and network analyses between taxa) as dry soils are rewetted and as frozen soils thaw multiple times in three cold desert soils. I am searching for continuity or predictability in the bacteria that are rapidly responding ecosystems to understand if there are coherent or universal patterns of the bacteria that respond to these stresses in cold desert ecosystems. I am looking at three cold deserts which include the Great Basin Desert, UT, The Junggar Desert, China, and the McMurdo Dry Valleys, Antarctica. Having the three deserts my results will: First, identify whether bacterial response to water stress is universal or only localized; second, bacterial adaptations are the same within similar but geographically isolated systems; third, whether this analysis will support or negate the hypotheses that every bacteria is everywhere and the environment selects dominant strains during discrete events; and fourth, through this process identify specific bacteria that are disproportionately contributing to CO2, a major greenhouse gas.

Briefly, my current real-time CO2 data shows that all pulses are not created equal. For example, in soil samples from China and the USA, freeze-thaw cycles produce slowly elevated CO2 over 3-5 days as fluxes reached a maximum of at most 598 ppm. In contrast, Antarctic soils generated cycles with higher maximums following soil thawing (335 – 265 ppm at -2°C) than rewetting (295 – 230 ppm at 5°C) and freeze-thaw pulses peaked more rapidly in soil samples from Antarctica (2 days) than China and USA soils. Our results suggest that the effects of soil rewetting and thawing on soil respiration are unique but not universal among ecosystems.

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Microalgae communities in Antarctic soils: changes along soil developmental stages and testing for geographical distribution

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The diversity of eukaryotic algae along a soil chronosequence, i.e. the lateral glacier retreat gradient, "Meseta" (Boy et al. 2016), in a glacier forefield of Fildes Peninsula, King George Island (Southern Shetlands, Maritime Antarctica), has been studied using two complementary culture-independent approaches, cloning and Illumina MiSeq (2x250) paired ends sequencing targeting the ITS2 rRNA gene. Group-targeted PCR amplification was required to minimize biases in biodiversity assessments because eukaryotic algae often seemed to be underrepresented in the DNA extracts from the soil samples. PCR primer pairs targeting various green algal classes (e.g. Trebouxiophyceae, Klebsormidiophyceae) and the stramenopile Xanthophyceae were employed. With those for the Xanthophyceae ITS2 rRNA genes of no other organisms were recovered. Long ITS1-5.8S-ITS2 amplicons were separated by cloning and sequenced. For Illumina MiSeq (2x250) paired-ends sequencing suitable shorter fragments comprising full ITS2 region were re-amplified using unspecific primers. This approach revealed a high algal diversity of 3299 green algal and 421 xanthophyte OTUs (97% identity level). Across the chronosequence total numbers of OTUs varied only little. However, no more than 184/15 green algal/xanthophyte OTUs were shared among all sites of the chronosequence. Based on OTUs the sites close and at middle distance to the glacier front were rather similar among each other, whereas the sites farthest from the glacier (oldest soil developmental stages) were clearly different from the younger stages. Cloning/sequencing resulted in a total of no more than 134 eukaryotic algal OTUs (97% identity level), i.e. from green algae (85 OTUs) and the stramenopile Xanthophyceae (43 OTUs). No saturation was reached. The scarcity of reference sequences available for the ITS2 region prevented assignment of most of the Ulvophyceae and Xanthophyceae OTUs to a more precise taxonomic position. Despite the NGS approach revealed a high diversity of xanthophytes, longer ITS2 sequences (> 380bp) as recovered by clone libraries for this algal group were absent, indicating that the xanthophycean diversity as revealed by NGS may have been biased. Ubiquitous species already known from geographic regions other than Antarctica as well as species probably confined to Antarctica, i.e. so far recovered only by our study, were revealed.

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Biodiversity of Eastern Antarctic microbiota: culture-based and metagenomic studies

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Little is known about bacterial communities in polar Antarctic ecosystems including their species composition, significance in various biogeochemical processes, mechanisms of cold adaptation [1]. In this study biodiversity of bacteria present in different environments near Belarussian field station in Eastern Antarctica (Thala Hills oasis, Enderby Land) was studied by culture-based and culture-independent techniques.

Using heterotrophic cultivation, collection of antarctic microorganisms, comprising more than 300 pure cultures, isolated from green snow, water, freshwater sediments, pit-run fines and other environments, was created.

Based on the data of microscopic and biochemical studies, MALDI-TOF MS protein profiling and 16S rRNA gene sequence analysis 46 bacterial cultures, isolated from green snow, were identified as representatives of Actinobacteria, Proteobacteria and Firmicutes phyla, mainly represented by genera Arthrobacter, Leifsonia, Salinibacterium, Cryobacterium, Pseudomonas, Psychrobacter. Green snow isolates grew at 4-28°C, for most cultures (78%) optimal growth temperature was 18-28°C, suggesting that they belong to psychrotrophs (facultative psychrophiles). Majority of strains formed biofilms composed of cell aggregates surrounded by exopolysaccharide matrix and had branched and unsaturated fatty acids Ci-15:0, Ca-15:0, Ci-16:0, C16:1, C17:0Δ, Ci-17:0, Ccis-18:1 in cell membranes, which may be regarded as mechanisms of cold adaptation. Most of isolates were sensitive to antibiotics of medical and veterinary importance. Evaluation of enzymatic activity revealed that isolates produce lipases, DNAses, proteases, cellulases, amylases active at low temperatures, prospective for biotechnological application.

Whole genome sequencing of two bacterial cultures was performed. Genome of isolate 3t.5.20 (4,862,000 bp, GC-content 40.3%, 2 plasmids) possesses high degree of identity with genome of Sporosarcina psychrophila DSM 6497. Genome of isolate 11t.7.20.2 (2,270,528 bp, 3 plasmids) was closely related to genome of Carnobacterium iners. Genes, coding for biotechnologically valuable properties, including urease and cold-tolerant beta-galactosidase production, were identified in sequenced genomes.

Analysis of metagenomic data using OneCodex Platform (OneCodex and RefSeq Complete Genome Databases) revealed that dominant bacterial phyla in green snow were Proteobacteria (72.6%), Bacteroidetes (24.9%), Actinobacteria (0.6%) and Firmicutes (0.4%). At genus level dominated Polaromonas, Chryseobacterium, Janthinobacterium, Pseudomonas, Flavobacterium, Sphyngobacterium, Psychrobacter. Comparison of culture-based and metagenomic data demonstrated that metagenomics resulted in a higher taxonomic diversity, but failed to detect some genera picked up by cultivation.

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Microbial community composition of Antarctic cyroconite holes is more variable for larger organisms

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How does the size of organisms impact the structure of the communities to which they belong? Microbial communities are particularly well-suited for answering this question, because of their large diversity in sizes (from bacteria 0.1µm long to ciliates >1mm long), the ease of generating exhaustive data sets with high-throughput DNA sequencing, and the fast turnover of microbes compared with long-lived plants and animals. Yet the degree to which microorganisms, particularly larger eukaryotes, are cosmopolitan has been subject to debate (Wilkinson et al. 2013). Microbial microcosms have been used to study community structure (Altermatt et al. 2015), but have limited ability to predict more complex communities with long-shared evolutionary history in a natural environment. In contrast, microbial samples from complex environments such as global soil surveys can limit inference due to confounding factors, including moisture and vegetation. We use Antarctic cryoconite holes as a system of natural microcosms, which bridge the gap in scale and complexity between in-vitro microcosms and more complex natural systems. Cryoconite holes form when sediment is blown onto a glacier, where its lower albedo melts a shallow hole in the ice (McIntyre 1984). We applied modern high-throughput amplicon sequencing to both prokaryotic and eukaryotic communities resident in cryoconite holes from three glaciers across a range of spatial scales (150m to 41km apart) along a known gradient of microbial diversity in the Taylor Valley, Antarctica (Virginia and Wall 1999) to ask how size affected community structure. The difference between two different sites' prokaryotic communities was a strong predictor of difference in eukaryotic community. The variability in community difference of bacterial and eukaryotic communities unweighted by abundance were of similar scale, but the normalized, abundance-weighted metric of community difference varied more between eukaryotic than between bacterial communities. Greater variability in weighted metrics is driven by more abundant organisms, which could reflect the more transient processes of local growth rather than dispersal (Lozupone et al. 2007). The greater variability in eukaryotic communities could be consistent with slower population growth and abundances of the larger eukaryotes, leading to greater stochasticity, but could also be consistent with more sensitive growth requirements of eukaryotes. Our findings that community structure of larger eukaryotes mirrors those of smaller prokaryotes in this system, but that the communities of larger organisms differ more, is consistent with larger eukaryotic microbes being as cosmopolitan as smaller prokaryotes in dispersal, but more variable in growth.

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Microbial Oceanography of Southern Ocean Water Masses

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The Southern Ocean (SO) is a major site for the sequestration of global anthropogenic carbon dioxide (CO_2), responsible for up to 40% of annual oceanic CO_2 uptake. Within harsh low temperature and high salinity environments of the SO, microbes dominate and support carbon sequestration and critical nutrient cycling processes. Carbon sequestration occurs mainly through a microbial-driven CO_2 fixation biological pump. The effects of climate change on the physical oceanography of the SO may have a globally significant impact on the microbial ecology and therefore the efficiency of this biological pump. The extent of this impact is unclear, because the diversity and functional capacity of the microbial assemblages inhabiting the SO is still not well understood. Water masses within the SO also have distinct physicochemical properties and are likely to harbor varying microbial communities. Additionally, the key environmental parameters controlling these microbial community variations are still poorly deciphered. To better understand this microbial community, we sampled seawater at multiple ocean depths from 4 different transects along the Australian and New Zealand region of the Southern Ocean (71°E-170°W). Sampling interval was every 0.5 – 1 degree from 42 - 66°S. This study will not only advance the depth and breadth of the SO's bacterial, archaeal and eukaryotic community composition through high vertical and spatial resolution metagenomics profiling using 16S and 18S rRNA gene tag sequencing, but combine this with physicochemical observations to investigate the potential triggers of the observed microbial community shifts. Preliminary bacterial 16S Operational Taxonomic Unit (OTU) data have shown community shifts before and after crossing major SO fronts, indicating the SO bacterial community to be endemic to hydrographically distinct water masses. Shifts were also at observed at depths between 200 and 1000m. Dominant bacterial communities within abyssal water masses were also observed to differ by latitude despite similar physicochemical conditions. These findings will contribute significantly to filling critical gaps of knowledge on how changes in Southern Ocean physical oceanography under forecasted global change scenarios might change the CO_2 uptake and biological pump in the Southern Ocean.

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Methane cycling in the High Antarctic – Paradigms lost?

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One of the key ecosystem services marine communities provide to global health is their consumption of the greenhouse gas methane prior to its release into the atmosphere. While climate models predict that Antarctica has the capability to release the same quantity of methane as all of the Arctic permafrost we lack even a fundamental understanding of those microbial taxa involved in methane cycling in the Southern Ocean, including whether paradigms based on more northerly habitats apply to the Southern Ocean. In 2012, we discovered an expansive microbial mat with methane present at 78 degrees S in the Ross Sea. This habitat formed in 2011. Through analysis of samples collected in 2012 and 2016, here we evaluate whether taxa involved in methane cycling in other parts of the globe are present and the successional pattern of fauna in this region. Through analysis of microbial community composition we found that anaerobic methanotrophic microbes, the dominant marine methane sink globally, were not yet present in 2011. However, methanogens (methane forming archaea) and aerobic methanotrophs (methane oxidizing bacteria) were present. These two groups fell within taxonomic lineages found north of the polar front. Through adding on to these initial findings with analysis of biogeochemical and molecular samples collected in 2016, we will be able to characterize this feature, its microbial succession and biogeography, and place it in a global context. The rate and trajectory of microbial colonization of methane-fuelled habitats may directly impact the rate of climate change while impacting the function of local marine communities in the Antarctic; this study is a first step towards understanding these critical marine ecosystem dynamics.

The BCCM/ULC collection to conserve the biodiversity and study the secondary metabolites of Antarctic cyanobacteria

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On the Antarctic continent, Cyanobacteria are key primary producers and main drivers of the food webs in a wide range of aquatic to terrestrial habitats. For example, they build benthic microbial mats in lakes and soil crusts. Their success in these harsh cold conditions can probably be explained by particular adaptations to survive freeze/thaw cycles, seasonally contrasted light intensities, high UV radiations, dessication and other environmental stresses.

The BCCM/ULC public collection is funded by the Belgian Science Policy Office since 2011. A Quality Management System ensures that the services of deposits (both public and safe) and distribution are well documented and efficient for the clients' satisfaction. It has obtained the ISO 9001 certification for deposition and distribution of strains, as part of the multi-site certification for the BCCM consortium. This collection aims to gather a representative portion of the Antarctic cyanobacterial diversity with different ecological origins (limnetic mats, soil crusts, cryoconites, endoliths…) and make it available for researchers to study the taxonomy, evolution, adaptations to harsh environmental conditions, pigments, and genomic make-up. It presently includes 216 cyanobacterial strains, of which 119 are of Antarctic origin (catalogue: http://bccm.belspo.be/catalogues/ulc-catalogue-search).

As shown by morphological identification, the strains belong to five orders (Synechococcales, Oscillatoriales, Pleurocapsales, Chroococcidiopsidales and Nostocales). The 16S rRNA and ITS sequences of the strains are being characterized. The first 85 Antarctic strains already studied are distributed into 25 Operational Taxonomic Units (OTUs = groups of sequences with > 97,5% 16S rRNA similarity), and thus represent a quite large diversity. Moreover, strains identified as members of the genera *Leptolyngbya* or *Phormidium* appear in several lineages. This supports the idea that there is a need to revise the taxonomy of these polyphyletic genera with a simple filamentous morphology.

In addition, cyanobacteria are known to produce a wide range of secondary metabolites (e.g. alkaloids, cyclic and linear peptides, polyketides) with bioactive potential. Genome sequencing of 11 strains has been started to enable genome mining for biosynthetic clusters. Pair-read data from illumina MiSeq runs were obtained and submitted to a bioinformatic pipeline dedicated to the assembly of genomes and search of sequences involved in the biosynthesis of secondary metabolites. Gene cluster prediction analysis allowed to characterize 20 clusters of NRPS, PKS and hybrid NRPS-PKS from 2 to 66kb. Surprisingly, none of the characterized operons had previously been described in the literature.

Response of *Pseudanabaena catenata* isolated from the Svalbard archipelago towards different quality and duration of light exposure: a case study of phycobilliprotein production

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Cyanobacteria are well known for their production of valuable compounds of pharmaceutical and commercial interest, such as antioxidants and pigments. The demand for natural bioproducts over their synthetic equivalents is also increasing. However, the potential applications of microscopic cyanobacteria species, including those associated with intense algal blooms and in particular those naturally occurring in extreme environments such as the polar regions, have largely been ignored to date because of difficulties in isolation and observation due to their relatively small cell/filament sizes. *Pseudanabaena* is a genus of microscopic cyanobacteria, cosmopolitan in distribution and known to be rich in phycoerythrins. Cyanobacteria are photosynthetic organisms, thus, one of the factors that influences their metabolism is the quality and quantity of incident light. Therefore, the aim of this study was twofold. First, to determine the influence of different light quality (white, green and red) and exposure (photoperiod of 12-24 h) on phycobilliprotein production in the strain *P. catenta* USMAC16 originally isolated from the High Arctic Svalbard archipelago. Second, to understand the adaptation of this strain to the extreme polar environment. The morphological and molecular characterisation of this strain of *P. catenata* identified 100% similarity with *P. catenata* SAG 1464-1 from Germany. Maximum phycoerythrin production was obtained under green light, while phycocyanin production was maximum under red light with a 16:8 L: D photoperiod. Very few cyanobacterial species have been found to be chromatically adaptable, or to be able to produce phycoerythrin under variable light qualities through employing chromatic adaptation. Our data support *P. catenata* being an effective producer of phycoerythrin when grown under green light, an ability that may have practical application in satisfying the increasing demand of consumers for natural antioxidants and dyes.

Theme 2
Adaptation and processes

Understanding the role of environmental conditions on the performance of Laternula elliptica (King & Broderip) in King George Island.

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Ecosystems from the Western Antarctic peninsula (WAP) are thought to be particularly vulnerable to global change, as this region is currently challenged by rapid rates of temperature rise. Global change has a cascading effect that is causing a variety of changes in marine ecosystems, influencing both their physical and biotic components. In that manner, global change is impacting the distribution and population dynamics of Antarctic marine organisms.

Life history, distribution and abundance of species are depending on the functioning of metabolic processes. Knowledge of these processes is essential to understand a species population dynamics, performance, and functional role within a given ecosystem. Dynamic Energy Budget (DEB) theory provides a framework to describe the process of energy uptake and allocation during the whole life cycle of an organism as a function of temperature and food availability, allowing the integration of a species' physiology with its physical environment.

The bivalve Laternula elliptica (King & Broderip) is a filter feeder with an important role in the bentho-pelagic coupling function in Western Antarctic Peninsula shallow ecosystems. To assess how global change affects this key species, we propose to study the mechanisms underlying its responses to changes in its environment. In this study, we have assessed the DEB parameters for this species, as inferred from field and experimental data. These parameters were used in conjunction with times series of biological traits obtained for King George Island (South Shetlands) populations, to reconstruct the feeding history of these species over two consecutive years. Feeding history was afterwards related to indicators of resource availability: chlorophyll levels, particulate organic matter, sediment load, duration of ice cover to assess the role of these variables in the observed patterns through a mechanistic link.

Chromosomal diversification and speciation in the Antarctic Nototheniidae (Teleostei): coping mechanisms facing environmental changes ?

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Multiple times in the last 20 My, glacial-interglacial cycles led to strong and repeated environmental changes in the Southern Ocean (habitat disturbance with iceberg scouring, habitat fragmentation during maximal glaciations) on the Antarctic continental shelf and peri-insular plateau. In this changing environment, notothenid fishes adapted through biochemical and physiological evolutionary innovations, most famously antifreeze glycoproteins and for some, loss of erythrocytes. They also diversified through several rounds of species radiation (including Trematominae), and now constitute the dominant group of Antarctic Teleosts in this sector (Eastman and McCune, 2000), with ecological, genetic and chromosomal differentiations. Among Trematominae, the genus *Trematomus* exhibits the highest chromosomal diversity, with diploid chromosome numbers ranging between 22 and 58, involving all the types of rearrangements probably linked to speciation (Morescalchi and al., 1992). However, the reasons for this unusual diversity remain unknown.

Transposable elements (TEs) are known to be involved in genome structuration and plasticity during evolution (Volff, 2005). They can lead to chromosomal rearrangements through ectopic recombination events (Bonnivard et Higuet, 2009), hinting at a role as drivers of specific-lineage diversification. Moreover, due to their epigenetic regulation, TEs can be mobilized when thermic changes occur ("epigenetic breakdown"). These bursts of transpositions might be concordant with species radiations (Rebollo, 2010), and are therefore especially interesting in relation to the trematomine diversification.

After identification of the Ty3-Gypsy, Ty1-Copia and DIRS-1 retrotransposons super-families in Nototheniidae, we evaluated their distribution, their structuration in those genomes (diversity, sequence identity) and relative abundance (copy numbers). Almost all genomes were found to contain four families of DIRS1, nine of Ty3/Gypsy and two of Ty1/Copia, all characterized by an interspecific intrafamily conservation (sequence identity over 90%). We detected dozens to hundreds of copies in each identified family. These TEs were also located on notothenid chromosomes by Fluorescent *In Situ* Hybridization (FISH). Some of them (especially the DIRS-1) accumulate in centromeric and pericentromeric regions. DIRS-1 hot spots of insertion might favor recombination mechanisms that could lead in different ways to fissions, inversions and centric or tandem fusions. These chromosomal diversifications linked with speciation and adaptation in relation to the phylogeny of these species provide novel evolutionary leads on the genomes of Nototheniidae.

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Galindez Island as a model area for studying Antarctic terrestrial vegetation dynamics

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Due to the fact that Argentine Islands are located in the epicenter of recent climate changes and has a rich archive of vegetation research, long-term program to monitor the impact of climate change and human impact continued here. For model area of Galindez Island (Ukrainian Vernadsky Station locality) the mapping of relief elements, streams, lakes, general vegetation and certain communities distribution in seasons 2014, 2016 have been realized. The relationship between certain vegetation communities' distribution and influence of animal and human impact additionally studied.

It had been shown that all types of vegetation were distributed mainly on relief elements that are towered above snow and ice, and therefore melting in the summer or even stay above snow cover during the winter. Depending on the heights and exposition, protection from the wind, duration of the period without snow cover, humidity, distance from the sea and organic input from seabirds, a mosaic of plant vegetation communities had been formed from the most sensitive in terms of vegetation period vascular plants, to the most hardy crustose lichens that can survive under the snow for a long time. The largest continuous stands are created by moss banks. *Deschampsia antarctica* and *Colobanthus quitensis* mainly grow in addition to wide spread moss carpet *Sanionia* community. Currently, on the Argentine Islands region and on Galindez Island in particular the expansion of penguin *Pygoscelis papua* is observed, which leads to increasing of organic input and destructive influence on the vegetation – initially at Marina and Penguin Points then at Pigeon Point. At the first two colonies localities, plant vegetation is totally destroyed. We also found mummified remains of moss banks at that area. A limited income of organic from seabirds promotes development of nitrophyl vegetation. Using of vegetation components for nests by seabirds, like *Larus dominicanus* and *Catharacta maccormicki* results into distribution of plants in this region.

The most anthropogenic transformation occurred due to station construction and on areas of regular station operations. However, the formation of new *Deschampsia antarctica* populations in protection of station's buildings as well as re-colonization of old constructions by lichens is also observed.

Due to presence of some unique karyotypes of *Deschampsia antarctica*, rare species of lichens and bryophytes, areas of undisturbed ecosystems in the region of Argentine Islands requires the creation of new strictly protected areas (Ia IUCN).

Collapse of a subantarctic ecosystem 8 years on

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In 2008, widespread death in the keystone, alpine cushion plant species *Azorella macquariensis* was first observed on subantarctic Macquarie Island. Over the next three years, additional death was noted and the endemic species was declared critically endangered. Examining this rapid collapse we concluded that a complex series of elements, including climate change and the possible emergence of a putative pathogen were the most likely causes of this event (Bergstrom et al 2015).

We examine the current situation on Macquarie Island, where there is both recovery and continued widespread death, in the framework of our current understanding and consider the future for the species and its associated ecosystem.

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Marine vertebrates control the community composition and diversity of coastal Antarctic terrestrial ecosystems

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As the coldest and driest environment on Earth Antarctic terrestrial communities are strongly controlled by temperature and water availability while biotic interactions and nutrient availability are assumed to play lesser roles. This frozen 'status quo' is however, rapidly changing due to the warming climate and retreat of glaciers which alleviates abiotic constraints for growth and reproduction but also changes the spatial sea ice conditions and food availability for marine vertebrates. Here we show that the presence of marine vertebrates, such as penguins and seals, have a greater impact on the biodiversity and community structure of Antarctic terrestrial ecosystems than climate warming at three sites along the Antarctic Peninsula (Signy Island: 60°S, Byers Peninsula: 62°S and Marguerite Bay: 67°S).

Penguins and seals greatly increased terrestrial invertebrate abundance, diversity and ecosystem respiration rates compared to sites without marine vertebrates and the community changes were larger than those found in climate manipulation studies following 10-13 yr. of warming. The impact of marine vertebrates on terrestrial ecosystems was driven by the nitrogen enrichment from fecal deposition which we could trace, using $\delta^{15}N$, through the air into the vegetation, the primary grazers and their predators up till 500 m inland. These results clearly show that current spatial patterns of terrestrial biota can be strongly affected by nutrient availability beyond existing latitudinal patterns of temperature and water availability. Biotic interactions, through bottom-up control of nutrient availability apparently play an important role in governing Antarctic terrestrial ecosystems along the Antarctic Peninsula. In addition, climate change can directly affect Antarctic terrestrial ecosystems by warming the local climate but its impacts through the spatial distribution of marine vertebrates along the Antarctic Peninsula will likely be much larger. Protection of the marine habitat is therefore just as important for Antarctic terrestrial ecosystems as it is for marine biota.

Responses of Antarctic Sponges to Climate Change: from Individual to Community Level

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The projected changes in temperature constitute major threats to ecosystem functioning, services and integrity, as they can affect key functional species and associated ecosystem processes. Sponges play important roles in community dynamics, as microhabitat providers and also positively influencing diversity and composition of Antarctic benthic communities. Recent evidence suggests their diversity and abundance in algae-dominated rocky reefs in the western Antarctic Peninsula (WAP) has been underestimated. This highlights that the existing knowledge on sponge assemblages and the functional roles they play in vast zones of the WAP is still incomplete. This work aims to evaluate the utility of sponge species as indicators environmental perturbation with Antarctic benthic communities. The objectives of this proposal, which are a step towards attaining the long-term goal, are to generate baseline data on the distribution of Antarctic sponge species and their microbial communities against which future temperature-induced changes can be assessed, and to undertake initial evaluations of the effect of temperature increases on the ecophysiological performance of Antarctic sponges. Semi permanent transects, sponge collections and laboratory experiments have been carried out around Doumer Island (64˚52'24"S; 63˚36'00"W), Palmer Archipelago, Antarctic Peninsula. Some of our surveys studying the abundance and distribution of sponge assemblages confirm the existence of diverse sponge assemblages in zones that are typically dominated by canopy-forming algae such as *Himantothallus grandifolius* and *Desmarestia* spp. In addition, high throughput sequencing of sponge-associated bacterial communities, shows the existence of diverse communities associated with different species of Antarctic sponges. We have also been able to resample after 12 months, tagged individuals to study temporal dynamics of the sponge-microbiome. We have obtained by a traditional PCR approach, several sequences of 70 kDa heat shock proteins from *Haliclona (Rhizoniera)* sp., *Mycale (Oxymycale) acerata* and *Dragmacidon* sp. and a transcriptomic approach by mRNA-seq will be used. This information will help us to assess the responses of these species to acute thermal stress under laboratory conditions. The information that this project will provide is critical to increase our understanding of the dynamics of Antarctic sponges from a molecular to community level. This will improve our understanding not only of current patterns, but also the responses of different species to increase temperature, which is essential for improving our ability to detect future changes in these communities resulting from Climate Change (Financial support by FONDECYT 11150129 is gratefully acknowledged).

Trophic plasticity of the Antarctic silverfish Pleuragramma antarctica

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The Antarctic coastal ecosystems, threatened by climate change, may be subject to dramatic variations in the near future. In particular, planktonic communities are known to be particularly sensitive (Mintenbeck et al., 2012). How the equilibria of the trophic webs will change? Present work aims at improving present knowledge on this issue by investigating the feeding flexibility of the plankton feeder and keystone species of the coastal trophic webs Antarctic silverfish (*Pleuragramma antarctica*).

An overall picture of the trophic ecology of the species has been provided in several previous studies (Pinkerton, 2017; Tavernier and Giraldo, 2017) nonetheless if it has opportunistic or selective feeding habits still remains to be clarified.

Therefore in the frame of the PNRA project RAISE (Integrate Research on AntarctIc Silverfish Ecology in the Ross Sea), we developed a study aiming at to evaluating the diet ductility of the Antarctic silverfish. Based on the analysis of stomach contents and other biological parameters (morphometric parameters and condition indexes) of specimens collected in different years and sectors of the Southern Ocean (Ross Sea, Dumont d'Urville Sea, and Antarctic Peninsula), possible differences in diet and condition across the schools were investigated.

Such a study highlighted that the relative importance of each item of prey, mainly composed by copepods and euphausiids, was different among areas. These differences were accompanied by different general conditions of the fish schools. At the same time, the rate of selectivity toward specific prey (observed in modified Costello diagrams, Amundsen et al., 1996) was high only where euphasiids were present (i.e. Antarctic Peninsula). This pray is associated to better conditions and seems to be preferential in the diet of the silverfish. According to our results, *P. antarctica* is a plastic predator, which can feed on a great variety of planktonic prey when euphasiids are not available.

Such a silverfish flexibility to alternate food sources, can have positive implications in terms of Antarctic silverfish adaptability to future ecological modifications, related to climate change known to be ongoing at a rapid pace in polar regions.

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The Antarctic silverfish resilience to climate change: clues from the mouth apparatus eco-morphological analyses

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Distributed along the Antarctic continental shelf (Duhamel et al., 2014), the Antarctic silverfish, *Pleuragramma antarctica* is a key species in the High Antarctic coastal ecosystem where it plays a major role by channeling energy from lower to higher trophic levels, from the plankton community to the top predators.

The key of such an ecological success might be searched in the use that the Antarctic silverfish does of resource-rich pelagic habitats throughout its entire life-cycle. Indeed, considerable data from various sectors of the Southern Ocean support the notion that *P. antarctica* is planktivorous at all stages of development. To date, the food resource partitioning during life-cycle is relatively clear, however to what extent the Antarctic silverfish is a generalist feeder that not exert preferences, or a trophic specialist adapted to a narrow spectrum of prey, is still unclear and needs to be elucidated.

This is particularly relevant and urgent in the light of current climate changes that, in certain areas of the Southern Ocean such as the Antarctic Peninsula, are already causing significant changes in the phytoplankton and zooplankton community structure (Mintenbeck et al., 2012). Here we report on the result of an eco-morphological study performed in the frame of the PNRA project RAISE (Integrate Research on AntarctIc Silverfish Ecology in the Ross Sea) with the aim of gaining insight into feeding behavior and plasticity in *P. antarctica*. The feeding performance and potential resource usage were evaluated through the morphometric analysis of the buccal apparatus. Key morphological traits of the head, jaw regions, and gill rakers were measured to estimate the suction capability and the ability in producing power during the bite. The values obtained were compared with those of two taxonomically close nototenioid species with different life-style and feeding habits, *Dissostichus mawsoni* (bentho-pelagic predator feeding on large items like fish and cephalopods), and *Trematomus bernacchii* (benthic opportunistic species).

Our results indicate that the adult silverfish can potentially feed on large size zooplankton (e.g. euphausiids) as well as on small plankton, owing to a modified gill rakers conformation. Such a feature can contribute to adult silverfish.

Trophic flexibility that in turn translates into a certain resilience of the silverfish populations to potential variations in prey availability due to climate changes. Further research is needed to assess if the diet flexibility deduced on an eco-morphological basis results in actual feeding plasticity for the species.

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Heat shock responses of the moss Sanionia uncinata under experimental warming and its implications for future changes in vegetation patterns in the maritime Antarctic.

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Bryophytes are major components of green landscapes in Antarctica's ice-free areas. Antarctic mosses, with more then 100 species, extend from maritime Antarctica well into the continent. *Sanionia uncinata* is one of the dominant species; its cover is most extensive on the Shetland Is. Archipelago, including King George Island. Our study focused on heat resistance of this bipolar moss to understand its growth pattern and responses to global climate change. We installed open top chambers (OTCs) for seven years on Fildes Peninsula, King George Island, to examine warming in bryophyte communities. We compared heat shock responses of bryophytes growing inside the OTC and in control plots. We observed no change in photochemical efficiency (Fv/Fm) one hour after heat shock (15-40ºC), with Fv/Fm values above 0.7. Interestingly, in the same samples one hour later, we observed, Fv/Fm values were decreasing for plants that experienced heat shock in the range of 20-30ºC, with the lowest Fv/Fm values (< 0.6) for plants that experienced higher levels of heat shock (36-40ºC). However, 24 h later, only gametophytes that experienced the highest level of heat shock (40ºC) did not recover photochemical efficiency. Surprisingly, values of Fv/Fm did not differ between OTC and control mosses, although during the experiment lipid peroxidation was higher in mosses inside the OTCs compared to mosses in control plots. Our results suggest that the photochemical apparatus in *Sanionia uncinata* is able to tolerate thermal shock, indicating that this moss could survive high temperatures in the future warming scenario. Grant FONDECYT 1120895.

Evolution at low temperature: protein structure and function in polar marine environments

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Under changing conditions, species may no longer remain adapted to the new conditions and could therefore fall outside their climatic niche. Of particular concern are "tipping points" where ecosystem thresholds can lead to irreversible shifts. Many ecosystems can undergo sudden jumps in response to changes in the proximity of these thresholds or tipping points. As environmental pressure exceeds the threshold or tipping point, the ecosystem rearranges and falls into an alternative state, leading to an abrupt change that we cannot predict. Empirical evidence suggests that, in complex, long-living species, physiological plasticity is often more important than genetic contribution. The critical rate of environmental change is generally lower for species with longer generation times; and as a consequence, these species will be at greater extinction risk.

The biological effects of increasing temperature on marine ecosystems are already evident. Temperature governs the rate of chemical reactions and pathways regulating the development and decline of life. Sensitivity to temperature influences the success of organisms in all habitats, and is caused by the susceptibility of biochemical processes, including protein function, to temperature change. Despite many advances in our understanding of structure–function relationships, we cannot yet predict how the replacement of a particular amino-acid residue can affect temperature sensitivity of protein function. Recent studies indicate that only minor structural modifications are needed to change the intrinsic stability of cold-adapted proteins, and that local rather than global flexibility may play an important role.

In this overview, we first summarise how cold temperature affects the physiology, then focus on the molecular mechanisms of cold adaptation revealed by recent biophysical, biochemical and genetic studies of a specific group: oxygen-binding proteins. Next, we also discuss the structural and functional features of cold-adapted globins, in an attempt to put into perspective what has been learnt about these proteins and their role in the biology of cold-adapted species.

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Moving backward to step forward: extending the seasonal timeframe of survey on the Antarctic silverfish nursery at Terra Nova Bay (Ross Sea)

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The Antarctic silverfish *Pleuragramma antarctica* is a dominant notothenioid fish living in high-Antarctic shelf and slope waters where the species plays a similar key role in the food web as does krill in the Seasonal Pack-ice Zone (SPZ). Despite reasonable understanding of many aspects of the Antarctic silverfish biology, knowledge on important components of the fish life cycle, including reproduction, is still limited. If sufficient evidence now supports the hypothesis that Antarctic silverfish reproduction occurs in austral winter/early spring (July to end of August, beginning of September) in coastal areas along major continental ice shelves, nonetheless breeding event hasn't been documented yet due to the logistic constraints that have historically limited year-round field observations close to the Antarctic continent.

Terra Nova Bay (TNB), in the Ross Sea, is the only area from where both embryonated eggs and newly hatched larvae have been recorded. Near term embryonated eggs have been found floating in large quantities among platelet ice under the sea-ice early in November and mass hatching has directly been observed later in the month (Vacchi et al. 2004, 2012; Guidetti et al. 2015).

A long term monitoring program was launched in 2005, under the Italian National Programme for Antarctic Research (PNRA), for assessing presence and distribution of Antarctic silverfish eggs in the Terra Nova Bay area. Until 2013 investigations have been temporarily limited to the late spring-summer period, when the Italian summer Station Mario Zucchelli is open. In 2014, under the umbrella of the framework agreement on polar research between Italy and Korea, a collaborative programme was started on the ecology of the Antarctic silverfish. The opening of the permanent Korean Jang Bogo Station has then allowed to extend to the winter and spring the monitoring of the nursery area. The occurrence of Antarctic silverfish eggs was surveyed under the sea-ice cover in Gerlache Inlet. Silverfish eggs were first recorded on the 18th of September. Following this finding, periodic sampling were performed at the same site until the end of October. Microscopic analyses of the egg samples allowed to recognize various developmental stages from cleavage to gastrula.

The opportunity of operate from a permanent station, extended back of about one month the seasonal sampling timeframe in the Antarctic silverfish nursery area, allowing to document that the Antarctic silverfish eggs are already present there, under the sea-ice, in September.

Lyallia kerguelensis, a Kerguelen endemic cushion plant from extreme environments in the face of climate change

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Rapid climate change is occurring in sub-Antarctic islands, mostly with temperature increase and loss of precipitations[1]. The native sub-Antarctic flora is poor and composed of perennial and often long-lived plants, potentially more vulnerable to rapid environmental changes[2]. Endemic species, ie the most geographically restricted should be even more at risk. *Lyallia kerguelensis* (Montiaceae), an endemic cushion plant in sub-Antarctic Iles Kerguelen is particularly infrequent on the archipelago and specialized in certain habitats. Recruitment appears low in populations. In addition, many cushions show more or less important necrosis. Our research aims at understanding the ecological and physiological limits of *L. kerguelensis* in its current range and to deepen the plant potential to respond to climate change. In a first approach, we aim to determine which environmental factors (abiotic, biotic) are most limiting for plant performance. We designed a field study that covered wide distribution and ecological ranges of the species in Kerguelen. Plant performance was described by the extent of necrosis within cushions. In each studied population, we quantified topographic and geomorphological features, climate (meteorological and local climatic recorders), edaphic parameters (soil profile, water content, conductivity, pH, texture, elemental composition and nutrients), epiphytes in cushions and the composition of the neighbouring community. To characterize the performance and morphology of cushions we developed a photointerpretation method. On a sample of individuals from each population, calibrated pictures were made. For each individual a view from above the cushion and eventually other views were chosen to extract phenotypic traits (cushion surface, perimeter, diameter, living/dead apices, living/necrotic cushion surface) using ArcGis[3]. Other morphological traits, e.g. shape and compactness were then calculated. Floral traits i.e. flower number and phenology were observed directly in the field. Trait variability at intra- and inter-population levels and correlations to environmental factors were investigated. Finally, morphology and flowering phenology were monitored across 10 years in one population. The results are interpreted in the light of the climatic data across this period. Furthermore, the results provide a hint for the temporal scale of morphological changes in the cushions. *L. kerguelensis* will be a model case for the response capacity of long-lived and possibly relict endemic plant species from past eras and climates to climate change.

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Effects of temperature on liver energetic metabolism of the Antarctic fish *Notothenia coriiceps*

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Climate change is already having significant impacts in the Southern Ocean. In particular, the Antarctic Peninsula is experiencing one of the strongest and fastest regional warming trends and as a consequence, physiology of organisms that live in this cold and stable environment can be affected. In fact, only a small increase in water temperature can alter the metabolic pathways which support the maintenance of the physiological integrity in stenothermal fishes under changing environmental conditions. Therefore, the study of the temperature effects on metabolism of Antarctic notothenioids fishes is of great interest. Therefore, to address the effects of temperature on energetic metabolism, we analyzed the activities of enzymes involved in glycolysis [hexokinase (HK); phosphofructokinase (PFK); pyruvate kinase (PK); lactate dehydrogenase (LDH)], Krebs cycle [citrate synthase (CS)] and a lipid-metabolizing enzyme, 3-hydroxyacyl-CoA dehydrogenase (HOAD). We also assessed the energy reserves and metabolic products (glycogen, glucose, lipid and lactate contents) in liver of the Antarctic fish *Notothenia coriiceps*. Metabolic parameters were determined in field-collected and laboratory-acclimated fishes. In laboratory, fishes were acclimated to 0°C and kept at 0°C (control) or exposed to 4°C for 1 and 6 days. A significantly reduced in the HK and PFK activities was observed in fish exposed to 4°C for 1 and 6 days, and in the PK activity after 6 days. A decrease in the CS and HOAD activity was observed in fish kept in 0°C or 4°C for 6 days, while the LDH activity was increased in fish exposed to 4°C for 6 days. The glycogen and lactate content were decreased in fish exposed for 1 day, while the lactate and lipid content was increased in fishes after a long-term exposure. The changes observed in HOAD activity and in the lipid contents suggest a reduction in fatty acid utilization as a metabolic fuel. In turn, the lower activity of glycolytic enzymes observed in fish exposed to 4°C indicates reduced energy availability via glucose metabolism while the increase in LDH and lactate accumulation can indicate a change from aerobic to anaerobic metabolism in this tissue. In general, this data are in agreement with the hypothesis that the thermal tolerance in Antarctic fish is limited by the capacity to cope with the increase in energetic demand in response to increasing water temperature and this inability for improvement oh the thermal plasticity makes *N. coriiceps* vulnerable to the increase in the Antarctic waters temperature.

Influence of environmental conditions on trophic niche partitioning among sea stars assemblages

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The Southern Ocean undergoes intense and contrasted impacts linked to climate change. The Western Antarctic Peninsula is one of the most rapidly warming regions of the world (Meredith and King, 2005), resulting in sharp sea ice cover decrease (Parkinson and Cavalieri, 2012). In contrast, surface temperature and sea ice cover remain stable in other regions such as the Weddell Sea. Sea stars (Echinodermata: Asteroidea) are a key group of the Southern Ocean benthos, considered to be quite resistant to seawater temperature changes (Peck et al., 2008). However, other more indirect environmental changes, might induce important shifts in food web structure and functioning, that may affect sea stars trophic ecology.

In this context, the aim of this study was to use stable isotopes ratios of C, N and S to study sea stars trophic ecology to characterise their trophic diversity and plasticity regarding food web changes. Sea stars were sampled during the austral summer in the South Georgia (sub-Antarctic) in 2011 and in the South Shetland (2006) and South Orkney Islands (2016), as well as in the Weddell Sea (2015-2016). Trophic diversity, i.e. differences of trophic ecology between sea star species, and variability, i.e. differences of trophic ecology between individuals of the same species, were investigated in each region by investigating isotopic dispersion and isotopic niche (proxy of the trophic niche) areas and overlap.

Difference in niche width and overlap between the regions may be the result of different environmental conditions, including sea ice coverage and dynamics. For example, in the South Shetland, sea stars had small and poorly differentiated isotopic niches. This result indicate that they may exploit the same benthic communities relying on few common food sources such as organic matter released during sea ice melting (Isla et al., 2006) or sinking phytoplankton (Mincks et al., 2008). Whether this situation leads to competition or not depends on the resources availability. In contrast, isotopic niches were larger and better separated for sea stars from South Georgia. South Georgia is an oligotrophic environment with no sea ice (Korb et al., 2008). As available food items are more limited but, perhaps, more diversified, a higher trophic segregation may appear between species. Ultimately, this project will help delineating processes determining trophic ecology of Southern Ocean sea stars.

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Understanding the climate vulnerability of *Antarctic* biodiversity

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The Antarctic continent is home to substantial numbers of endemic species, including moss, lichens, springtails, tardigrades, mites, nematodes and seabirds. Whilst it is largely considered to be pristine, and a "nature reserve, devoted to peace and science", it is actually under threat from multiple pressures, including climate change, invasive species and anthropogenic disturbance (both tourism and science). The Antarctic Peninsula has experienced one of the most rapid temperature rises in the Southern Hemisphere and managing invasive species has been labelled as the number one priority of the Committee for Environmental Protection (Vaughan et al. 2003; Mulvaney et al. 2012). Climate change impacts on the rest of the continent are likely to become more pronounced over the 21st century and as climate ameliorates, it will become easier for alien species to establish in regions currently inhospitable to them (Turner et al. 2016; McGeoch et al. 2015). Despite this, we know relatively little about how resilient most Antarctic taxa are to climate change and invasive species. Here we assess the climate vulnerability of different taxonomic groups using life history and mechanistic traits. We consider exposure, sensitivity and adaptive capacity of different species to determine which groups are the most vulnerable and why. We then explore whether the resilience of these groups will be further impacted by invasive species. We demonstrate substantial differences in vulnerability amongst terrestrial biota, varying both within and across taxonomic groupings, and spatially across biogeographic regions. These results will inform conservation planning by identifying climate vulnerable groups and regions that may benefit from targeted management actions.

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Stable isotopes reveal effects of *environmental* changes on ecological niches of Iphimediidae amphipods

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When faced with environmental changes, organisms are expected to have some intrinsic ability to adapt through ecological plasticity. However, this process is still poorly understood in many Antarctic invertebrates. Here, we focused on Iphimediidae amphipods, as this widely distributed family shows important ecological diversity. In total, 248 amphipods (19 species) from two widely different zones (the West Antarctic Peninsula, or WAP, and Adélie Land, AL) were studied to elucidate how environment can influence ecological niche parameters. Ecological niches were explored using stable isotope ratios of carbon and nitrogen and the SIBER approach (Jackson et al., 2011).

The isotopic niche of the whole amphipod assemblage was wider in WAP than in AL. This was true for both total (proxy of the whole range of resources exploited by animals) and the core (proxy of the most commonly used resources) isotopic niches. The ratio between total and core isotopic niches was smaller in WAP than in AL (4.13 vs. 5.74), suggesting that in WAP, animals commonly use a greater relative percentage of the resources to which they have access.
Niche modelling at the specific level revealed that this trend was not found in all taxa. For example, niches of *Gnathiphimedia sexdentata* and *Iphimediella microdentata* were bigger in WAP than in AL, following the general pattern. On the other hand, niches of *Echiniphimedia echinata* and *E. hodgsoni* had the same width in both areas. Moreover, relative niche overlap between these two species was much higher in WAP (42%) than in AL (20%).

Our results indicate that the widely different environmental conditions encountered by the animals in these two zones clearly influence their ecology. Overall, Iphimediidae amphipods tend to exploit more resources in WAP, i.e. in the zone where impacts of global change (temperature increase, sea ice cover decrease) are the strongest. Niche overlap between some closely related (i.e. congeneric) species was also more important in WAP. Ultimately, environmental changes in this region might reinforce these trends, which might lead to competition and perturb amphipod community structure.

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Assessing the down-fjord mechanistic relationships of biodiversity and abundance of Antarctic benthic macrofauna of Andvord Bay

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Glaciomarine fjords, which exhibit substantially different ecosystem forcing than adjacent continental shelves, have shown to be highly sensitive to climate warming. Extensive research in the Arctic has shown that subpolar fjords are heavily influenced by sediment inputs from glacial meltwater, resulting in high turbidity and seafloor burial rates, and thus, macrofaunal communities with low abundance and species diversity. In contrast, poorly-studied sub-polar fjords along the Western Antarctic Peninsula (WAP) are subject to weak meltwater processes, resulting in comparatively low turbidity and seafloor burial rates. Thus, seafloor communities in WAP fjords may not currently be limited by turbidity and burial disturbance, and have the potential to foster highly abundant and diverse seafloor faunal communities. However, as warming continues along the WAP, increased glacial meltwater input to WAP fjords is expected, potentially causing a shift in benthic community structure toward that of Arctic sub-polar fjords.

This study characterizes the benthic macrofauna community of Andvord Bay, a subpolar fjord along the warming WAP. Using interdisciplinary research, we compare the distribution of benthic macrofauna in the fjord to potentially important ecological drivers, particularly sediment burial rate (a source of burial disturbance) sediment Chlorophyll-a concentrations (an indicator of labile detritus availability), and sediment-community respiration (an indicator of detrital carbon flux to the seafloor). In addition, we compare the down-fjord burial-disturbance model for benthic macrofauna from subpolar Artic fjords to macrofaunal patterns in Andvord Bay.

Megacore samples were taken at a total of five locations in Andvord Bay, the Gerlache Strait and at Station B (shelf locations), during Nov-Dec 2015 and an April-May 2016. We find high macrofaunal abundance in the middle to outer fjord in comparison to the shelf stations, with reduced abundance in innermost fjord basin where sediment accumulation rates are relatively high. Abundances are up to an order of magnitude larger than was recorded in Arctic fjords. The middle basin station had the highest abundances of macrofauna, which may be attributed to a high flux of detritus to the seafloor and moderate sediment disturbance. Here we draw connections between macrofaunal abundance and diversity to sedimentation rate, Chl-a concentrations, and respiration in the fjord basins and at the shelf locations.

Analysis of RGB data of photographs for long-term vegetation survey of terrestrial ecosystem on Antarctica

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The quadrat method has been widely used in vegetation monitoring. The method is performed to set some quadrats in a field and survey plants in the quadrat with investigator's naked eyes then the method need monetary cost and human resources. Recently, an approaches analyzing photographs of the investigation object taken by compact digital camera as one of the remote sensing techniques is increasingly attempt to diminish the costs of vegetation monitoring (Richardson 2007, Sakamoto et al. 2011). However the method is never applied to communities constructed by extremely small plants such as mosses, cyanobacteria and lichens. Remote sensing survey for vegetation of these plants require data at resolution of a few centimeters.

Then, we attempt to develop an analytical method of RGB data of photographs by digital video camera for vegetation survey and we analyzed photographs for permanent quadrat. The analyzed photographs are of permanent quadrat for vegetation survey near Showa station on the north east Antarctica. The permanent quadrat for vegetation survey has been set and kept since 1984 in the Antarctic Specially Protected Area No. 141 and taken photographs using compact digital camera each quadrats by Japanese Antarctic Research Expedition since 1988. The quadrat is chosen places growing mosses, cyanobacteria and lichens in the area. The RGB data ware derived from these photographs and analyze using canonical discriminant analysis (CDA) and Naïve Bayes classifier (NB) to detect the cover degree of whole plant community and each taxonomic groups. We compared accuracy of the two methods and the accuracy of CDA totally was high than the results of NB. The error of confusion Lichen with gravels was large because the colors of that are not much difference. And the results show that discrimination gravels and that of cyanobacteria or lichen has trade-off relations.

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Changes in health of Windmill Islands vegetation: a decade of monitoring

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Continental Antarctic vegetation communities are good baseline environments for climate change research, with little human impact, simple trophic structures and fewer interactions than more complex ecosystems. In addition, they are expected to be more sensitive to environmental changes than communities in less severe conditions.

In the East Antarctic, there is little evidence of warming, however changes to the Southern Hemisphere Annular Mode (SAM), primarily driven by the Antarctic ozone hole, have caused stronger circumpolar westerly winds, which have migrated poleward by 1-2° of latitude since the late 1970s. Existing moribund and lichen-encrusted vegetation patterns in the Windmill Islands, East Antarctica suggest that this region is currently undergoing a period of long-term drying, with contraction of bryophyte communities to areas with reliable moisture supply.

In order to monitor recent vegetation changes in the Windmill Islands region, a long-term monitoring system was established in 2003. Here, we present the results from the first decade (2003-2013) of repeat long-term vegetation monitoring at two sites in the Windmill Islands, East Antarctica (ASPA 135 and Robinson Ridge). Vegetation cover, health and species composition were assessed at four time points, along a series of transects spanning a community gradient from pure bryophyte stands in the wettest areas, to drier lichen-dominated communities higher up the slopes.

Moss health state changes were observed between healthy, stressed and moribund over the decade of monitoring. A marked increase in stress and decline in health was observed in 2008, due to some stress event prior to the 2008 sampling. Moss health then markedly improved by 2013, with a return to baseline levels of health at ASPA 135, and regaining health to 2/3 of baseline levels at Robinson Ridge. An associated increase in moribund moss was found at both sites. This indicates that these vegetation communities are resilient; however moss can become moribund if there is stress of high intensity or for extended periods.

This long-term monitoring system informs Australian State of the Environment Indicator 72*, regarding terrestrial Antarctic vegetation. These results will help to inform policy and management of vegetation in the Australian Antarctic Territory.

* https://data.aad.gov.au/aadc/soe/display_indicator.cfm?soe_id=72

Life at extremes: Ferns in a modern warming "Pleistocene" environment

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Ferns have an interesting global distribution. Since the late Cretaceous, they have tended to occur in low-productivity habitats, usually limited to shaded or low nutrient environments, and rarely dominant in their native ranges(Schneider *et al.*, 2004; Tosens *et al.*, 2016). They are, however, currently dominant in some high alpine and tundra environments. This might be an indicator that these ferns might be relics from Pleistocene-type environments, preferring cold locations and outcompeting angiosperms in these habitats. They would also be quite sensitive to the increase in global temperature, with larger predicted upslope movement than other vascular plants. Such movement upslope has been observed on Marion Island, where the ferns and fern allies have increased their ranges significantly(Le Roux and McGeoch, 2008). The dominant fern and our study species is *Blechnum penna-marina*, which has the highest biomass of any vascular plant on the island.

In this talk, I will attempt to unify remote sensed abiotic and photosynthetic data, combine it with gas exchange data collected at different desiccation intensities, as well as different temperature acclimations and try to show how these plants are coping with some of the most challenging conditions on the planet. I will discuss how both desiccation and acclimation affects photosynthesis. Preliminary results show that plants acclimated at higher temperatures had lower dark respiration, electron transport rates and Rubisco activity. *Blechnum penna-marina* can withstand desiccation for up to 14 days, well above the current limit for rainless days. I will touch on how the light regime, which is neither a fully shaded nor a high light environment, may force the ferns to be well adapted to both light conditions. Early results show that leaf temperature, while being governed by solar radiation and air temperature, not affected by high wind speed. I will show how extremely high wind speeds and the vapour pressure deficit can limit photosynthetic capability. I will then indicate where the next steps in this research could lead.

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Towards estimation of blue carbon sink potential of sub-Antarctic continental shelf benthos

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Continental shelves around Antarctica are a globally important carbon sink, due to both oceanographic CO2 absorption and biological fixation and trophic cascading. Most carbon passing through the foodweb is pelagic and is recycled through microbial loops. However significant masses are accumulated and immobilized (within calcareous skeletons of benthos), accounting for sequestration potential of 106 tonnes per year. Burial potential is enhanced by being largely untrawled by human harvesting and too deep for iceberg scouring. Yet these are also true for subAntarctic island shelves where there are considerable phytoplankton blooms, little or no sea ice and warmer sea temperatures (enabling faster meal processing time by benthos) – yet their potential as a carbon sink has been largely ignored. We report on the Antarctic Seabed Carbon Capture Change (ASCCC) project which sampled most of the high southern latitude continental shelves during the 2016/17 Antarctic Circumnavigation Expedition (ACE). Video and photo-equipped trawls collected imagery and benthos samples allowing us to estimate changes in intra and inter-shelf variability in benthos density and biomass. Growth models constructed from age structure of sampled species with growth check lines (e.g. bryozoans, bivalves, brachiopods etc) enable annual carbon accumulation to be estimated. Preliminary data and analyses suggest that continental shelves of 40-55°S may be globally significant, both in terms of absolute carbon storage but also in trying to reduce error in climate models. See www.asccc.co.uk

Responses to environmental pressure of fungal component in the Antarctic lithic communities

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The airspace of rocks represents a common niche for microbial life in harsh environments. In the McMurdo Dry Valleys, Antarctica, the best analogue for Martian environment, rocky outcrops support the largest standing biomass (Cowan et al., 2014) and endolithic life-style remains the most widespread and often the sole possibility of survival (Friedmann, 1982). Over the past 50 years some Antarctic areas experienced the most rapid changes in mean air temperatures on Earth (Steig et al., 2009). As border ecosystems, endolithic Antarctic communities are expected to be very sensitive to external variations. Despite recent advances, data on biodiversity in these communities are still scant and nothing is known about how and if is affected by the environmental pressure. Since it is virtually certain that the progression of warming will continue and intensify in the future, we can expect a direct influence on the delicate equilibrium of these border ecosystems. The distribution of epi- and endolithic colonization, up to the limit of extinction, was recently mapped in the North Victoria Land, Antarctica (Zucconi et al., 2016). Here we studied the biodiversity, with special focus on fungi, of Antarctic epi- endolithic microbial communities, its variation and community structure, according to environmental pressure. Rocks of different typologies were analyzed since porosity is hypothesized to influence microbial diversity (Cockell et al., 2003). Sampling was performed along an altitudinal gradient up to 3600 m asl and sea distance up to 100 km in the Victoria Land, Antarctica, and biodiversity studied with Denaturing Gradient Gel Electrophoresis (DGGE) approach. Lichenized fungi were largely predominant and the biodiversity heavily influenced even by minimal local variations. The n-MDS analysis showed that altitude and sea distance affect biodiversity while sandstone is the best substratum for the maintenance of high biodiversity indexes. The Pareto Lorenz curves indicate that all the communities analysed are very adapted but scarcely resilient, so any external perturbation may have irreversible effects on these weak ecosystems. Data will give clues for monitoring and predict any future variation related to Climate Change.

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Spatial distributions of Southern Ocean mesozooplankton communities have been resilient to long term surface warming

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The biogeographic response of open-ocean planktonic communities to climatic change has a large influence on the future stability of marine food webs and the functioning of global biogeochemical cycles. Temperature plays a pivotal role in determining the distribution of these communities and ocean warming has the potential to cause major distributional shifts, particularly in polar-regions where the thermal envelope is narrow. We considered the impact of long-term ocean warming on the spatial distribution of Southern Ocean crustacean mesozooplankton communities through examining plankton abundance to sea surface temperature relationships between two distinct periods, separated by an interval of around 60 years. Analyses considered 16 dominant mesozooplankton taxa (in terms of biomass and abundance) in the Atlantic sector of the Southern Ocean, south of the Polar Front, from net samples and *in situ* temperature records collected during the *Discovery Investigations* (1926-1938) and contemporary campaigns (1996-2013). Sea surface temperature was found to have increased significantly by an average of 0.74°C between the two eras. The corresponding sea surface temperature at which community abundance peaked was also significantly higher in contemporary times, by 0.98°C. Spatial projections indicated that the geographical location of community peak abundance had remained the same between the two eras despite the poleward advance of sea surface isotherms. If the community had remained within the same sea-surface thermal envelope as in the 1920s-1930s, community peak abundance would be 500 km further south. Studies in the North Atlantic and North Pacific have found that dominant taxa, such as calanoid copepods, have conserved their thermal-niches and tracked surface isotherms polewards. The fact that this has not occurred in the Southern Ocean suggests that other selective pressures, particularly food availability and the properties of underlying water masses, place greater constraints on spatial distributions in this region. It further demonstrates that this community is thermally resilient to present levels of sea surface warming.

Optimal field conditions for photosynthesis in Antarctic mosses

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Global warming, ozone depletion and their interaction have led to substantial changes in Antarctic terrestrial ecosystems. Differences between plant species' capacity to maintain and optimise photosynthesis as environmental conditions vary could lead to changes in community composition and species distribution. However, the optimal environmental conditions for photosynthesis in Antarctic mosses are not known. The inherent daily and seasonal variability in photosynthesis is also an important context for understanding the impact of a shifting climate on moss health and survival.

Photosynthesis in three Antarctic mosses was measured at noon (± 2 hours) on 22 days over a summer growing season using chlorophyll fluorescence with corresponding measurements of water availability, solar radiation, moss turf temperature and air temperature. Optimal noon-time conditions for photosynthesis were then estimated using a generalised additive model. Diurnal measurements were also conducted on the endemic species *Schistidium antarctici* across a water gradient.

Photosynthesis is strongly seasonal in Antarctic mosses and this has implications for the timing of measurements in inter-annual studies. We found photosynthesis was well adapted to strong sunlight and frequently proceeded at relatively warm temperatures (>10°C) with daytime moss turf temperatures reaching well above ambient. Photosynthesis increased until 10-day mean air temperature reached -2□C, a threshold that may correspond to the cessation of overnight freezing events. Noon time photosynthesis was rapidly responsive to the ephemeral variables water content, moss turf temperature and photosynthetically active radiation in the two cosmopolitan species, but less so in the endemic species *S. antarctici*. This lack of responsiveness may indicate an inability to optimise photosynthesis as conditions vary. Furthermore, this species requires wetter conditions and may be most suited to colder temperatures so could be disadvantaged under a warmer, drier climate change scenario.

Evidence for mass mortality events of Antarctic Silverfish (Pleuragramma antarctica) in the Ross Sea

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Mass mortality in Antarctic fishes is a very poorly explored issue. The first evidence of an extensive die-off of fish in Antarctic waters dates back to the heroic era of Antarctic exploration. Shackleton's diary of the 1914-1917 Antarctic expedition reports: "…*Thousands of small dead fish were to be seen, killed by a cold current and the heavy weather. They floated in the water and lay on the ice, where they had been cast by the waves. The petrels and the skua-gulls were swooping down and picking them up like sardines off toast"*. At that date, 13 April 1915, Shackleton and his crew were on board the *Endurance* lifeboats, between Elephant Island and Hope Bay (Antarctic Peninsula).

More than 40 years after Shackleton's observation, on 22 March 1952, an enormous quantity of dead fish, all *Pleuragramma antarctica*, were reported by Argentinian scientists floating on the sea surface over a stretch of many miles west of Adelaide Island, Bellinghausen Sea. Another Antarctic fish mass mortality event was reported in February 1982, in proximity of Davis Station (Vestfold Hills region), where several thousand specimens of *Pagothenia borchgrevinki* were found dead after a blizzard.

During our ecological surveys in the the Ross Sea Region, repeated findings of dead *P. antarctica* made us consider possible mass mortality in this species. First a conspicuous number of silverfish remains (mainly constituted by decomposed trunk parts and whole adult specimens) were noted in December 2009 trapped under the fast-ice of Terra Nova Bay and also sampled by SCUBA divers. More recently, in February 2015, during the New Zealand cruise on the research vessel Tangaroa, we observed thousands of dead adult *P. antarctica* floating on the sea surface, in two distinct sites of the western Ross Sea.

This contribution is intended to draw the attention of Antarctic scientists engaged in ongoing and future ecological studies to Antarctic fish mass mortality, to better understand the scale of this phenomenon and its relevance for the Antarctic fish life histories, as well for the Antarctic ecosystem dynamics.

Assessing the roles of sea ice and chlorophyll in the winter diets of euphausiids in the northern Antarctic Peninsula region: implications for predicting responses to climate change

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Few studies have addressed the winter biology of Antarctic krill (*Euphausia superba*), and fewer have addressed the winter biology of other Southern Ocean euphausiid species. Here we examine the winter diets of five species of euphausiids (*E. superba, E. crystallorophias, E. frigida, E. triacantha,* and *Thysanoessa macrura*) in the northern Antarctic Peninsula (nAP) region. We analyzed data on stable isotope and lipid content collected over five consecutive winters (2012 – 2016) with varying environmental conditions. Despite inter-annual differences in sea-ice coverage and water-column chlorophyll-a concentration, the relative trophic positions and diets of all five species, as inferred from $\delta^{15}N$ and $\delta^{13}C$, were relatively consistent among years. Although diets remained consistent and were distinct among species, the mean lipid contents of all species varied coherently among years. The species-specific patterns of change in percent lipid were also not related to changes in ice coverage or chlorophyll-a. Our results suggest that during winter, euphausiids in the nAP region are feeding specialists and consistently rely on similar prey items despite changes in environmental conditions. Fluctuations in lipid content may be the result of either reduced quality or availability of prey, or a combination of both. Furthermore, the consistent pattern in annual lipid fluctuation among species suggests that species are responding to large-scale, rather than habitat-specific, changes in environmental conditions. This study is the first to establish winter baselines for important metrics of euphausiid feeding behavior and body condition in the nAP. Our results have implications for predicting future responses of euphausiids to environmental change. Euphausiid responses to climate change may be difficult to assess without annual, in-situ measurements of trophic position and lipid content because variability in these measures of diet cannot be explained by environmental changes that are commonly observed from space, sea-ice coverage or chlorophyll-a concentration.

What is the impact of human disturbance on the stress response of Adélie penguins breeding in Antarctica?

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One of the thematic set of questions of the SCAR first Horizon Scan deals with the impact of human presence on the Antarctic environment and wildlife. Questions 74 (How can natural and human-induced environmental changes be distinguished, and how will this knowledge affect Antarctic governance?) and 75 (What will be the impacts of large-scale, direct human modification of the Antarctic environment?) represent pressing issues that still lack scientific data to be addressed, despite investigations conducted in the Peninsula region where human presence is more acute than elsewhere. In addition, impact studies on wildlife, especially upper vertebrates, are often confined to observational studies, possibly masking underlying physiological responses of wildlife to human exposure. In this context, our study aimed at examining the physiological response of Adélie penguins (*Pygoscelis adeliae*) from Terre Adélie, East Antarctica, to various degrees of long-term human exposure using a standardized stress protocol. When exposed to stressors, a hormonal stress response is indeed activated to shift energy investment away from reproduction and/or growth and to redirect it towards immediate survival. In vertebrates, this stress response is achieved through a release of glucocorticoids hormones (corticosterone in birds). One of the most common method to measure such a hormonal response, is to subject individual to a standardized capture/restraint/stress protocol. In our experiment, two sites with sustained and continuous human activity (on Petrels Island where the scientific base of Dumont d'Urville is installed since 1952) were opposed to two sites on neighbouring islands with little or no human activities (Island Lamarck and Bernard). Stress response experiments were conducted on fifteen adults per site from nests with equal value (2 eggs or 2 chicks per nests) several times during the reproductive season, on incubating females, incubating males, chick-rearing males and females. Around 15 large chicks were also tested per site. Within 0 to 3 minutes after capture, an initial blood sample was collected to measure baseline corticosterone levels. Birds were then restrained for ca. 15 minutes and a subsequent sample was collected to measure maximum stress-induced corticosterone levels. We expected birds from sites with little human impact to present greater elevation in corticosterone concentration following restraint. Although we do not want to spoil the results in this abstract we can tell that the story has a – probably counter-intuitive – happy-ending, bringing valuable information for the Standing Committee on the Antarctic Treaty System to develop scientific advice to the Antarctic Treaty Consultative on this hot topic.

Adaptation to a threatened world: What the immune system of the Antarctic penguins can tell us?

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Parasites are the most abundant species in the Earth. Antarctica and the wildlife inhabiting this continent is not free of these organisms although the information about their presence and their effects are scarce and fragmented. Along the evolution, hosts have developed mechanisms to defend themselves against the action of parasites. Penguins as vertebrates have a very well developed immune system composed by a great variation of components, such as the innate or the acquired immunity, or the humoral and cellular immune response. Parasites are affected by global change by increasing their distribution, their abundance and virulence and this trend should also be present in a region like Antarctica and specifically the Antarctic Peninsula, where huge environmental changes due to the increase of temperatures and the increase of the human presence are present. Such changes can affect penguins increasing the risk of exposure to new parasites or emergent diseases or simply producing population changes in the endemic parasites or diseases which could increase their effects. To avoid or reduce such effects, penguins should response through its immune system. Here we give information about the functioning of the immune system in these species from a spatial a temporal perspective. We show that some components of the immune response have a genetic basis while others seem to show a high environmental component; how the immune system can be affected by environmental changes such as variation in snow precipitation, how differences in parasite prevalence can affect the response by penguins, how different physiological stages could also influence the immunological response and how human activity can also affect penguin immunity. As a conclusion, considering that penguins are sentinels of the changes in Southern Ocean and that the immune system responds to a great variety of factors, immunity can be considered as an indicator of the health status at both population and individual level in penguins, then monitoring its variability seems to be crucial for surveillance the health of the Antarctic continent.

Reproductive strategies in Gentoo penguin (Pygoscelis papua): to cheat or not to cheat?

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The use of new molecular markers has confirmed reproductive strategies in monogamous birds, such as (1) extra-pair paternity (EPP), when the social father is not the genetic father of the chick and (2) intraspecific brood parasitism (ISBP), which occurs when a female lays eggs in the nest of another conspecific female and she does not aid in the process of incubation and the care of chicks. Preliminary studies found that these reproductive tactics are infrequent in seabirds' species, especially in penguins. However, studies with more advanced genetic techniques (such as microsatellites) have discovered that they are not as rare as had been postulated. Through the use of microsatellite markers, we determined a parentage analysis, along with the sex of 60 adults and 30 chicks. Our results showed a 27% rate of inconsistency between social parents and their chicks; 18% corresponded to EPP and 9% to ISBP. These EPP and ISBP rates are the highest recorded in penguins; these numbers, however, remain low when compared to terrestrial birds. Penguins presents high and extended parental care, specially in *P. papua* and this could explain the low rate in EPP; on one hand, a male must invest a lot of time caring for his offspring, therefore decreasing the rate of EPC. On the other hand, females are able to restrict the attempts of EPC when there is risk of partial or total reduction of paternal care of the nest when it's fundamental for the survival of the offspring. In the case of ISBP, the high parental care would avoid this practice; since it would be more difficult to place eggs in a nest guarded by parents. Moreover, has been proposed that colonial breeding may favour EPC (by facilitating encounters between individuals) and ISBP, where it is easier to infest the closest nests. However, behavioural and genetic studies alone are inconclusive. So, it's necessary to work in conjunction to ensure the causes of those strategies. This study is one of a few contributing to understanding the reproductive strategies in seabirds and penguins. The reproductive strategies can be affected by diverse environmental and/or anthropogenic factors, which in turn would affect the species evolution. Therefore, it is important to further comprehend alternative reproductive strategies in seabirds associated with biotic and abiotic variables and to establish their causes and effects in different populations and species.

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Reproductive effort affects the annual dive behavior of adult, female Weddell seals

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Given forecasted changes in sea-ice cover, understanding the baseline and seasonal activities of apex predators is a scientific priority. Our objective was to characterize the annual foraging behavior of adult, female Weddell seals (*Leptonychotes weddellii*) in the Ross Sea, Antarctica during 2013-2017. We hypothesized that following the lactation period, post-parturient seals would increase diving effort to regain body mass prior to their annual molt. To test this hypothesis, we deployed time-depth recorders (TDRs) on the flippers of 57 seals during the austral summer, including seals that had produced pups in a given year (post-parturient; n=34) and seals that had not (non-parturient; n=23). The tags were recovered between 39 and 436 days later and together comprise more than 135,000 dives from 5,642 seal days. During summer, seals that pupped were active divers (mean ± standard deviation 48±11dives day^{-1}, with dives averaging 12±2min, 177±73m) whereas seals that had not pupped spent less time foraging (22±7dives day^{-1}, 18±5min, 158±62m). Coincident to the higher diving activity, seals that pupped gained mass over summer (0.6±0.5 kg day^{-1}) whereas seals that had not pupped lost mass (-1.0±0.4kg day^{-1}). Despite marked inter-annual differences in sea ice extent (range 17 to 110km from McMurdo research station to ice edge), behavioral patterns and mass change dynamics were consistent across years, suggesting the relative resilience of this species to changes in sea ice extent. In all years, seals showed a clear pattern during late summer where dive depth gradually shallowed from >400m to <150m across two weeks and subsequently returned to >400m. Because the number of dive-depth-wiggles (a proxy for prey capture events) was significantly higher during this brief period, shallow diving could correspond with altered prey dynamics following the seasonal phytoplankton bloom. In the seven over-winter records, seals dove 3x more frequently and 50% deeper than summer, although dive durations were similar. Differences in dive metrics between post-parturient and non-parturient seals were not evident in the winter records. Our utilization of flipper-tag TDRs provides the first look at year-round Weddell seal behavior. These behavioral data are crucial for understanding predator responses to Antarctic change.

Life in the fast lane: differences in foraging behavior between lactating and non-lactating Antarctic fur seals (*Arctocephalus gazella*) at high latitude

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The study of Otariids foraging ecology have been traditionally based on the analysis of lactating females lacking a proper comparison with non-rearing females. This comparison is fundamental to understand the additional effort associated with lactation. The Antarctic fur seal (*Arctocephalus gazella*) is a good example of this. Up to date, research has shown that, in climatic extremely variable years or places, individuals operate at their highest field metabolic rate and will modify trip duration when necessary but not their diving effort. Onderkant formulier

The study of Otariid foraging ecology has been traditionally based on the analysis of lactating females, frequently lacking proper comparisons with non-rearing females. This comparison is fundamental to understanding the additional effort associated with lactation especially across latitudinal gradients in rapidly changing and seasonally-variable environments. At its most southerly breeding range, the Antarctic fur seal (AFS) operates at its highest field metabolic rate in an environment challenging the physiological limits for energy acquisition and expenditure for fur-bearing marine mammal. Using time-depth recorders (TDRs) we tested the hypothesis that diving effort is modified to cope with increased demand for energy associated with lactation using age- and size-matched controls. A total of 6 non-lactating controls (NLC) and 16 lactating females (LF) were captured and instrumented with TDRs during the breeding seasons of 2015/16 and 2016/17, at Cape Shirreff Livingston Island, Antarctica (62.47°S). Foraging behavior was compared between NLC and LF throughout seasons using 14 variables that represent three different categories: trip duration, recovery time (time ashore and at surface between dives) and diving effort. Overall, trip durations were long in NLCs even though some LFs did longer trips throughout the season. Short trips of LFs maybe related to offspring attendance not present for NLCs. In addition, NLCs spent considerably more time onshore between trips and more time at the surface between dives (recovery time) than LF. Diving effort variables such as bottom time, average maximum depth and dive duration were also higher in LF. Our study confirms previous studies (without suitable controls), that rearing offspring requires considerable modification in behavior and foraging strategy. Further, the magnitude of the increased effort suggests that the demands of lactation and increased energy acquisition associated with breeding at higher latitudes drive lactating seals closer to their physiological and ecological limits. These modifications may have been missed by previous studies that did not have NLCs. Additional studies of field metabolic rate of non-lactating females compared to lactating females would be valuable in understanding the true cost of rearing offspring and how time budgets and energy allocation change under different environmental scenarios. Such studies are especially important in the face of climate change and increased demand by fisheries that can change predator-prey dynamics resulting in increased vulnerability.

Bulk and Compound-specific Isotope Analyses of Seal Mummies reveal the Vulnerabilities of Antarctic Seals to Environmental Change

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Anthropogenic climate change is rapidly altering polar systems. Analysis of the response of organisms to past climate events provides insights into their present vulnerabilities. Over the mid-to-late Holocene, sea ice duration and extent likely increased in the Ross Sea. Wave-formed, raised beaches on the Victoria Land Coast (VLC) of the Ross Sea indicate that liquid water once reached this coastline, which is largely rimmed with land fast ice today. The presence of fossil southern elephant seals (SES, *Mirounga leonina*), which are missing from the modern Ross Sea, also suggest the VLC was less icy earlier in the Holocene since SES require rocky beaches to breed and molt.

We used bulk stable carbon and nitrogen isotope ($\delta^{13}C$ and $\delta^{15}N$, respectively) analyses of ~700 fossil Antarctic pinnipeds, complimented by isotopic analysis of individual amino acids, to investigate biological and biogeochemical responses to Holocene climate change. Bulk isotope values of Weddell seals (*Leptonychotes weddellii*) decrease around 700 YBP ($\delta^{13}C$ by ~1.5‰ and $\delta^{15}N$ by ~3‰). Similarly, bulk $\delta^{15}N$ values of fossil southern elephant seals are higher than modern SES, suggesting a Holocene environmental transition in the Ross Sea. The isotopic transitions of these predators could result from a drop in Ross Sea productivity, a switch to lower trophic level prey, or both. In contrast, crabeater seals (*Lobodon carcinophagus*) show no temporal change in their bulk isotope values, but they have greater isotopic variability in the past, indicating more diverse foraging habits. Amino acid $\delta^{15}N$ analysis allows discrimination between trophic switching and baseline shifts in $\delta^{15}N$ values. Weddell seal amino acid $\delta^{15}N$ values support a late Holocene baseline drop of ~3‰ in the Ross Sea, consistent with higher past productivity. Amino acid $\delta^{15}N$ values of SES individuals foraging in the Ross Sea also support higher baseline values in the earlier Holocene. Crabeater seal amino acid $\delta^{15}N$ values indicate diets consisting of more fish and use of a different region of the Ross Sea than the Weddell seals.

Our findings indicate that crabeater seals may have a higher adaptive capacity and lower sensitivity to climate change than Weddell seals and SES. The crabeater seal appears to have more heavily relied on fish up to ~250 YBP and, thus, only recently shifted to a diet dominated by krill. In contrast, Weddell seals and SES show no significant variability in trophic position and diet over the Holocene and, thus, have less flexibility in their foraging strategies.

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Maternal constraints on the timing of weaning in Weddell seals

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For many Antarctic species, critical life history events are concentrated during the short austral summer when weather is good and productivity levels are higher. During their ~6 week nursing period in October and November, Weddell seal (*Leptonychotes weddellii*) pups double in size while females lose ~30% of their body mass. In many young mammals, development of heme stores (hemoglobin; Hb and myoglobin; Mb) is constrained by limited iron delivery in milk. Heme stores contribute to marine mammals' total body oxygen stores (TBO_2) and are particularly important for diving and foraging capacities. Late lactation female Weddell seals have higher serum iron levels (mean±SD 290±88µg dL^{-1}) than non-lactating females (130±53µg dL^{-1}, p<0.001), indicating mobilization to milk. However, the amount of iron transferred from mother to pup during lactation may reflect a trade-off between the pups' need to develop heme stores and the mothers' need to defend hers. Soon after weaning, adult females have lower TBO_2 and aerobic dive capacities (pre-weaning: 123±9mLO_2 lean kg^{-1}, post: 102±15mLO_2 lean kg^{-1}, p=0.002) suggesting that females were not able to allocate as much iron for Hb and Mb self-maintenance during lactation, an unexplored cost to a capital breeding system.

Following weaning, both females and pups forage on local prey resources. While females can utilize these resources to recuperate their body mass by ~1kg day^{-1}, pups still lose mass for the next 6 weeks. It was presumed that the pups' shorter and shallower dives were due solely to still-developing heme and aerobic capacities; however, recent work shows that adult females also dramatically reduce average dive depths for ~2 weeks during late summer (mean±SD 224±66 meters to 96±30 meters, p<0.0001), coinciding with the local phytoplankton bloom. Being able to forage at shallower depths may facilitate mass and heme recovery by post-partum females. This sudden prey availability may also improve foraging success of newly weaned pups by bringing prey into a range that they can efficiently exploit despite reduced capacity. Indeed, dive depths and duration of weaned pups plateau, and pups shift from mass loss to mass gains concomitant with this shallowing of adult dives. This is followed by a secondary increase in pup dive capacity. In combination, these findings suggest that Weddell seal pup weaning is timed to coincide with a brief period of shallow prey abundance, which in turn may allow pups to develop and females to recover TBO_2 stores, prior to the onset of winter darkness.

Different chick provisioning strategies in Antarctic petrels and Southern fulmars

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On Ardery Island, Wilkes Land, Antarctic petrels (*Thalassoica antarctica*) breed 2.5 weeks earlier than the closely related Southern fulmars (*Fulmarus glacialoides*). In this pilot study we investigated how this different timing of breeding affected the chick-provisioning strategies in both species. We fitted 9 ARGOS satellite transmitters on 8 Antarctic Petrels and on 13 Southern Fulmars in the late chick phase (23 January - 23 March 1999). Transmitters were reused on different individuals and each device was on average attached for 13 days (range: 2-31 days).

Southern fulmars had foraging trips for on average 32 hours and during these trips they travelled less than 600 km during one trip. Kernel analysis showed that Southern fulmars foraged in a restricted area west of the breeding colony in a relatively shallow area over the Antarctic continental shelf. Individual trips of Southern fulmars were difficult to detect because of the short distances they fly and the low satellite coverage (long time intervals between two locations). Therefore, only 15 complete individual foraging trips could be distinguished.

In comparison, Antarctic petrels had much longer foraging trips of 73 hours (based on 27 trips) and flew almost 1700 km during one trip. The foraging area was much larger and the locations were more evenly distributed. A substantial part of the locations was situated near the shelf break, within the highly productive, seasonal sea-ice zone. Possibly due to their long foraging flights, Antarctic Petrels must leave their chick unattended at an earlier stage than Southern fulmars. On average the guarding stage of Antarctic petrels ended 7 days earlier.

There are no differences in food preference between both species that could explain the differences in foraging strategies. Earlier studies on Ardery Island showed that both species were feeding similar food to their chicks (both around 80% fish, mainly *Pleurogramma antarcticum*). In this presentation we discuss other factors (such as bathymetry and temporal sea ice cover) that influence how both species exploit the habitat in a different way.

Eggs finding and steps forward the knowledge of the biology of the Antarctic toothfish from the First Winter Survey (northern Ross Sea Region, June-July 2016)

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The Antarctic toothfish Dissostichus mawsoni represents an important fishery resource and plays a major ecological role as a top predator (Stevens et al., 2014; Pinkerton and Bradford-Grieve, 2014). Although biological and ecological data have greatly improved since the fishery began in 1997, crucial aspects of the species' life cycle, including spawning, remain hypotheses (Hanchet et al., 2008, 2015). Such gaps are mainly due to limitations in data collection, associated with the fishing activities being carried out only during the summer months and mainly on the continental slope.

The First Winter Survey in the northern Ross Sea Region, was aimed to expand the seasonal and geographic frame of Antarctic toothfish reproductive biology investigations. The survey was carried out in June and July 2016 on board of the New Zealand longline vessel FV Janas in the Ross Sea Subareas 88.1B-C, where deep seamounts, potential features for toothfish reproduction, are present (Hanchet et al., 2008; Ashford et al., 2012; Hanchet et al., 2015). Main aim of the journey was to investigate timing and location of spawning in the study area. Secondary objectives included evaluating fertilized eggs buoyancy, and characterize the early ontogenetic stages of Antarctic toothfish.

The biological characteristics of 1050 males and 392 females were documented. Male toothfish were often captured with ripe gonads, while running ripe females were caught only near the end of the survey. The eggs from two females were used for in vitro fertilization experiments. Fertilized eggs were incubated for several days allowing us to follow the first developmental stages and to measure buoyancy in a density gradient chamber. In each subzone of fishing, plankton nets were deployed in the attempt to capture Antarctic toothfish eggs or larvae set in the water column. For the first time, 19 presumed Antarctic toothfish eggs have been captured at the same locations where running ripe specimens were caught. These results represent an important contribution to the knowledge of the D. mawsoni life cycle, and open the way to further investigations.

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Integrative studies of Southern Ocean food webs and Pygoscelis penguin demography: mechanisms of population response to environmental change

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Unraveling the proximate physiological, ecological and evolutionary mechanisms that underlie population responses to environmental variability is an increasingly important challenge facing conservation biologists and is the primary motivation of the work described here. We studied *Pygoscelis* penguins that breed west of the Antarctica Peninsula (AP). Along the western AP, breeding populations of Adélie (*P. adeliae*), chinstrap (*P. antarctica*) and gentoo (*P. papua*) penguins are undergoing pole-ward range shifts that correlate with long-term warming trends of the region. However, mechanistic relationships that link marine ecosystem variability with demographic parameters that drive population change are rarely quantified. Our data support the following conclusions. At Anvers Island, where reductions in sea ice have been notable, *Pygoscelis* penguins became more similar isotopically throughout the breeding season, due to a depletion in δ13C and δ15N of blood tissue. Here, crèched chicks of all species occupied similar trophic levels and isotopic mixing models indicated that the proportions of prey provisioned to crèched chicks were generally similar across species within years. Crèched Adélie chicks were isotopically enriched at Avian and Charcot Islands, southern rookeries where sea ice is more prominent, and their trophic level increased with latitude. Penguin food webs are isotopically wider in regions with greater sea ice coverage. At Anvers Island, I detected little evidence of trophic foraging influencing body and egg mass of adult penguins and chick body mass. However, regional analyses suggested that a provisioning diet enriched in δ15N, such as that found at southern rookeries, resulted in heavier five-week-old Adélie penguin chicks. Corticosterone hormone did not mediate individual variation in *Pygoscelis* breeding performance. I found no overall genetic structure among Adélie penguins based on microsatellite and mitochondrial DNA markers, however, pairwise comparisons including Charcot Island were significant. Gene flow was asymmetrical from the species' regional core to its northern range. In conclusion, variability in sea ice-associated food webs of the western AP is an important determinant of *Pygoscelis* penguin reproductive performance, but not at the physiological level. A lack of genetic structure implicates dispersal as an important demographic factor that may structure population responses to future ecosystem change.

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Insight into an Adélie penguin colony

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Adélie penguins (*Pygoscelis adeliae*), like 95% of seabirds, nest in colonies, a form of social reproduction in which individuals aggregate within densely distributed breeding territories that contain no resources other than nesting sites. This structure is the product of numerous constraints and the patterns of bird distribution within a colony is complex.

To explore how a penguin colony functions across space and time scales, we monitor a colony of 350 Adélie penguin pairs breeding in Adélie Land with a new and ongoing methodological approach. Using automatic monitoring systems we can detect, weigh and spatially track an individual marked electronically (i.e. implanted subcutaneously with small Passive Integrated Transponders weighting less than a gram), without human intervention and disturbance, from its entrance inside the colony to its nest location, and vice versa.

Inside this particular and undisturbed colony, all the chicks and some adults have been implanted every year since 2006 (10 years of data) leading to a total of 2300 birds tagged. Since a transponder detection system is connected to an automatic weighing system (6 years of data) and 3 high-definition cameras (3 years of data) we can monitor, with the help of software already developed, the reproductive cycle of each penguin and track their movement inside the colony.

Thus, we have built a spatiotemporal database to evaluate the mechanisms determining the distribution of Adélie penguins within a colony according to their age and individual history (birth sites, kinship, past breeding performance, mate and site choice and fidelity) and to climatic conditions (marine and terrestrial), without the bias associated with earlier techniques. In other words, we can determine how environmental and social pressures are shaping reproductive strategies of undisturbed individuals.

Ultimately, we aim to determine how individuals manage their energy reserves and how the allocation of resources between reproduction and maintenance (decision to breed or to abandon) are affected by changes in the environment.

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Endocrine regulation of body stores varies with reproductive status in female Weddell seals

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Female Weddell seals (*Leptonychotes weddellii*) undergo rapid fluctuations in mass and body condition (% lipid) during the summer in association with reproduction and molt, but the physiological regulation of these changes is poorly understood. Recently, we determined that post-partum females rapidly deposit lean mass across summer after they wean their pups. In contrast, females that did not give birth start the summer larger and in better condition than post-partum seals, but then lose lipid mass across summer while completing the annual molt. We hypothesize that these mass dynamics are regulated by differential activities of hormones involved in metabolism and nutrient allocation. To examine how endocrine profiles varied with mass trajectories, we handled prime-age multiparous Weddell seals in early summer (n=72, Nov/Dec, late lactation) and again in late summer (n=70, Jan/Feb, molt period), and compared study animals that had pupped to those that did not give birth in the study year. We measured mass, condition, and a suite of serum hormone concentrations: cortisol, a marker of stress, thyroid hormones T4 and T3, which regulate metabolic rate, and growth hormone (GH) and insulin-like growth factor (IGF)-1, which modulate protein and lipid stores.

While Weddell seals lose up to 35% of their body mass during lactation, post-partum female cortisol levels were not elevated near weaning in early summer, suggesting weight loss in nursing females does not invoke an adrenal stress response. In contrast, cortisol was higher in smaller females in late summer, as might be expected for animals experiencing continued nutritional stress. Elevated T3 in post-partum females in early summer suggested that T3 plays a role supporting the metabolic demands of milk production; in non-lactating seals, T3 values mirrored those of T4. Relationships between mass and T4, GH, and IGF-1 were consistent between early and late summer. GH was elevated in smaller seals (R^2=0.51, $p<0.0001$), likely to defend lean mass and facilitate protein deposition, while T4 and IGF-1 levels were higher in larger seals (T4: R^2=0.22, $p<0.0001$; IGF-1: R^2=0.17, $p<0.0001$). Both T4 and IGF-1 increased significantly in post-partum females over summer, as expected from their roles supporting elevated metabolism and anabolism during positive energy balance. Our findings demonstrate that endocrine regulation of metabolism and body stores in Weddell seals varies seasonally and with reproductive status. These dynamics must be carefully considered when comparing endocrine profiles between populations or applying hormone levels as markers of nutritional stress.

The diet of leopard seals (Hydrurga leptonyx) at Cape Shirreff, Antarctic Peninsula examined with scat and stable isotope analysis

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Leopard seals are a widespread and important predator in Antarctic coastal ecosystems. Previous studies have identified a wide range of prey items; however, due to anecdotal or otherwise limited information leopard seal diets remain largely unresolved by seal sex, inter-individual variability, age class, region or season. As a result, leopard seals are widely reported as generalist predators. Over two summer field seasons we collected visual, scat and stable isotope tissue (blood and plasma) data from nineteen adult female leopard seals foraging near mesopredator breeding colonies at Cape Shirreff. We summarized a priori diet information and applied a two isotope ($\delta^{13}C$ and $\delta^{15}N$), four source (fish, fur seal, krill, penguin) Bayesian mixing model to examine temporal variability in both prey sources and leopard seal tissues, and define their trophic position within the local food web. Leopard seals known to be foraging on Antarctic fur seal pups, showed a trophic signature co-incident rather than above their prey suggesting that krill are a major prey source despite a priori evidence to the contrary. Although variability in leopard seal isospace values was low, 3 of 9 seals from 2014 showed a significant $\delta^{15}N$ shift indicating the possibility of individual-based foraging specialization. Additionally, $\delta^{15}N$ values were consistently enriched for plasma versus red blood cells implying a seasonal diet change. While the four prey groups appear to explain the entire leopard seal diet, their linear distribution in isospace prevented informative posterior probabilities of prey proportions.

An Accurate and Adaptable Photogrammetric Approach for Estimating the Mass and Body Condition of Pinnipeds Using an Unmanned Aerial System

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Measurements of body size and mass are fundamental to pinniped population management and research. Manual measurements tend to be accurate but are invasive and logistically challenging to obtain. Ground-based photogrammetric techniques are less invasive, but inherent limitations make them impractical for many field applications. The recent proliferation of unmanned aerial systems (UAS) in wildlife monitoring has provided a promising new platform for the photogrammetry of free-ranging pinnipeds. Leopard seals (*Hydrurga leptonyx*) are an apex predator in coastal Antarctica whose body condition could be a valuable indicator of ecosystem health. We aerially surveyed leopard seals of known body size and mass to test the precision and accuracy of photogrammetry from a small UAS. Flights were conducted in January and February of 2013 and 2014 and 50 photogrammetric samples were obtained from 15 unrestrained seals. UAS-derived measurements of standard length were accurate to within 2.01 ± 1.06 %, and paired comparisons with ground measurements were statistically indistinguishable. An allometric linear mixed effects model predicted leopard seal mass within 19.40 kg (4.4% error for a 440 kg seal). Photogrammetric measurements from a single, vertical image obtained using UAS provide a noninvasive approach for estimating the mass and body condition of pinnipeds that may be widely applicable.

From genes to ecosystems, adaptation of introduced salmonids to a changing sub-Antarctic environment.

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Polar regions undergo rapid changes to which both native and non-native species must adapt. Long term and well documented monitorings are paramount to understand the various processes and scales that participates to adaptation. The case of introduced salmonids to sub-Antarctic Kerguelen islands offers a rare opportunity to envision adaptation at these various scales. Our monitoring encompasses 8 introduced salmonid species over five decades and tenths of hydrosystems. Some of these species did not adapt, some managed to persist, and some thrived. We here give a report of these different outcomes in relationship with their introduction conditions (numbers, stages, origins, genetic diversity). We then browse a panel of recent or ongoing research, picturing how adaptation processes may be investigated through different scales, taking the brown trout as the model species. At the genes level, we seek footprints of selection on the colonization front by monitoring heterozygosity fitness relationships generation after generation, in populations where genetic variation is minimal. At the organism level, we show plastic behavioural adaptation in terms of feeding to these trophically limiting environments. At the population level, we investigate the temporal and spatial environmental aspects that trigger and facilitate colonization of virgin habitats throughout the archipelago. And at the ecosystem level, we investigate how fish may impact their new environment, and how in turn they may be used as markers of environmental change driven by other species, and how strong is this current change. We finish by underlining connexions between these processes and scales, their role in the dynamics of diversity, and by identifying the potential of our findings for other rapidly changing polar regions.

Elephant seal mothers expend more on their offspring when conditions are favourable and less when they are poor

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In mammals, maternal expenditure on offspring is a mix of several factors including the species' mating system, offspring sex and the condition and age of the mother. While theory suggests that in polygynous species mothers should wean larger male offspring than females when resources and maternal conditions allow, the evidence for this remains equivocal. Southern elephant seals are highly dimorphic, polygynous capital breeders that live in an environment with highly variable resources and should therefore provide clear evidence to support the theoretical expectations of differential maternal expenditure in male and female pups. We quantified maternal size (mass and length) and pup size at birth and weaning for 342 elephant seal mothers at Macquarie Island. The study was conducted over 11 years of contrasting sea-ice and Southern Annular Mode values, both indices of maternal prey resources. Overall, large females weaned male pups that weighed 17 kg (15.5%) more than female pups. Maternal condition varied by as much as 59 kg among years, and was positively related to SAM, and negatively to maximum sea-ice extent. Smaller mothers weaned relatively larger male pups under favourable conditions, this effect was less apparent for larger mothers. We developed a simple model linking environmental variation to maternal masses post-partum, followed by maternal masses post-partum to weaning masses and then weaning masses to pup survival and demonstrated that environmental conditions affected predicted survival so that the pups of small mothers had an estimated 7% increase in first year survival in "good" vs "bad" years compared to 1% for female pups of large mothers. The co-occurrence of environmental quality and conservative reproductive tactics suggests that mothers retain substantial plasticity in maternal care, enhancing their lifetime reproductive success by adjusting reproductive expenditure relative to both prevailing environmental conditions and their own capabilities.

Under-shelf ice foraging of Weddell seals

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The Drescher Inlet is a 25km long crack in the Riiser-Larsen Ice Shelf, eastern Weddell Sea, and is characterized by a stable fast ice layer. The fast ice represents an attractive habitat for Weddell seals, aggregating along the tidal cracks of the inlet in numbers of ca. 200 – 300 individuals. Multiple field campaigns aimed to investigate the seals' diving behaviour and foraging ecology in relation to their environment. A recent joint seal and ROV project was focussed on the investigation of the cryo-benthic community underneath the floating ice shelf of the Drescher Inlet, which were previously detected by seal-borne cameras, and 3D-multi-channel dive loggers (Watanabe et al. 2006; Liebsch et al. 2007). Images show dense aggregations of isopods that likely represent an attractive food horizon, where seals could benefit from a local hotspot of high biological productivity. This context triggered a retrospective analysis of available high-resolution dive profile data to identify within-dive hunting phases and correlate those to the local physical environment.

A total of 34 adult Weddell seals were instrumented with different types of dive loggers (time-depth recorders, digital still image loggers) in the course of six summer field campaigns between 1990 and 2016. Dive profiles were zero-offset corrected to reduce noise in the dataset and subsequently only dives deeper than 20m were regarded as 'true' dives, accounting for the thickness of the local fast ice and platelet ice layer. An automated broken stick algorithm (Heerah et al. 2014) was used to separate the dive into different segments. Segments with a high sinuosity were considered to indicate hunting. Segments characterized by a straight dive trajectories (low sinuosity), were assumed to be transit phases with no hunting behaviour.

A tri-modal distribution of mean hunting depths suggests that Weddell seals concentrated their foraging activities in three depth strata. A peak in hunting depths below 370m corresponds to the sea floor of the Drescher Inlet, indicating demersal foraging. A second peak between 110 and 160m matches with the depth of the underside of the floating ice shelf, which suggests shelf ice associated foraging. The third peak probably represents hunting in the pelagic realm.

Our investigation highlights the importance of the shelf ice underside as an attractive food horizon for Weddell seals suggesting a re-evaluation of trophic interactions and bentho-pelagic processes in the coastal Antarctic ecosystem.

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Postweaning behaviour of southern elephant seal´s pups at Isla 25 de Mayo, King George Island: wean mass and activity patterns.

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After a suckling period of 23 days southern elephant seals weanlings usually stay on beaches fasting for a variable time of 5 to 8 weeks (Ling & Bryden 1981). This period may be crucial for a successful first foraging trip since pups gradually enter the sea in order to perfect their swimming and diving abilities (Arnbom et al 1993). Not all pups are weaned with same amount of fat reserves, thus in theory the animals should optimize the energy expenditure. The aim of this work was to determine if there are differences in weanling's activities and/or ambient frequented in relation to their weight at wean. During 2003 breeding season at the Antarctic Specially Protected Area (ASPA) N132 "Peninsula Potter" we weight 200 weaned pups. From those, we randomly select 15 pups weighting less and 15 weighting more than the average weight (154.5 kg) and we mark them. From December 10 to 27 we carried out daily census of the beach registering in which ambient there were the marked pups (sea vs. land) and the temperature of those places was measure in each period with a mercury thermometer (0.1°C precision). The censuses were carried out from 7 am, every three hours, until 10 pm. We used Spearman Rank Order Correlations to test for association between the number of animals of each group (heavier vs. lighters than the average) in each ambient and the temperature of that ambient. A positive correlation (Spearman's rho = 0.58, $P < 0.05$) between both groups of pups and the ground temperature was observed, corresponding to day times when the temperature on the ground is higher (although always below the one in the sea). In contrast, a significant and negative correlation (Spearman's rho =-0.36 $P < 0.05$) was registered between sea temperature and weight only for the group of the animals weighting more than the average. From our results it seems that the all weaned pups tend to remain resting on land during daylight hours even when ground temperatures are lower than those of sea. On the other hand, when sea temperature was lower than ground temperature, mostly heavier weanlings were swimming at sea. Thus, at "Peninsula Potter" been heavier could improve diving capabilities during the post lactation fasting period since allows to spend more time practicing swim and dive capabilities even during periods of low se water temperatures.

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Setting a baseline for monitoring studies: leukocyte levels in pack-ice seals from western Antarctic Peninsula

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Global warming and its consequences constitute one of the main stressors for organisms worldwide affecting different factors such as the distribution, and abundance of parasites, which in turn can affect the immune system of organisms. Therefore, it is important to have baseline information on immune parameters of organisms in order to make future comparisons in this changing ecological context. The use of haematological parameters such as leukocyte counts is becoming popular in the analysis of health status. Leukocytes are one of the key components of an animal's immune system, with different leukocyte types offering protection against a variety of parasites and pathogens. In the present study, we report for the first time the leukocyte numbers of three species of Antarctic seals: the Weddell (Leptonychotes weddellii), the leopard (Hydrurga leptonyx) and the crabeater (Lobodon carcinophagus). During the summer 2014/15 and 2015/2016 we sampled 65 seals at Punta Cierva, Danco Coast, Antarctica. We evaluate if exist differences on leukocyte counts among species and presence/absence of ectoparasites. Smears were prepared with a drop of fresh blood and placed on slides, fixed with ethanol and stained. They were examined under a light microscope to obtain total leukocyte counts, proportion of each leukocyte type classified into basophils, neutrophils, eosinophils, lymphocytes, and monocytes, and neutrophil/lymphocyte ratio (N/L) as a physiological stress index. Neutrophils were the most abundant leukocyte type for crabeater and Weddell seals, followed by lymphocytes whereas, leopard seals showed the inverse pattern. Leukocyte numbers showed differences among species. Basophils ($H(2,65)= 9.8$, $p<0.05$), eosinophils ($H(2,65)= 8.3$, $p<0.05$) and lymphocytes ($H(2,65)= 6.1$, $p<0.05$) were higher in leopard seals; while the relation N/L ($H(2,65)= 7.6$, $p<0.05$) and the total amount of neutrophils ($H(2,65)= 9.7$, $p<0.05$) were higher for crabeater seals. The Weddell seal was the only species that showed a positive relationship between neutrophil counts and consequently N/L and presence of lice ($R= 0.42$ and $R=0.4$, $p<0.05$, respectively). There was no relationship between leukocyte counts and the presence of lice for the crabeater and leopard seals. The immune cells measured here serve as baseline for a sustained monitoring of changing populations of Antarctic pack ice seals. Future research will incorporate additional comparative indices of conditions and stress, such as levels of cortisol and oxidative damage, as well as other measures of immune function.

Keywords: Leukocyte counts, pack-ice seals, Antarctic peninsula, health status

Physical features of multi-species habitat in the face of climate change

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Compared to the terrestrial environment the open ocean is seemingly homogeneous, but in reality it is dynamic on both spatial and temporal scales. Remote sensing promotes a better understanding of the physical mechanisms shaping the marine environment, and addresses major challenges monitoring these inaccessible regions. From an ecological perspective, marine physics is important because lower-trophic-level resources (i.e. plankton) are strongly structured by nurtient-rich oceanographic features such as fronts, eddies and filaments. These features are also likely to be ideal foraging habitat for higher trophic-level groups, such as top marine predators. However, we cannot interpret satellite-derived maps in terms of resources, habitat vulnerability, and climate change if we do not incorporate biological data.

Marine predators are sensitive to environmental change, making them useful sentinel species of the ecosystem. Consequently, the resilience and response of top predator populations to resource variability is an ongoing question in marine ecology. Our team has collated telemetry tracks of Antarctic predators - collected by French and Australian researchers – including over 2000 individuals from 12 species (including seals, penguins and flying seabirds). These species are particularly useful because they interact with important frontal features of the open ocean while carrying multiple sensors that record an individual's location, behaviour and surrounding environment (e.g. temperature and salinity). Our first goal is to use these data to identify areas of ecological significance (AES) in the Southern Ocean. Our second goal is to apply new analytical methods, developed at Laboratoire d'Océanographie et du Climat: Expérimentation et Approches Numériques (LOCEAN), to these data to understand the impacts of complex fine-scale physical ocean dynamics on these AES. This comes at a time when signs of change are being observed in the Southern Ocean, and when concerns about conservation in the region are increasing (e.g. managing future fisheries).

We are using contemporary diagnostic tools for altimetry satellite data to identify key fine-scale oceanographic features encountered by our tracked individuals. This information will be used to validate and extrapolate multi-species habitat models to understand underlying physical mechanisms and predict future ecological trends in the context of climate change. Here, we present key marine habitat for multiple species in the Indian sector of the Southern Ocean. We also discuss the diagnostic tools developed at LOCEAN that will be used to examine important physical mechanisms driving ecology in the region.

Weddell seal reproductive phenology challenges the notion that all pinnipeds have embryonic diapause

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In polar environments, animals experience temporal constraints on reproductive events (birthing, lactation, breeding) imposed by dramatically-changing ambient conditions. The Erebus Bay population of Weddell seals (Leptonychotes weddellii) provides a unique opportunity to elucidate how high latitude pinnipeds have balanced the energetic costs of reproduction to maximize fitness, due to a long-term demographic study and high site fidelity of individuals. Female Weddell seals give birth in October/November each year, nurse their pups for the next 5-7 weeks, and then are bred (mid-December). To align energetically-costly reproductive events with the narrow window when environmental conditions are most benign, pinnipeds include a period of embryonic diapause within their annual cycle. In January/February 2014-2017, we used transrectal ultrasonography to determine the length of embryonic diapause and detect early pregnancy in Weddell seals. We handled mature females that did not give birth during the study year (no birth; n=25), and females that gave birth early (October; n=27) and late (November; n=25) in the pupping season. Nineteen seals were captured for a second examination for longitudinal measures of embryonic growth.

Using ultrasonography in combination with re-sight efforts shows that reproductive history strongly influences future pregnancy at multiple levels. Overall, late birthing females were slightly less likely to become pregnant (72%) as compared with no birth and early birth seals (84% and 85%). Of late birthing females that had started a new pregnancy, embryos were significantly smaller (4.5±1.7cm²; $P<0.001$) than the other study groups (no birth: 13.5±4.5cm²; early birth: 7.2±1.1cm²) showing that implantation occurred later. Embryo measurements were incorporated into growth curves and showed that the Weddell seal's implantation period could be delayed by a maximum of 2-3 weeks, making the adaptive advantage of employing embryonic diapause in this species unclear. That embryonic diapause does not synchronize gestation in Weddell seals was further supported by late birthing females having later parturition dates the next year (no birth: Oct.27±1.6d, early birth: Oct.24±1.6d, late birth: Nov.4±1.6d; $P<0.001$). Late birth females were also most likely to experience pregnancy loss (no birth: 13%, early birth: 16%, late birth: 27% loss rates), keeping the birthing window short. Earlier research indicates that Antarctic phocids have a relatively short diapause, and our work suggests that it may be absent from the Weddell seal's reproductive cycle altogether. Instead, a longer gestation would reduce daily costs of pregnancy in Weddell seals, but would extend the time that the developing fetus would be vulnerable to environmental perturbations.

Regulating heat loss while molting in the cold: skin temperature and heat flux patterns in Weddell seals

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Thermoregulatory challenges of pinnipeds in the Antarctic environment are multifaceted. As semi-aquatic mammals in a polar climate, they must conserve heat in both air and water. Primary adaptations to reduce heat loss to the environment include a thick subcutaneous blubber layer of low conductivity (K), and the ability to limit blood flow to the peripheries via vasoconstriction. These adaptations decrease the temperature gradient between the animal and the environment (ΔT, T_{skin}-$T_{environment}$), and so reduce heat flux ($Q = -K\Delta T$). However, during the annual molting period, epithelial cells may need more constant perfusion in order to support hair development, resulting in higher rates of heat loss to the ambient environment and higher metabolic costs. Furthermore, cooling environmental conditions may lead to increased thermoregulatory costs for animals molting later in summer.

Across a four year study, skin temperature (ST) and heat flux (HF) was directly measured at multiple sites on the body of 65 individual female adult Weddell seals (Leptonychotes weddellii) both before the molt (Nov/Dec), and again during the molting period (Jan/Feb). Infrared thermography (IRT) was additionally used to assess regions of high heat across the surface of each seal. As predicted, environmental conditions played the largest role in HF/ST observed; animals subjected to high winds, low solar radiation and colder ambient temperatures experienced lower ST measurements, and few, if any, thermal windows were evident in IRT images. However, ΔT was similar in animals handled prior to, and late (stages 3-4) in the molt, but animals earlier (stages 0-2) in the molting process maintained higher ΔT. Additionally, IRT images revealed regions of increased heat along the dorsum during early molting stages. This “dorsal stripe” was less evident once the new pelage grew in, suggesting increased perfusion to the dorsum as the visible molt was initiated. These changing patterns of HF/ST during the molt suggest that seals limit the surface area which is actively perfused at one time in order to reduce overall thermoregulatory costs associated with molting in a polar climate.

Patterns in microbial gene expression during the transition from winter to spring along the western Antarctic Peninsula

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During the transition from winter to spring the Antarctic marine microbial community shifts from a regime defined by chemoautotrophy and mixotrophy to one defined by phototrophy and heterotrophy. Because sea ice imposes a strong control on the flux of sunlight to the water column during the polar spring, we hypothesize that sea ice influences the mechanism and degree of microbial carbon acquisition and exchange. Future changes to sea ice extant and duration will thus impact primary production at this base of the foodweb. To test the influence of sea ice on water column microbial processes we took advantage of unique sea ice conditions in Arthur Harbor on Anvers Island off the western Antarctic Peninsula during the 2015 spring-summer seasonal transition. Over a five week period we sampled water from below land fast sea ice, in the marginal ice zone at nearby Palmer Station B, and conducted an ice-out experiment with incubations of water collected below the land fast ice. Analysis of bacterial production, primary production, chlorophyll a concentration, and fluorescence induction and relaxation (FIRe), show strong differences in community physiology and ecophysiology between treatments. To develop a mechanistic understanding of these responses we sequenced whole community metatranscriptomes for each time series. Here we will present preliminary results of our metatranscriptome analysis, as abundances of transcripts binned by enzyme commission number and genome. This approach will allow us to identify microbe-specific responses to increased light during the critical winter-spring seasonal transition.

The effect of climate change on the carbon balance between photosynthesis and respiration in planktonic and benthic microalgae

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The Southern Ocean is an important sink for the atmospheric CO_2 due to the physical and the biological photosynthetic activity of phytoplankton. The anthropogenically increased emissions of CO_2 (IPCC Fifth Assessment Report) and variations in the climate are also believed to strongly influence the ecological status of the marine ecosystem. Some studies have investigated the photosynthetic activity of the benthic and pelagic producers (Petrou and Ralph 2011, Palmisano et al. 1987), but there is only very scarce knowledge about the carbon losses due to respiration. The reason for this lack of information is principally methodological limitations. It has been reported (Vona et al. 2004) that the ratio photosynthesis/respiration (rP/R) is species-specific. Additionally, other factors such as temperature, nutrient availability (e.g. iron) and light are expected to influence the rP/R and by consequence, the primary productivity. The aim of the project is to investigate the range of variability of rP/R in response to different growth conditions. In this respect, two key species of the Southern ocean are investigated: the diatom *Fragilariopsis cylindrus* and the prymnesiophyte *Phaeocystis antarctica*. Both are ubiquitous in the Southern Ocean, often forming large blooms around much of the Antarctic continent (Kropuenske et al. 2009). The former is a typical psychrophilic species, predominantly found in the sea ice with cold and high saline water but also in the meltwater (Ugalde et al., 2013). The latter has been observed in both deep and shallow mixed layers in the Southern Ocean (Arrigo et al. 2010).

F. cylindrus and different isolates of *P. antarctica*, obtained from Dr. Gäbler-Schwarz (AWI, Bremerhaven) are grown at three different temperatures (i.e. -2 °C, 1°C and 4°C). The cultivation is performed under light-limited conditions (≤ 10 µmol photons.m^{-2}.s^{-1}), with a 16:8 hour light-dark cycle. The photosynthesis and respiration rates are determined by oxygen evolution and consumption rates (Clark electrode), respectively. In addition, PAM-fluorescence analysis will allow an estimation of the relative electron transport rate and the potential of non-photochemical quenching. First results show that the ratio rP/R is generally different for both investigated species. In addition, rP/R is variable in dependence on experimental conditions and work is in progress to assess the impact of these changes for potential biomass production.

In conclusion, the aim of my work is to investigate the changes in the rP/R in relevant Antarctic algal species under global climate change conditions, namely: different temperatures, water salinity and in dependence on iron availability.

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Adaptability to a warmer world – a new view of Antarctic notothenioid heat shock response

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Antarctic notothenioid fishes evolved remarkable cold adaptations that empowered life in the otherwise inhospitable frigid Southern Ocean. Evolution in unvarying cold also inexorably led to cold stenothermality and cold specialized physiologies, which now may become vulnerabilities should sea temperatures rise rapidly under climate change. One key concern arising from Antarctic notothenioid cold specialization is the apparent loss of the classic heat shock response (HSR) that acts to mitigate cellular damages by heat. Earlier studies led to the general notion that HSR loss pervades across Antarctic notothenioids, intimating broad susceptibility of the clade to climate change. Detracting the robustness of this conclusion is the limited species studied, disparate heating regimes between studies, and the lack of appropriate basal comparison to establish the ancestral state of HRS in Notothenioidei. We therefore carried out a large study using standardized Critical Thermal Maximum (CTMax) protocol as acute heat stress to reliably compare thermal tolerance, and to interrogate cellular responses induced by heat using Northern blot analyses and RNA-Seq transcriptomic analyses among three strategically selected lineages: the temperate notothenioid *Eleginops maclovinus*, the basal nearest sister species to the Antarctic clade and the most appropriate ancestral proxy; the highly cold-adapted cryopelagic *Pagothenia borchgrevinki* from McMurdo Sound; and one of the highly derived, hemoglobinless icefish *Chionodraco rastrospinosus* from West Antarctic Peninsula waters. Mean CTMax temperature was 30.5±0.5°C for *E. maclovinus*, and nearly 3-fold lower for *P. borchgrevinki* (12.1±0.8°C) and *C. rastrospinosus* (10.3±2.8°C). Northern blots of *E. maclovinus* tissue RNA showed massive heat-induced HSP70 mRNA expression, and RNAseq transcript profiling confirmed a robust cellular wide HSR in action, inclusive of cytosolic and ER molecular chaperones and other families of stress responding genes. A robust HSR is therefore a plesiomorphy in Notothenioidei. In stark contrast, *P. borchgrevinki* response was extraordinarily muted in all analyses, suggesting wholesale HSR loss. HSP70 expression in the icefish was negligible on Northern blot, and corroborated by RNAseq transcript profiling, but surprisingly a robust response was found in other cellular networks of stress responding genes, akin to *E. maclovinus*. The disparate transcriptional responses to heat stress in two key Antarctic lineages counter the common notion of uniform HSR loss. Cold specialization might have in fact evolved to varying extents among Antarctic notothenioid lineages, with varying impact on their capacity to adapt to a warming world. This work was supported by NSF award ANT1142158 to CHCC. LVC was supported by DID UACH, Fondap-Ideal Grant Nº15150003.

Diet, antioxidants and oxidative status in the Gentoo penguin

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Changes in the Antarctic environment due to climate change can lead physiological, behavioural and evolutionary shifts. Diet as well as feeding strategies can affect the physiology of the organisms in several ways. Both can affect either the antioxidant defenses or the production of reactive oxygen species (ROS). Indeed, oxidative stress is defined as the imbalance between pro-oxidants and antioxidants defences. If such imbalance is in favour of the former, leading oxidative damage (i.e.: oxidative destruction of biomolecules such as lipids, proteins, and DNA), oxidative stress would increase. However, the way animals adjust their oxidative balance in relation to their diet, feeding strategies and dietary antioxidants in free-ranging animals remained unstudied as far as we know. Penguins are an interesting biological model to assess such comparison because their diet based on krill and/or fish present marked differences in terms of dietary antioxidant absorption depending on their habitat. Therefore, we investigated diet (δ15N), foraging strategies (δ13C), dietary antioxidants (retinol, α-tocopherol and astaxanthin) and oxidative status (OXY and ROMs) in the Gentoo penguins (Pygoscelis papua) breeding at Hope Bay, Antarctica. Gentoo penguins appear to exploit lesser krill in favour to fish in more coastal and benthic waters. Further, even showing high astaxanthin levels which is known for its antioxidant power, they presented a bad oxidative status. In conclusion, Gentoos foraging plasticity seem to trigger their huge oxidative imbalance. As well, since they present a carotenoid-based trait (i.e. orange beak), their oxidative physiology appears to use more endogenous antioxidants compared to other species because the dietary ones are necessary to maintain astaxanthin unoxidised for their carotenoid-based trait.

Genomic analysis of the psychrophilic alga *Chlamydomonas* sp. UWO241suggests that gene duplication plays an important role in adaptation to life in the cold

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Chlamydomonas sp. UWO241 is a unique, psychrophilic green alga isolated seventeen meters below the ice surface of the Antarctic Lake Bonney. This alga has adapted to cope with a plethora of extreme conditions including relentlessly cold temperatures, high salinity, extreme shading and prolonged darkness during the polar night, which is reflected in its unique cellular and physiological features (1). Despite the importance of eukaryotic algae as the primary source of organic carbon in polar environments, relatively little is known about how these organisms have adapted to such extreme conditions. Here we report the sequencing of the genome of UWO241, the first psychrophilic green alga to be sequenced. This opens the door to comparative evolutionary and functional analyses with important model organisms, such Chlamydomonas reinhardtii — the leading unicellular photosynthetic research system (2). Our data reveal that UWO241 has one of the largest green algal genomes known to date, which can be attributed to the presence of high levels of non-coding intronic DNA. Furthermore, we show that several key genes involved in photosynthesis and protein folding are present in two highly similar copies in the genome of UWO241. This is in contrast with their mesophilic counterparts which are present as single copies in C. reinhardtii and other green algae and plants. We provide detailed analysis of the duplicated gene encoding chloroplastic ferredoxin (Fd), a key enzyme involved in the distribution of photosynthetic reducing power (3). We show that the duplication of this gene leads to the presence of two highly similar Fd proteins and that UWO241 accumulates high levels of these proteins under optimal growth conditions compared to the mesophile C. reinhardtii. We propose that gene duplication leads to increased amounts of important proteins in the psychrophile UWO241, which may be an evolutionary strategy for adaptation to permanently cold environments.

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Antifreeze Activity Associated with Freezing Avoidance in Antarctic Notothenioid Fishes Involves Contributions of Blood Antifreeze Glycoproteins and a Newly Discovered Antifreeze Potentiating Protein.

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Freeze avoidance in most all Antarctic notothenioid fishes is associated with high levels (25 to 40mg/ml) of blood born antifreeze glycoproteins (AFGPs). Species inhabiting the high latitudes have twice the level found in lower latitude (Antarctic Peninsula) species. One low latitude species, Lipidonotothen squamifrones lacks AFGPs but survives by inhabiting the deep waters where the temperatures are above their freezing point, -0.78o C and ice is absent. Quantification of blood AFGPs of high latitude species living at -1.9 o C, in the presence of ice, using HPLC and freezing point/melting point differences (hysteresis) of native and heat treated serum indicate that they account for only half of the freezing point depression of the native serum . A search for the unknown entity responsible for the remainder of the freezing point depression revealed a heat label protein present at concentrations of 2 to 3mg/ml of serum. Isolation by ammonium sulphate precipitation and column chromatography yielded a protein lacking carbohydrate with a molecular weight of 15,000. Using Edman protein sequencing and cDNA sequencing a sequence was obtained and protein data base searches indicated that it is similar to one of the vertebrate complement proteins, C1Q. The antifreeze activity on a weight basis is similar to the high molecular weight AFGPs, but interestingly when combined doubles the antifreeze activity of the AFGPs. Hence this new found AF was named an antifreeze potentiating protein (AFPP). Its potentiation affects only the large AFGPS (1-4) but not the smaller AFGPS. The potentiation of the large AFGPs suggests that it binds to those growth sites on ice crystals that the large AFGPS cannot adequately mask. The AFPP was crystallized and it structure obtained. One of its surface is flat and displays serine and threonine residues that are located on anti-parallel strands on a beta-sheet with a spacing that corresponds to the spacing between ice oxygens suggesting that these residue OH groups can hydrogen bond to the prism planes of hexagonal ice. Further characterization of the interaction of AFPP with ice indicated that ice grown in its presence grows primarily along the a-axes thus indicating that it inhibits growth along the c-axis, in contrast to the AFGPs where growth is primarily along the c-axes and ice binding is on the prism planes. Together the AFGPs and AFPs account for all of the antifreeze activity in the notothenioid fish blood.

Strategies of controlled anabiosis II: Desiccation metabolomes of three Antarctic lichen photobionts

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Lichens dominate the Antarctic flora in terms of species diversity and in terms of total biomass across Antarctica. As symbiotic associations of a photosynthetic partner (photobiont) and a fungus (mycobiont), lichen holobionts represent stable systems with autonomous primary carbon acquisition. Due to their photosynthetic activity and also their poikilohydric lifestyle, lichens strictly depend on the environmental water and light regime for metabolic activity. By photosynthetic activity the photobiont provides nutrition for the mycobiont for processes of e.g. growth, differentiation and formation of secondary metabolites. It can be postulated that the photosynthetic partner of the lichen symbiosis developed particular adaptation mechanisms to be able to successfully colonise terrestrial sites across the Antarctic. The research presented focuses on the characterisation of the metabolome profile of isolated lichen photobionts in correlation with desiccation. To avoid damage of cellular proteins and membrane structures due to desiccation and subsequently, the rehydration process, photobionts possess different mechanisms of desiccation tolerance. The study addresses photobionts of the genus Trebouxia which are dominant in the macro lichen flora across Antarctica. Understanding the mechanisms during desiccation and rehydration, isolated photobionts of different Antarctic lichens (Buellia frigida, Pleiopsidium chlorophanum, Umbilicaria antarctica) were studied and compared with an isolated photobiont of a lichen (Fulgensia bracteata) from a more moderate habitat in southern Sweden. The potential to cope with extreme environmental conditions as desiccation followed by rehydration combined with light-stress has been tested on the level of photosynthetic activity (chlorophyll fluorescence measurements of photosystem II and I) and in correlation with the metabolome profile. The metabolite profile of each isolated photobiont was created during a desiccation process with focus on sugars, polyols and amino acids. The isolated photobionts from Antarctic lichen species differed in reactivation kinetics, differences in concentrations and dynamics of the metabolite profiles and a clear divergence to the photobiont of the Swedish lichen could be recognized. The higher reactivation kinetics and concentrations of specific metabolites of the isolated photobionts from Antarctic lichens indicate a higher tolerance towards abiotic factors of the severe Antarctic terrestrial environments. The results will fundamentally support the knowledge hitherto mainly achieved on the physiological level considering the adaptive potential of the lichen symbiosis. Knowledge on the potential of adaptation on the genetic level of the lichen symbiosis will increase the knowledge on their prerequisites to cope with future climate change.

Chemioreception in the Antarctic toothfish: clues from the morphology and histology of the olfactory organ and bulb

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The Antarctic toothfish Dissostichus mawsoni is the most important piscine top predator in the Southern Ocean, where it is also commercially fished. Fishery is managed by the Commission for the Conservation of Antarctic Marine Living Resources (CCAMLR) through an ecosystem-based approach. Accordingly, scientific data that broaden current knowledge on the biology and ecology of the Antarctic toothfish are awaited to refine sustainable fishery.

In this frame, we undertook the study of the toothfish sensory capability, aiming at contributing to current knowledge on this fish feeding ecology and interactions with other elements of the ecosystem.

Chemical senses (olfaction and taste) are often used in fish to enhance capability to locate preys. In particular, olfaction is a key sensory component, allowing fish to sample chemical stimuli from the environment and influencing their feeding behaviour. To date, poor information is available on the sensory organs of the Antarctic toothfish. A proportionally large olfactory bulb has been described (Eastman and Lannoo 2011), but no data are available on the peripheral olfactory organ of the species.

Here we report on the morphology and histology of the olfactory organ and bulb of the Antarctic toothfish. Olfactory organ and bulb were sampled from adult males and females collected under the sea-ice in McMurdo Sound, and fixed for later histological analyses.

The toothfish olfactory organ consists of a central raphe and several lamellae (varying in shape and size according to the position in the organ) organized in two rows. From the base of the organs, the olfactory nerves run toward the brain, collecting the axons of the olfactory receptor neurons and projecting them to the olfactory bulbs that are large and clearly distinguishable from the telencephalon. In agreement with the relatively large olfactory bulb of this species, the extent of the sensory epithelium is relevant, covering the whole lamellar faces. On a single olfactory organ, the sensory surface area (that is the area covered by the sensory epithelium) was calculated to be about 10 cm2 (female specimen, 129 cm total length). As common in bony fish, ciliated and microvillous sensory receptor neurons have been observed scattered in the olfactory epithelium. A number of rodlet cells, whose role is unclear, are also visible.

On the whole, the gross morphology, and especially the size, of the olfactory organ and bulb of D. mawsoni suggests a key role of olfaction in relevant ecological tasks such as migration and food searching.

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Transcriptomic and Phenotypic Response to Environmental Change in a Developing Antarctic Fish

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The sensitivity of long-lived, slow reproducing Antarctic fishes to near-future environmental change (ocean warming and acidification) depends largely on their plasticity to tolerate novel conditions. Previous transcriptomic analyses in adult Antarctic fishes have provided insight into observed phenotypic responses to warming and acidification, such as time to acclimation, mechanistic stress responses, and altered energy homeostasis. While early life stages show enhanced sensitivity to environmental change during their very different physiological states, the transcriptomic response has yet to be characterized. For this study, using dragonfish Gymnodraco acuticeps collected from McMurdo Sound in the Ross Sea, we used transcriptomics to a) characterize transcript differences between embryos and adults and b) assess transcriptional response to warming and ocean acidification across development time matched with whole organism performance. Using Next-Generation Sequencing (Illumina Hiseq3000 and Miseq), we created a de novo reference transcriptome for Gymnodraco acuticeps (378 M PE150 and PE300 reads) from individually indexed pools of embryo (2) and adult (1) dragonfish tissues. After assessing assembly quality and completeness, we identified genes both unique to and shared across adult and embryonic life stages. Next, we assessed differential gene expression from individual embryos from 2 temperatures (-1 and 2˚C) x 2 pCO2 (440 and 1100 µatm) x 3 time points (n = 6, total =72, average 44 M PE50 reads; Illumina Hiseq 3000) using the de novo transcriptome. Significantly up- and down-regulated genes and pathways were further integrated into phenotypic data measuring metabolic rate, development, and survival to integrate physiological processes across different levels of biological organization. Results from this study provide both provide possible mechanistic responses and biomarkers into the response of Antarctic fish embryos to environmental change, as well as a new genomic resource for comparative study of notothenioid fish physiology and evolution.

Plasticity or Stability? Ocean warming effects on the physiological and transcriptional responses of Antarctic marine invertebrates

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Changes in environmental conditions as a result of the global effects of human activities, are occurring in the Polar Regions at faster rates than elsewhere. The uniquely adapted fauna and flora of these regions are vulnerable to shifts in climate. Due to their slow growth, increased longevity, delayed maturity and little capacity to resist warming, the Antarctic marine fauna has a very poor ability to cope physiologically to climate change. In order to understand the ecological and potential evolutionary responses of Antarctic marine invertebrates to rapid changes in sea surface temperatures, we investigated the physiological and transcriptional responses of natural populations of the limpet Nacella concinna under projected scenarios of climate change. Our results evidence that: i) physiological plasticity is the main response to the stress induced by increased temperatures; ii) the degree of plastic responses differ among populations; iii) ocean warming affect the gene expression profiles of natural populations of Antarctic limpets; however, the transcriptomic profiles differ among populations. Our findings suggest that local adaptation may constraint the degree of plastic responses (physiological and transcriptional) to ocean warming in populations from more stable areas in the south of the Antarctic Peninsula compared to populations in areas with greater environmental variation in the north of the Peninsula. Considering geographical differences in plasticity, tolerances and sensitivities to rising temperatures will provide more accurate predictions for species responses to future ocean warming.

Coping with cold: the physiological role of globins in the Antarctic marine bacterium *Pseudoalteromonas haloplanktis* TAC125

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Evolution allowed Antarctic microorganisms to grow successfully under extreme conditions (low temperature and high O2 content) through a variety of structural and physiological adjustments in their genomes and development of programmed responses to strong oxidative and nitrosative stress. The availability of genomic sequences from an increasing number of cold-adapted species is providing insights to understand the molecular mechanisms underlying crucial physiological processes in polar organisms. The genome of Pseudoalteromonas haloplanktis TAC125 (PhTAC125) contains multiple genes encoding three distinct truncated globins (2/2Hbs) exhibiting the 2/2 □ helical fold, encoded by the PSHAa0458, PSHAa0030 and PSHAa2217 genes and one flavohemoglobin (flavoHb) encoded by PSHAa2880 gene (1). To our knowledge, PhTAC125 is the first example of coexistence of genes encoding a flavoHb and three 2/2Hbs (2). The high number of globins in the PhTAC125 suggests that these proteins fulfil crucial functional roles perhaps related to the peculiar features of an O2-rich and cold habitat as the Antarctic Ocean. One of these globins has been extensively characterised by spectroscopic analysis, kinetic measurements, computer simulation approaches and X-ray diffraction (3-6). The results indicate unique adaptive structural properties that enhance the overall flexibility of the protein related to the O2 concentration and low kinetic energy of molecules, experienced by organisms living in the Antarctic environment (6). Recent results on a genomic mutant strain highlight the involvement of the cold-adapted globins in the protection against the stress induced by high O2 concentration, hydrogen peroxide and nitrosating agents, confirming their potential role in reactive oxygen and nitrogen species scavenging (7-8). All results presented in this study are discussed in the attempt to clarify the hypothetical physiological function of the 2/2Hbs in the Antarctic bacterium since in only few cases a functional role has been demonstrated in vivo for these globins.

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Antioxidants and chaperones gene expression in immune cells of Antarctic sea urchin by stress inductors.

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The Antarctic sea urchin Sterechinus neumayeri has evolved under a cold and thermally stable environment for million years, as most of the Antarctic coastal benthic organisms. Antarctic sea urchins have a low metabolic rate; however the activation of the immune response is possible at low temperatures. Those responsible for initiating the immune response are the coelomocytes. These cells are capable to mediate immune response by mechanism recognition, phagocytosis, encapsulation of foreign particles, in conjunction with the release of antimicrobial molecules. These cells are part of coelomic fluid, which can be considered similar to seawater, for this reason these cells could be considered as sentinels of environmental stress. The transcriptome analysis done by RNA-seq produced a several sequences related to stress response, like heat shock proteins (Hsps) and antioxidant proteins. In previous work we demonstrated that adult sea urchins exposed to elevated temperatures triggers the synthesis of Hsps which help protect cells against high temperatures and a variety of other potentially toxic agents. As an alternative to whole animal tests that require a large number of animals, the in vitro study was conducted to evaluated the gene expression of short-term primary cells culture of coelomocytes exposing to proteasome inhibitor (MG-132) and heat stress (3°C and 6°C). Four chaperones (Hsp70, Hsp90, Grp 78 and Grp120) and three antioxidant enzymes (Superoxide dismutase (SOD), catalase (CAT) and metallothionein (MT)) were chosen for qPCR analysis and their expression levels were measured relative to housekeeping genes (18S and GAPDH). The chemical inducer MG-132 result in a significant decrease expression of Hsps after exposure to 50µM and 100µM, however the expression of MT was the only gene induced. When cells were exposed to heat stress, it caused an increase in the Hsp90, Grp78 and Grp120 levels after 24 h at 6°C, however the expression of Hsp70 it was not changed respect to the control levels. mRNA expression levels of CAT and MT were significantly higher, while expression levels of SOD mRNA were decreased following the acute exposure.

The primary cells culture of S. neumayeri are capable of overexpressing stress proteins as a result of stress inductors, however, this response is delayed and to a lesser degree compared to other Antarctic or temperate species. Antarctic sea urchin coelomocytes could be a sensitive cell culture system for environmental studies and it is possible their use for the analysis on the effects of increased temperature and ocean acidification.

Expression of antioxidant defenses in response to acute temperature

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Extreme cold temperatures present in polar environments allow increased oxygen solubility; this situation could produce a high rate of oxidation by formation of reactive oxygen species (ROS) and also affect the stability of proteins in Antarctic marine invertebrates. In addition, warmer temperatures could potentially result in increased oxidative stress, and it is not known whether stenothermal Antarctic sea urchin (Sterechinus neumayeri) can cope with this on a molecular, cellular and physiological level. We evaluated the effect of warming in the antioxidant response of S. neumayeri exposed to thermal stress. During the acute thermal stress and long term thermal stress (3 weeks) the transcriptional activity of superoxide dismutase (SOD), and catalase (CAT) was measured by real time RT-PCR. The expression of SOD and CAT during the acute thermal stress at 3˚C and 6 ˚C was measured in short- term cultures of coelomocytes, while the expression a long term was measured in coelomocytes obtained from the adult sea urchin stressed during three weeks at 3˚C. During the acute thermal stress the expression of catalase increased significantly at 6˚C, whereas the superoxide dismutase decreased at 3˚C after 1h and 24h. The heat shock at 3˚C during a long period of three weeks did not produce a significant response of superoxide dismutase and catalase in coelomocytes. Sequences obtained by RNA-seq sequencing showed that Cu-Zn SOD and catalase proved highly conservative with respect to amino acid sequence as well as to catalytic sites when compared to others temperate antioxidants enzymes. Using the sequence information we have produced specific antibodies. We determined that CAT and SOD proteins decrease significantly their expression after thermal stress at 3˚C during the week two and three. Following long-term exposition at 3˚C we determined that low transcriptional expression for these genes may be correlated by a lesser protein expression. After three weeks, the expression of antioxidant enzymes was not significantly different at 3˚C. These data show that under long periods of moderate thermal stress the immune cells of adult S. neumayeri seem to maintain their rate expression of antioxidants enzymes, with relatively little measureable effect. These results indicate that this species has the ability to alter levels of endogenous antioxidants during acute thermal stress, but that this response is transient and may be insufficient to protect against oxidative damage.

The endocrine stress axis responses to temperature in Notothenia rossii and Notothenia coriiceps – a fish continuum or a singular flock?

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Antarctic fishes evolved in isolation in stable thermal conditions, ranging from circa -1.9ºC to about 3ºC. Many recent studies have shown that several mechanisms mediating the stress response are sub-responsive or inefficient in these species, such as is the case of the lack of heat shock protein (HSPs) reaction to increased temperature. However, little is known about the sensitivity, velocity and amplitude of the endocrine response and how other pathways and components of the stress axis (HPI) perform in response to different stress factors or in comparison to fish inhabiting different waters. Here we looked at the HPI sensitivity by evaluating plasma cortisol, interrenal secretion and HPI gene expression upon chronic and acute thermal, osmotic and handling challenges.

Notothenia rossii and Notothenia coriiceps, collected around Rothera(UK), Arctowski(PL) and Great Wall(CN) stations in Adelaide and King George Islands were transferred to experimental tanks and acclimated for 10 days (0-2ºC) before the experiments. Time-course of the stress response was evaluated for 48 hours upon a single handling/air exposure event or transfer to increased temperature (8 ºC). The influence of temperature on stress response were evaluated in fish at 2ºC or slowly acclimated to 6ºC and then sampled, or further stressed by a single handling/air exposure event. The different HPI pathways were studied by injecting modulators or blockers of the cortisol secretion and/or glucocorticoid receptors, prior to temperature acclimation. Plasma samples were used for cortisol analysis and tissues collected for gene expression by QPCR and full transcriptomics. Interrenals in culture medium were used in a perifusion system to evaluate the effect of temperature/previous stress on its sensitivity to ACTH spikes.

Increased temperature reduced overall activity and response to stimuli, with no clear effect on most energetic substrates although pharmacological modulation of HPI pathways showed temperature always induced a glucose rise irrespective of cortisol levels. Both cortisol and gene expression of metabolic-related proteins and glucocorticoid-receptors were modified after heat shock, and the cortisol response to handling appeared reduced in fish at elevated temperatures, indicating loss of sensitivity. Genes for heat-shock proteins HSC70, HSP70 and HSP90 showed little change while GRP78 appeared increased by temperature. Over 2000 genes showed at least a two-fold change in warmed fish when compared to control conditions, but their implications are still under evaluation. In conclusion, these fish reactive to environmental change, but their ability to accommodate long-term adaptive responses may be compromised. The involvement of the several HPI axis pathways on temperature-related metabolic response is still under study but overall Antarctic fish responded to HPI manipulation in a way similar to temperate species.

Osmoregulating without filters – Notothenia rossii 's renal and branchial responses to salinity and temperature changes

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The Antarctic Ocean is one of the most extreme marine environments, with temperatures reaching -1.9ºC. Antarctic fishes evolved in stable thermohaline conditions for roughly 30 million years, currently displaying a number of structural and functional features that result from adaptation or inherited from resilient ancestral species. A common feature is the presence of aglomerular kidneys and cold-adapted enzymes. Recent climate changes have contributed to rises in water temperature and forecast models indicate the rate of such changes will increase in coastal regions of maritime Antarctica, leading to ice melting and freshening of shallow waters in enclosed areas. Fish, Notothenia rossii, collected around Arctowski(PL) and Great Wall(CN) stations in King George Islands were transferred to experimental tanks and acclimated from natural temperatures (0-2ºC) to 4-8ºC using thermostat-controlled heaters, and from 32‰ to 20-10‰ by addition of freshwater to recirculating tanks, over a period of up to 10 days. Plasma and urine electrolytes and renal and branchial Na+/K+-ATPase were determined, and tissues were collected for immunohistochemistry and gene expression. Altered conditions had no effect in immediate mortality, but reduced overall activity and startling time. Cortisol and gene expression of osmotic-related proteins such as aquaporins and claudins, were modified after heat and salinity shock. No clear changes were observed in HSPs, but important changes were observed in gluco- and mineralo-corticoid receptors. Temperature induced dependent decreases in plasma osmolality, increasing the osmotic gradient between extracellular fluid and seawater and resulting in increased branchial/renal Na+/K+-ATPase activity, whitout modifying gene expression of either alpha or beta subunits. Low salinity reduced both plasma and urine osmolality, with fish showing a marked increase in urine production, and significant changes in urine ionic composition and urine/plasma ratio. Large amount of magnesium-concentrated, low-sodium urine was found in most urinary bladders. Overall, the data shows that increased temperature increases osmoregulatory challenges but that these marine fish can partially cope with reduced salinities. Results also indicate these fish possess important mechanisms for water elimination despite their aglomerular kidneys. The reasons for such large amounts of urine in marine fish will be discussed.

Factors driving the production of defensive secondary metabolites in the Antarctic red seaweed Plocamium cartilagineum

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Inter- and intraspecific interactions between organisms are often mediated by chemicals such as secondary metabolites. These chemically-mediated interactions can be either a form of communication, environmental sensing, or defence. Sessile marine organisms such as sponges and macroalgae commonly produce chemical defences against grazers, pathogens, as well as biofoulers. The biomass of macroalgal forests around Palmer Station on the Western Antarctic Peninsula is comparable to temperate kelp forests and provide vital functions to the ecosystem. Plocamium cartilagineum is a finely branched red understory alga that is common in these macroalgal forests. It supports a very high abundance of amphipods. However, most of these amphipods are not able to feed on the heavily chemically defended P. cartilagineum. Instead they gain refuge from predation by hiding within the macroalga and in return feed on epiphytes which would otherwise be overgrowing it. This is a community-wide mutualism. As to everything, there is an exception: the amphipod Paradexamine fissicauda is significantly more abundant on P. cartilagineum than any other macroalgal species around Palmer Station. In feeding choice experiments, P. fissicauda readily consumes its preferred host and it is able to sequester the secondary metabolites and therefore gain additional protection against predators. Different P. cartilagineum individuals produce differing mixtures of halogenated secondary metabolites and these unique chemical signatures are referred to as chemogroups. Around Palmer Station a total of 12 different chemogroups have been identified from 105 individuals. Those individuals were collected from two different depth ranges at 19 sites. The 12 chemogroups fit well into two distinct genetic groups (but not different enough to be considered different species) identified by the cox1 and rbcL genes. These data suggest that chemogroups are to some extent site specific and they have some correlation with depth. Clearly there is also an underlying genetic differentiation. These data will be expanded based on experiments and observations during February-May 2017 field season. The effect differing chemogroups have on the ability of P. fissicauda to feed on P. cartilagineum will be examined; along with initial analyses of whether differences in chemogroups are driven by differential expression due to environmental factors, underlying genetic differences with isolated gene flow, or a mixture thereof.

Using fisheries samples to investigate seasonal and regional variation in Antarctic krill lipids

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Antarctic krill lipids (oil) is a large industry and is predicted to grow in the coming decades. Knowing how Antarctic krill lipids change in time and space is therefore of critical importance to managing and maintaining a sustainable krill fishery both now and into the future. Using samples collected by the krill fishery over a 3 year time period, this study examined how the lipid and fatty acid content of Antarctic krill varies seasonally and spatially. Krill were staged, sexed, weighed and measured before undergoing lipid analysis. Our results show a continuous fine-scale seasonal cycle for lipid content and composition in Antarctic krill. Levels of the ecologically and commercially important and health-benefitting omega 3 polyunsaturated fatty acids varied between seasons, giving us an enhanced insight into variations in the krill diet and health throughout the year. Our data can be used as a baseline for future studies assessing lipid levels under stressors such as ocean acidification and warming. These results also serve as a baseline for lipid levels in the energy budget of krill throughout their life history and between the sexes.

Constitutive expression of DREB/CBF-like genes from an Antarctic vascular plant Deschampsia antarctica, resulted in improved cold tolerance in transgenic rice plants

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Deschampsia antarctica is an Antarctic hairgrass that grows on the west coast of the Antarctic peninsula. In this report, we have identified and characterized two transcription factor, D. antarctica C-repeat binding factor 4 and 7 (DaCBF4 and DaCBF7) as transcription factors functioning in process of cold resistance. Both proteins contain a single AP2 domain and were predominantly localized to nuclei showing traditional feature of AP2 transcription factor. The interaction of DaCBF7 with the C-repeat/dehydration responsive element (CRT/DRE) core sequence (ACCGAC) was also confirmed in vitro. DaCBF4 and DaCBF7 were induced by abiotic stresses, including drought and cold, but salinity induced only DaCBF7. To investigate its possible cellular role in cold tolerance, a transgenic rice system was employed. Both transgenic rice plants overexpressing DaCBF4 (Ubi:DaCBF4) and DaCBF7 (Ubi:DaCBF7) exhibited markedly increased tolerance to cold stress. Their survival ratio under cold treatment were higher than wild type rice plants within range of 3.5 and 5 fold without growth defects; however, overexpression of these genes exerted little effect on tolerance to drought or salt stress. Transcriptome analysis of a Ubi:DaCBF7 transgenic line revealed 13 genes that were up-regulated in DaCBF7-overexpressing plants compared to wild-type plants in the absence of cold stress and in short- or long-term cold stress. Five of these genes, dehydrin, remorin, Os03g63870, Os11g34790, and Os10g22630, contained putative CRT/DRE or low-temperature responsive elements in their promoter regions. Transcriptome analysis of a Ubi:DaCBF4 transgenic line revealed 22 genes that were up-regulated in DaCBF4-overexpressing plants compared to wild-type plants with or without cold stress. Among them, 9 genes were induced significantly in both transgenic lines in common, which encoding PR protein, protease inhibitor, glutathione peroxidase, malate dehydrogenase, ribonuclease family protein, and several unknown proteins. These results suggest that overexpression of CBF transcription factor genes of D. antarctica directly and indirectly induces diverse genes in transgenic rice plants and confers enhanced tolerance to cold stress across different taxa.

Transcriptomic analysis of physiological effects for acute salinity change on Antarctic fish

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In the Antarctica peninsula region, the melting glaciers and sea ice contributes freshwater to the surface waters seasonally, and it could affect the physical and biological environment. The rate of melting glaciers and sea ice in the Antarctica is speeding up dramatically caused by global warming and climate change. However, the potential impacts of the environmental changes on marine organisms are not well characterized. Along the significant increase of air temperature, decreased salinity cause the discharging freshwater can influence the marine ecosystem including phytoplankton, diatom, and fish. In teleost, Notothenioids have evolved successfully to adapt to specific Antarctic marine ecosystems, and Antarctic bullhead notothen, Notothenia corriceps, a typical Antarctic notothenioid teleost, is one of the main Antarctic fish in the Southern Ocean having higher abundant in the Antarctica peninsula. In order to improve our understanding on direct biological effects of Antarctic marine organism on the acute salinity change, transcriptomic analysis performed by RNA-Seq analysis after exposing N. coriiceps, to diluted salinity series (25 and 15‰) comparing control (35‰) respectively for 6 and 24 hours. Four tissues (gill, head kidney, intestine, and skin) were dissected from the fish in each group of treatment. The next-generation sequencing transcriptome library was constructed using RNA extracted the tissues. A differential expression analysis and a quantitative real-time RT-PCR was performed. The results could help to grasp biological strategies of polar marine teleost to the extreme environment.

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Alpha amylase from Geomyces spp. fungi isolated from the Antarctic and Arctic

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Microfungi are vital in carbon and nutrient cycles in soil ecosystems worldwide. In polar ecosystems, Geomyces spp. soil fungi play a key role. They are common and often dominant species in soils in various parts of the Antarctic and Arctic. They are known to produce various hydrolase enzymes, such as endoglucanase, keratinase, glucose oxidases, esterase, protease, phosphatase and lipase. This ability and the production of various secondary metabolites make them successful decomposers in the polar regions. We conducted this study in order to assess any differences in characteristics of the same enzymes obtained from members of the same genus isolated from the two physically remote polar regions. Soil samples were collected from King George Island, maritime Antarctic, during the 2007/8 austral summer, and from Svalbard, High Arctic, during the boreal summer in 2006 and 2010. Soil microfungi were isolated from the samples and screened for amylase activity. One strain with highest relative enzyme activity from each region was chosen for more detailed enzyme activity analysis. Alpha amylases were purified using a forced affinity chromatography column with the help of Fast Protein Liquid Chromatography (FPLC). The purified enzymes were run on SDS PAGE to confirm the quality of the separation. Thirty-three Antarctic and four Arctic Geomyces spp. were screened for amylase activity. Of these, 25 Antarctic and all four Arctic strains showed significant relative amylase activity in the preliminary screening. The best amylase producers from each region were chosen for further analysis. Enzyme activity of crude amylase from the Antarctic isolate was higher than that of the Arctic strain. Purified alpha amylase of both isolates had an optimum temperature for enzyme activity of 10°C, and an optimum pH of 6.6. SDS PAGE showed both alpha amylases had molecular weights around 70kDa. The differences in enzyme activity between the two strains, even though they are from the same genus, indicates different levels of adaptation to their physically extreme natural habitats.

Physiology of uncultivated atmospheric CH_4 oxidizing bacteria informed by genome from metagenome

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Atmospheric CH_4-oxidizing bacteria is responsible for CH_4 uptake observed in aerated soils including the active layers in High Arctic (79°C). However, because of the absence of isolates and genomes, phylogenetic identity and physiology of atmospheric methane-oxidizing bacteria have remained a mystery. Recently, a draft genome of Upland Soil Cluster gammaproteobacteria (USCγ) has been obtained from incubated pavement soil samples collected from the Taylor Dry Valley, Antarctica (S 77°39', E 163°05'). This first genome of its kind possesses a high-affinity form of particulate methane monooxygenase (encoded by pmoBAC), suggesting its high affinity methanotrophic activity. Subsequent methanol oxidation to CO_2 is also proven. As with the genomes of other gammaproteobacterial methanotrophs, the USCγ draft genome encodes all essential genes for a complete serine biosynthesis pathway for formaldehyde assimilation (glycerate-3P → serine). All genes necessary for a complete tricarboxylic acid (TCA) cycle and a complete Embden-Meyerhof-Parnas pathway, with the exception of 6-phosphofructokinas, were identified. Genes for the Calvin-Benson-Bassham cycle, the pentose phosphate pathway, glycogen biosynthesis were also identified. The diversity of genes for central carbon metabolism indicated that in addition to CH_4, USCγ could potentially gain cellular carbon through multiple pathways. The 16S rRNA gene fragment (488 nt) shared 99% identity to uncultured bacteria occurring in terrestrial ecosystems such as Antarctic, Arctic and Tibetan permafrost and caves. It was 94% similar to *Thioalkalivibrio* and *Ectothiorhodospira* of the gammaproteobacterial order Chromatiales, which is phylogenetically closely related to Methyloccoccales but includes no methanotrophs. Ongoing analysis aims to depict the metabolic potential and physiological requirements of atmospheric methane-oxidizing bacteria.

Evolutionary adaptation in two bivalve sibling species (Yoldia) from Subantarctic and Antarctic environments

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Understanding the adaptive capacity of species to survive environmental change is a fundamental requirement to make predictions about the Antarctic community response to climatic change. This project aims at establishing the Antarctic protobranch bivalve *Yoldia eigthsi* and its congener the Magellanic *Yoldia woodwardi* as a "species models" to understand the phenotypic and genomic traits that support adaptation in both climatic zones (Polar vs. Subpolar). We want to put our concept and approach up for discussion at the beginning of a PhD project. The approach is to generate a comprehensive dataset of genomic, transcriptomic and morphometric information for both species in combination with the evaluation of metabolic performances under in situ and stress conditions. Fieldwork will be carried out in two summer expeditions in the Magellanic region (Punta Arenas, October 2017) and in Western Antarctic (Potter Cove, King George Island, January 2018) in which *Y. woodwardi* and *Y. eigthsi* will be collected respectively. Stress experiments will be performed in both sites to test for the separate and combined effects of temperature and hypoxia in both species. Our working hypothesis is that a combination of genetic drift and differential adaptation following the interruption of gene flow between both species have caused inter-specific differences in gene expression profiles and shell morphometry. Specifically, temperature and oxygen availability are two key factors that individually and synergistically modulate physiological responses of *Y. eightsi* and *Y. woodwardi*. The estimated divergence time between both sibling species is relatively short (3.9 Ma) so that we expect to find many similarities, but also important differences in metabolic functioning and in the patterns of gene expression in situ as well as in response to mild stress exposure.

Photo-physiology of Adenocystis utricularis and Desmarestia species along latitudinal gradients on the Antarctic Peninsula´s west coast

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Macroalgae are exceptionally important primary producers and contributors to the global aquatic primary production. Especially in coastal, polar regions, macroalgae are key indicators of environmental changes due to their susceptibility to stressors such as marked spatio-temporal oscillation in photoperiod, ice-abrasion and temperature. Such stressors may exacerbate along the Antarctic Peninsula´s north–south gradient. Macroalgal rapid, physiological (photosynthetic) response may determine the fate of the community and of the ecosystem entirely.

Using pulse-amplitude modulated (PAM) fluorometry, we determined photosynthetic parameters of four macroalgae species (three endemic to Antarctica) from eight sites between the South Shetland Islands (62ºS) and Marguerite Bay (~68ºS) along the western Antarctic Peninsula (WAP). We applied increasing irradiances (1 to 750µmol photons $m^{-2}s^{-1}$) to determine the electron transport efficiencies (α_{ETR}), maxima (ETR_{max}) and irradiance saturation points (E_k) of *Desmarestia menziesii*, *D. Antarctica*, *D. anceps* and *Adenocystis utricularis* in 2013 and 2017. ETR–light curves were fitted with Platt et al.´s (1980) equation. Pigment content was quantified for Desmarestia species (2013) and is currently being quantified for samples of *A. utricularis* and *Desmarestia* (2017).

Results thus far, show that α_{ETR} remains largely constant between study sites, but ETR_{max} and E_k decrease towards higher latitudes in all species. Spatial and interspecific differences in light harvesting pigment composition was observed among *Desmarestiales*, with increasing chlorophyll *a*, *c* and fucoxanthin concentrations with increasing site latitude. Pigment analyses in *A. utricularis* are underway, but similar patterns are expected (Zacher et al. 2007, Mansilla et al. 2016) because its photosynthetic performance reveals higher E_k and ETR_{max} at sites near South Shetlands (62°S) than in Marguerite Bay (~68°S).

This suggests physiological acclimation to low light conditions, i.e., to irradiance regimes of high latitudes or those under extended ice-cover (68ºS) rather than acclimation to other variables measured (water temperature, salinity). Photoacclimation is achieved through changes in ETR_{max} capacity. The different photosynthetic responses we see in *A. utricularis* and endemic *Desmarestia* species may relate to their life cycle and habitat occupied along WAP (e.g., low intertidal *A.utricularis* versus the subtidal, perennial *D. menziesii*), underlying their biogeographical and evolutionary components.

Understanding the process by which macroalgal populations form, acclimate, adapt and diverge is key to understand how biodiversity is generated and maintained over time. Our results may be central to predict responses of vital macroalgal populations to on-going climate changes, emerging environmental conditions and habitats in polar regions.

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Effects on physiology (PSI and PSII) depending on water content and light intensity of three Antarctic Umbilicaria species from southern maritime Antarctic

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Lichens form together with bryophytes the dominant vegetation across Antarctica. Lichens are symbiotic organisms consisting of a fungus (mycobiont) and a green alga or cyanobacterium (photobiont) essential for carbon nutrition of the symbiosis. They are characterised by a poikilohydric life style that means, for metabolic activity the symbiotic organism is depending on water availability. At terrestrial Antarctic sites water availability is restricted to minor times during a year and poikilohydric organisms must be well adapted to desiccation. Much research has been done on the effect of long term desiccation on metabolic processes of lichens during the summer season. It could be proofed that the lichen symbiosis at terrestrial sites is well adapted to desiccation. But during snow melt the water availability may be quite high leading to a high water content in the lichen even for a shorter time only. The question arises, how do the lichens cope with times of high water content during daylight? The study focuses on the reaction of Photosystem I and II by high water content and different light intensities in the lichens *Umbilicaria antarctica, U. decussata* and *U. umbilicarioides* under laboratory conditions. The lichen species have been collected in the southern maritime Antarctic (67˚35'S, 68˚16'W) on Lagoon Island, Ryder Bay. The three lichen species differed conspicuously due to differences in morphology/anatomy, photobiont species of the genus *Trebouxia* and the topography of the respective colonised microniches. Based on the results it can be assumed that the lichen symbiosis may be characterised by a high plasticity considering environmental parameters.The results clearly show, to understand how these symbioses function and survive under extreme environmental conditions it is of high importance to recognise the high complexity of lichens. The study presented will give fundamental additional information on the physiology of lichens by high water content and provides a baseline for the recognition of the consequences of environmental change in future decades.

Spatial sorting and phenotypic differentiation of the populations of the invasive carabid beetle Merizodus soledadinus at the Kerguelen Islands

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The fast growing populations of aliens, their ecological niche shifts during biological invasions, and their accelerating expanding range in the introduced areas remain under deep investigation. It has been assumed that traits enhancing dispersal may be favoured in alien individuals at their expanding range edges, and the assortative mating among the dispersers could further enhance this phenomenon. Meanwhile, our current understanding of the evolutionary processes generating such phenotypic variation in dispersal ability remains incomplete. Here, we aimed at decrypting the fingerprint of dispersal evolution, and more generally phenotypic differentiation of the populations long the invasion gradient, using the well-known invasion chronosequence of a carabid insect at the French Kerguelen subantarctic islands. The flightless predatory carabid *Merizodus soledadinus* (Coleoptera: Carabidae) was uniquely introduced from the Falkland Islands 102 years ago at one site of the Kerguelen Islands. Since then, it colonized a large geographical area of the Kerguelen Islands. First, we examined if there are there are morphological variation along the invasion succession could be related to dispersal power? Second, physiological experiments (metabolomics) were conducted to identifying evolutionary network changes associated with differences in dispersal abilities. We mapped metabolomics data onto genome-scale metabolic networks so that we could restore the connectivity among identified metabolites. We observed that beetles sampled at the range margins were characterized by distinct physiological strategies as compared with their relatives sampled at the invasion core; large differences were observed in dispersal behavior, management of energetic budgets (starvation resistance) and metabolic signatures. Finally, survival durations to multiple environmental stressors in adult *M. soledadinus* insects collected along the invasion gradient revealed a significant correlation between residence time and stress resistance. Altogether, our data constitute a solid basis for post-introduction expansion modelling and further tests for evolutionary invasion analysis.

An approach in assessing nutrient limitations in polar, tropical and temperate microalgae: nutrient-induced fluorescence transients (NIFTs)

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Nutrient-induced fluorescence transients (NIFTs) approach has a potential in assessing nutrient limitations in laboratory cultures as it is rapid and cost-effective compared to conventional methods. 9 polar species (*Chaetoceros neglectus*, *Chaetoceros neglectus*, *Fragilariopsis curta*, *Fragilariopsis obliquecostata*, *Navicula directa*, *Navicula glaceii*, *Odontella weisflogii*, *Proboscia alata* and *Thalassiosira tumida*), 9 temperate species (*Alexandrium catanella*, *Amphidinium massartii*, *Alexandrium minutum*, *Euglena gracilis*, *Emiliania huxleyi*, *Gymnodinium catenatum*, *Karlodinium veneficum*, *Tabellaria flocculosa* and *Tetraselmis suecica*) and 13 tropical species of microalgal cultures (*Chaetoceros* sp., *Chloropsis* sp., *Isochrysis* sp., *Nannochloropsis* sp., *Tetraselmis* sp., *Alexandrium affine*, *Alexandrium minutum*, *Alexandrium tamiyavanichi*, *Bysmatrum* sp., *Coolia malayensis*, *Gambierdiscus* sp., *Nitzschia* sp. and *Prorocentrum* sp.) were grown under nutrient-limited conditions and NIFTs' responses were measured following re-supply of possible limiting nutrients (nitrate, phosphate or silica) by using Pulse Amplitude Modulation (PAM) fluorometers. We observed NIFT responses differ across microalgal taxa. For polar species, 5 out of 9 species were undetectable by NIFT. Only *N. directa* showed positive NIFT responses following re-supply of phosphate and silica. For temperate species, *G. catenatum* the only species undetectable by NIFT. *A. catanella* nad *A.minutum* showed positive NIFT responses following re-supply of phosphate and silica. For tropical species, *A. minutum* and *C. malayensis* showed positive NIFT response following re-supply of nitrate. Addition of phosphate induced positive fluorescence changes in *A. minutum* and *Gambierdiscus* sp. Positive NIFT responses indicated there were nutrient limitations in the cultures. These results suggest that NIFT is species-specific because not all species respond well to NIFT. This method offers potential for assessing the importance of nitrate, phosphate or silica as nutrient sources to microalgal populations and as a diagnostic tool for nutrient limitations.

Seasonaltrophic ecology of the dominant Antarctic coral Malacobelemnon daytoni (Octocorallia, Pennatulacea, Kophobelemnidae)

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Antarctic ecosystems present the most marked seasonal patterns in energy input, which in turn determines the biology and ecology of marine invertebrates species. This relationship is stronger at lower levels of the food web while upper levels could be less dependent of the primary production pulses. The pennatulid *Malacobelemnon daytoni*, is one of the most abundant species in Potter Cove, Antarctica. In order to assess its trophic ecology and energetic strategies, biochemical (carbohydrates, proteins and lipids), fatty acid (FA) and stable isotopes (SI) ($\delta^{15}N$ and $\delta^{13}C$) compositions were studied along a year-round period. FA and SI profile suggest an omnivorous diet and opportunistic feeding strategy of the species. These results, together with biochemical analysis (higher lipids and carbohydrates concentration observed in July and October 2009), support the hypothesis that resuspension events could be an important source of energy, reducing the seasonality of food depletion periods in winter. The evidence presented here give us a better insight of the success that this specie has in Potter Cove and under the current environmental changes experienced by the Antarctic Peninsula.

Ecophysiology and Habitat Characterisation of the flightless midge Halirytus magellanicus (Diptera: Chironomidae)

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Halirytus magellanicus (Jacobs, 1900) is a flightless midge originally described for the genus *Belgica* Jacobs, 1900 and recorded for Tierra del Fuego, South America. It has barely been studied along the last hundred years and, thus, not a lot is known about the species. However, Delettre et al. (2003) argued that the genus *Halirytus* Eaton, 1875 should be synonimised to *Telmatogeton* Schiner, 1866. This discussion remains to be resolved as there is still a possibility that the species might actually belong to *Belgica*. More recently, we rediscovered the species in the Chilean Patagonia, more specifically in Navarino and Cape Horn Islands. In order to better understand how the species is related to other sub-Antarctic and Antarctic midges (known for their incredible hardiness [Brundin, 1962]), we are taking a novel approach of linking molecular data through phylogeography (still in its early stages) with physiological data through ecophysiological experiments (temperature and salinity stress tolerances), both of which have separately been done for *Belgica antarctica* Jacobs, 1900 and to a lesser extent with *Parochlus steinenii* (Gerke, 1889) and *Eretmoptera murphyi* Schaeffer, 1914. Additionally, we are doing the first habitat characterisation for *H.* magellanicus, through transect-quadrant sampling coupled with floral and invertebrate fauna composition, has shown the species to be highly restricted to the mid-intertidal zone, rarely occurring in the low-intertidal zone and not in the high-intertidal, apart from stray adults. Furthermore, it is most commonly found among filamentous algae growing on top of bivalves. This is particularly interesting in comparison to *Belgica antarctica*, considered a sister-species, which occurs mostly on land among nitrophilous algae and on damp sites. To assess the resilience of *H. magellanicus* to stress tolerance, larvae are put under temperature (from -12ºC to 35ºC) and salinity gradients (from ~0 $mOsm^{-1}$ to saturated solutions of ~2000 $mOsm^{-1}$). So far larvae have survived for more than 30 days in freshwater and recovered from freezing at temperatures as low as -6ºC for periods of 24h, akin to what has been seen in the aforementioned related species.

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Isolation and characterization of noble Growth promoting bacteria from Zub Lake, East Antarctica.

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The bacterial isolates were recovered from a sediment core sub-samples from Zub lake (12 meter deep), Schirmacher Oasis, (70°46'04"–70°44'21"S, 11°49'54"–11°26'03"E), Dronning Maud Land, East Antarctica. The culturable bacterial isolates were orange, yellow, and cream in colour. Physiological tests such as effect of temperature, pH and salinity on growth of the isolates were studied. All the isolates grew at 4 to 22°C. The optimum growth temperature was 15°C and optimum pH was 7. The isolates had preference to utilize the simpler form of carbon sources.16S rRNA gene sequence of isolates exhibited 99-100% homology with Gene bank database. Out of several bacteria isolated from core samples; four bacterial species (Bacillus amyloliquefaciens, B. megaterium, B. mycoides and Brevundimonas diminuta) showed excellent plant growth promoting ability in addition to their cold tolerance. A set of pot experiment was performed to evaluate the effect of bacterial strains on root and shoot growth of cucurbitaceous and leguminous plants. The experiment results showed that isolates increased the root and shoot growth in comparison to control (Fig 1a,b). The bacterial isolates were also tested in vitro for inhibitory effect against different fungal strains (Sclerotinia sclerotiorum, Fusarium oxysporum, Rhizoctonia solani, Phytophthora sp. and Sclerotiorum roflsii) by using plate bioassay method (Fig 1c). Antifungal activity was recorded as zone of inhibition. Besides this the four bacterial species showed good ability for phosphate solubilisation (Fig. 1d). In order to decipher the plant growth promoting ability and cold tolerance, whole genome sequencing of Bacillus amyloliquefaciens was performed. The genome sequence was established with a whole-genome shotgun strategy using 316™ chip and 200-bp chemistry on the Ion Torrent PGM platform (Life Technologies, USA). Gene prediction and functional characterization was performed with the help of Rapid Annotation using Subsystem Technology (Aziz et al. 2008). The annotation predicted 3.7 mbp genome size including 3214 coding sequences, and 72 total RNAs (11 rRNAs and 61 tRNA genes). A total of 330 unique genes responsible for different functions were found with the subsystem. The genome analysis of Bacillus amyloliquefaciens revealed the presence of genes encoding for biosynthesis of plant growth promoting hormones (auxin, cytokinin, abscisic acid, ethylene, salicylic acid and indole acetic acid) were detected indicating its survival strategy in oligotrophic environment and immense potential to be used as a Plant Growth Promoting Rhizobacterium (PGPR) in cold environments. Besides this there are genes encoding for Cold-shock proteins (CSPs), illustrating the survival strategies in cold environments.

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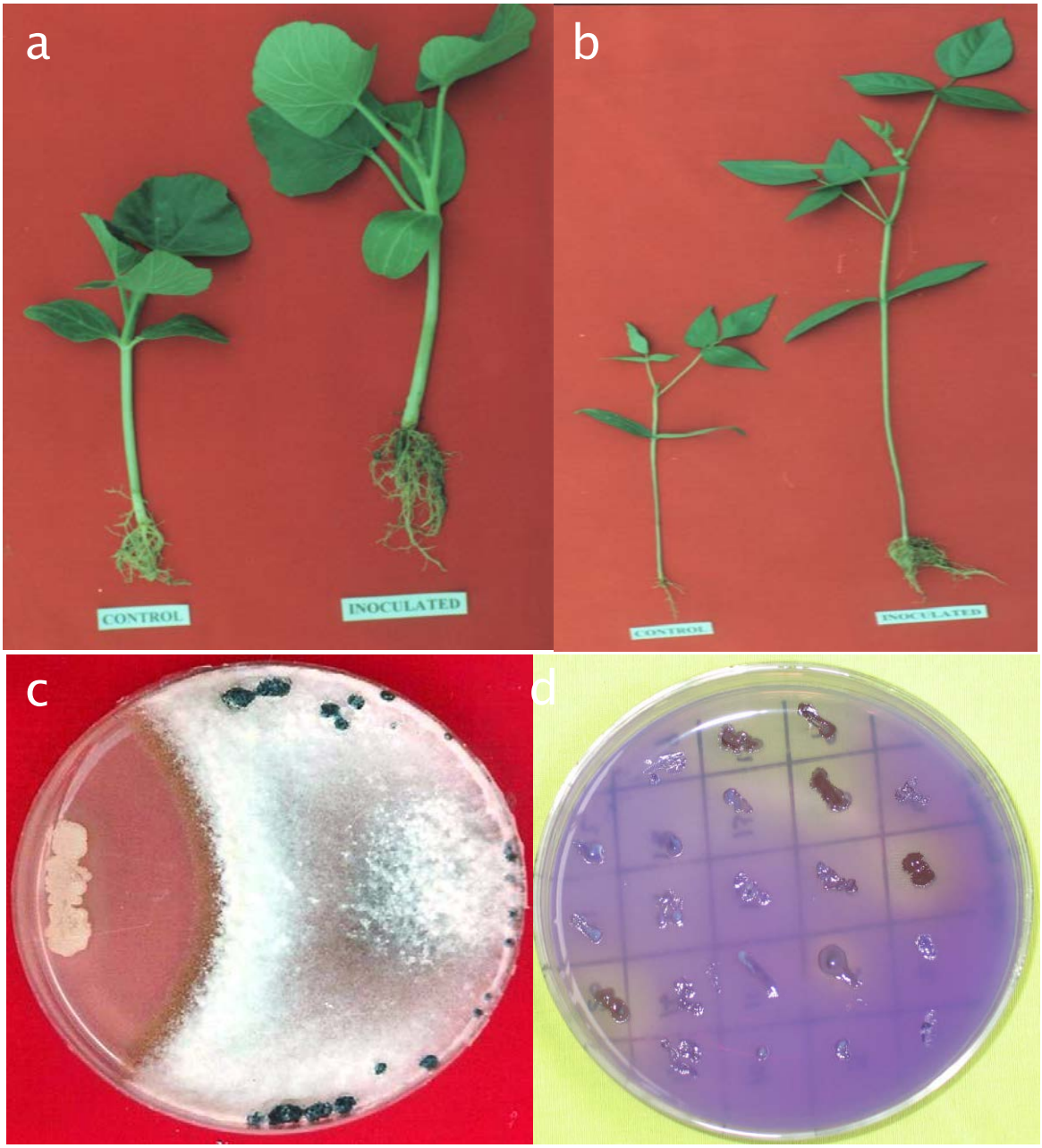

Figure1. a,b) Growth promotion in Cucurbitacaeous and Leguminous plants by Antarctic lake sediment Bacteria, c) Screening of isolated bacteria against *Sclerotinia sclerotiorum*, d) Screening of isolated bacteria to solubilize phosphate in selective media.

Expression of aryl hydrocarbon receptor-regulated genes in *Pachycara brachycephalum* exposed to Benzo(*a*)pyrene

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Ligand-binding to the Aryl hydrocarbon Receptor (AhR) pathway mediates many, if not all, responses of fish to dioxin-like compounds. The Southern Ocean was long time considered as one of the last pristine environments on earth. Nowadays, it is progressively exposed to increasing concentrations of anthropogenic pollutants. Antarctic fish are known to accumulate those pollutants, however, nothing is known about their capability to induce chemical biotransformation via the AhR pathway.

The objective of this paper was to investigate if Antarctic eelpout *Pachycara brachycephalum,* respond to anthropogenic pollutants by activation of the AhR and one of its target genes, i.e. cytochrome P4501A (CYP1A), and if pollutant exposure causes oxidative stress.

We exposed *P. brachycephalum* to benzo(*a*)pyrene (BaP), a model polycyclic aromatic hydrocarbon (PAH), specifically to 10 and 100 mg BaP per kg body weight, over a time course of 10 days. We measured the expression of AhR, CYP1A and superoxide dismutase (SOD) in liver tissue via quantitative RT-PCR at day one, three and 10 after start of the exposure.

We identified at least two distinct AhR isoforms in the liver of *P. brachycephalum.* Antarctic eelpout responded to BaP exposure by an up-regulation of both AhR isoforms and by a strong induction of CYP1A expression in a concentration- and time-dependent manner. Both AhR and CYP1A expression was up-regulated following the third day of BaP-exposure and remained high until day 10 of the exposure time. SOD activity was up-regulated after the 10th day of the 100 mg BaP/kg BaP-exposed eelpout.

Our data suggest that *P. brachycephalum* possesses the potential to upregulate xenobiotic biotransformation pathways. However, the time course of the AhR- and CYP1A response points to a slow response towards xenobiotics exposure.

Ice-binding proteins from psychrophilic *Chloromonas* sp. enhance freezing tolerance in transgenic *Arabidopsis thaliana*

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Genus *Chloromonas* is cosmopolitan green algae which is secondary larger group in Chlorophyceae. *Chloromonas* species was often found in extreme environments such as snow surface, alpine and polar region. Microalgae in polar region have developed their own strategies to protect the cells under repeated freeze-thaw cycles of ice crystals. Ice-Binding Proteins (IBPs) which are widely spread in polar fungi, slim mold, bacteria, diatom and microalgae, possibly play a key role making the microenvironment surrounding cells more habitable. Recent studies have identified that two types of IBPs are more abundantly present in Chlorophyceae in low temperature environments. Among them, type 2 IBP has been found only Antarctic green alga *Chlamydomonas* CCMP681. To discover more IBP genes, we performed type 2 IBP gene screening using psychrophilic Arctic/Antarctic *Chloromonas* strains and confirmed that these IBPs are more frequently found in this genus but not in *Chlamydomonas* species. For focusing on cold acclimation, we carried out transcriptome analysis under 4, 8, 12, 16, 20°C conditions using one of the psychrophilic *Chloromonas* (KCCPM KNF032). By comparison, we selected 39 up-regulated transcripts under low temperature specific. More than half of annotated transcripts were revealed as type 2 IBPs and those proteins were shared structural properties: conserved TXT motifs and none predictable domains. Transgenic *Arabidopsis* plants overexpressing CmIBPs (*Chloromonas* IBPs) revealed to increase a freezing tolerance through ion leakage assay. Furthermore, these heterogeneous IBPs in plant more stabilized under cold acclimation (CA) than non-cold acclimation (NA) condition. Recombinant protein expressing by *E. coli* system were used to characterize a freezing inhibition activity. Characterization of these proteins and predictable biological functions will be discussed.

Silicon recycling in the Southern Ocean: multi-analysis of incorporated silica from digested diatom frustules in Antarctic sponges

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Sponges and diatoms rely on biogenic silica to build their internal and external skeletons, respectively. However, the mechanisms by which they construct them are remarkably different. While diatoms polymerize their silica within intracellular silicic acid deposition vesicles (Hildebrand & Wetherbee 2003), sponges are able to do it both intracellular and extracellularly (Uriz et al. 2003, Maldonado & Riesgo 2007). Biogenic silica present in sponge spicules is usually considered to proceed from seawater uptake and posterior polycondensation using enzymes called silicateins. Interestingly, sponges can feed upon a wide variety of microorganisms, including diatoms from the phytoplankton. In the Southern Ocean, the rate of diatom uptake in sponges has been shown to be higher than in other latitudes, mainly due to their exceptional abundance in the seawater. Whether sponges can actually recycle the silica contained in the digested diatom frustules currently remains untested.

We sampled 5 demosponge species (*Mycale acerata, Isodictya kerguelensis, Phorbas areolatus, Hemigellius pilosus* and *Haliclona penicillata*) from Deception Island (Antarctica) and fixed their tissues for TEM and SEM and electron probe microanalysis (EPMA), and silicon isotope analysis (as well as seawater and diatoms). Our results show multiple indications of demosponge silica uptake from the digested frustules of diatoms. First, within the mesohyl of the demosponges we observed many diatoms, some of them being digested intracellularly by archaeocyte-like cells. Second, we detected many vesicles in archaeocyte-like cells containing silica (analyzed by TEM and EPMA) that were not spicule-forming sclerocytes. Third, our SEM observations showed evidence of digestion also in the diatom frustules obtained from the tissues of the sponges, also observed in their counterparts from tropical latitudes. And fourth, our silicon isotopic analysis shows that spicules are more depleted in ^{30}S than diatoms frustules, which in turn are more depleted than seawater. This is consistent with a two-step absorption process, i.e., from seawater to diatoms and from diatom frustules to sponges, although it is also common in other sponges with little or none diatom feeding. Our results open a new avenue to explore silica deposition in sponges, and suggest a new method of biogenic silica uptake at least in environments with an abundance of diatoms.

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A tiny genome for a tiny midge: physiology and genomics of the world's southernmost insect

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The Antarctic midge, *Belgica antarctica*, is the only true insect endemic to Antarctica and is found exclusively along the western Antarctic Peninsula. Larvae feed during the austral summer and take two years to complete development, after which adults briefly emerge, mate, and lay eggs. This midge is among the most resilient insect species described, surviving a range of environmental stressors including freezing, desiccating conditions, immersion in fresh and sea water, and anoxia. While cold is the most conspicuous feature of terrestrial Antarctica, water availability is perhaps the greatest challenge for polar arthropods, as water is frozen and thus unavailable for much of the year. Larvae of B. antartica have an impressive ability to tolerate desiccation and can survive dehydration down to 35% of their original body mass. To identify genetic mechanisms that contribute to extreme stress tolerance, we sequenced the genome and transcriptome of *B. antarctica* (Teets et al., 2012; Kelley et al., 2014). The most conspicuous feature of the genome is its size: at 99 megabases, the genome of B. antarctica is the smallest insect genome sequenced thus far. Despite its small size, the genome contains a similar number of protein-coding genes as other Diptera, and the size reduction is primarily a consequence of low repeat density and reduced intron length. In response to desiccation, we observed a complex reorganization of the transcriptome. Genes related to cell preservation, including the ubiquitin-mediated proteasome and autophagy, were upregulated, while genes belonging to nearly every metabolic process were downregulated. To our surprise, the transcriptional response to desiccation stress was highly divergent from that of another polar arthropod, the Arctic collembolan *Megaphorura arctica,* suggesting there are distinct transcriptional mechanisms to cope with polar environments. In future work, we will sequence additional species from Antarctic and sub-Antarctic habitats to work towards a comprehensive understanding of the evolutionary mechanisms that permit survival in extreme environments.

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Comparative transcriptome analysis of the Antarctic tardigrade, *Acutuncus antarcticus*, in response to changes in temperature

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Terrestrial ecosystems in parts of Antarctica are currently experiencing sometimes drastic climatic and environmental changes. Understanding how individual species – and hence the populations and communities of which they are part - respond to these changes is recognized as a key research challenge affecting our ability to predict how ecosystem structure and function might alter.

Tardigrades are important members of the simple faunal assemblages found in the extreme terrestrial and freshwater environments of continental Antarctica. In lakes and pools, in particular, they are one of the major community components (Gibson et al. 2007; Tsujimoto et al. 2014). The species *Acutuncus antarcticus* is often the most common and dominant species in these communities (Velasco-Castrillón et al. 2014).

In this study, we set out an RNA-seq analysis to provide insights into the gene regulations of *A. antarcticus* including metabolism by the comparative transcriptome analysis under different temperature settings. Cohorts of *A. antarcticus* were incubated at either 20˚C, 15˚C, 10˚C, 5˚C for 48h and analyzed in triplicates.

The number of differentially expressed genes (DEGs) were limited, in the range of hundreds of genes between two conditions. Of these, the 20˚C condition resulted in the largest number of DEGs. DEGs were primarily enriched in embryogenesis and development-related genes, and a down regulation of mitochondrial activities was suggested for lower temperature conditions.

The previous study conducted on the life history of *A. antarcticus* under the same temperature settings indicated the optimal reproductive performance under 15˚C and 10˚C and the remarkably short lifespan under 20˚C. Together with the present study, only a relatively small change in habitat temperature may significantly affect the metabolism, reproduction and survival, thus the population growth of *A. antarcticus*. They also suggest possibly rapid changes in the influence of these tardigrades on community structure and function in the terrestrial and freshwater ecosystems of continental Antarctica.

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New scenario of temperature and salinity modified the osmotic response in Antarctic fish Harpagifer antarcticus

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In teleosts, temperature and salinity are important factors that affect the physiology, therefore, changes in environmental temperature-salinity, outside of the optimum species-specific range, have profound effects on physiological processes (Farrel et al. 2011; Schulte 2015; Somero 2014). An important physiological process for teleost fish, "the osmoregulation", is strongly affected by temperature-salinity. The new scenario of climate change may be modifying these responses, especially in areas where low increase of temperature or low decrease of salinity would be affecting the fauna, especially fish. The *Harpagifer antarcticus* is an Antarctic species called the spiny plunderfish, it is a marine notothenioid. *Harpagifer antarcticus* are small (7–12 cm standard length) benthic fishes generally characterized by narrow and shallow bathymetric ranges (Eastman 1993). The aim of this study was to evaluate the changes in the osmotic response according a new scenario of climate change, where increase the temperature and freshening of the Antarctic sea could be affecting the Antarctic fish *Harpagifer antarcticus*. Adults of *H. antarcticus* (n=75) were catched by turn over the rocks from the lower intertidal area of Georges King Island. After one week of acclimation the fish were exposed at 2, 5, 8, 11 and 14°C and three different salinities (33, 18 and 23 psu), being the control group fish keeping at 2°C and 33 psu, and simulating other 14 different environmental condition (n=5 per condition). After 10 days the fish were killed by overdoses of anaesthetic and gills, kidney and foregut portion were removed to determinate changes in osmotic response by quantifying the Total ATPase and Na^+,K^+-ATPase activity (NKA) by McCormick method (1993). The results showed mortality at 14°C in all salinity groups, being this temperature critical for *H. antarcticus*. Gill NKA and Total ATPase activity increased at temperature and salinity experimental condition to respect at control group. Kidney and foregut showed different pattern of the NKA and Total ATPase activity according temperature and salinity experimental condition. At 11°C in all tissues sampled the NKA activity was lowest at 28 and 23 psu. The results suggest that *H. antarcticus* will respond to the new thermal-salinity scenario with effects on osmotic process, with different responses depending on the tissue, but having critical effect over 8°C. This study provides information relevant for understanding how new scenario of climate change would be affecting the osmotic response of this Antarctic Notothenioid fish. This work was financed by DID UACH, Fondap-Ideal Grant Nº15150003.

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Heat tolerance and its physiological response in Antarctic fish Harpagifer antarcticus

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The critical thermal maximum (CTMax) is a commonly used technique equating an animal's heat tolerance to the temperature at which it loses the ability to escape from constant rapid warming (Paladino et al., 1980). The *Harpagifer antarcticus* is an Antarctic species called the spiny plunderfish, it is a marine notothenioid. *Harpagifer antarcticus* are small (7–12 cm standard length) benthic fishes generally characterized by narrow and shallow bathymetric ranges (Eastman 1993) and by the presence of a long free-living larval stage (Kock and Kellermann 1991; White and Burren 1992). The aim of this study was to evaluate two methods of CTMax ramp and the physiological response according to both CTMax trials. The adults of *H. antarcticus* (n=23) were caught by turning over the rocks from the lower intertidal area of Georges King Island. After one week of acclimation the fish were exposed at two CTMax heating rates, 0.3˚C and 1˚C per minute and after the loss equilibrium were put in recovery tanks for 2 and 4 hours. Gills, kidney and foregut portion were removed to determinate changes in osmotic response by quantifying the Total ATPase and Na^+,K^+-ATPase activity (NKA) by McCormick method (1993). The CTMAX temperatures were similar from both velocity of ramp, being 18.23 $\pm$ 0.37˚C and 18.63 $\pm$ 0.29˚C for the 0.3˚C and1˚C per minute, respectively. The NKA activity showed different response depending on heating rate, recovery time and tissue type. The gills Total ATPase and NKA activity showed increasing osmotic response, with the highest level at 2-4 hours of recovery at 0.3˚C per minute rate, and decreased response at 4 hours of recovery at 1˚C per minute rate, relative to the 0.3˚C per minute group. Kidney and foregut presented the highest level at 1˚C per minute rate in 2 and 4 hours of recovery respectively, contrary to gill that presented highest level at 0.3˚C per minute rate. This study provides information relevant for understanding the differences between two different of CTMax methods and recovery time on osmotic response of this Antarctic Notothenioid fish. This work was financed by DID UACH, Fondap-Ideal Grant Nº15150003.

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Heating up the ocean: effects of in situ warming on marine benthic recruitment and community development

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With coastal sea temperature predicted to increase 1.5-2ºC by 2050, it is important to assess how the communities of coastal marine habitats will respond, in order to predict overall biodiversity and ecosystem level impacts. Elevated temperature effects have been tested in laboratory settings on numerous sessile invertebrate species, however these are predominantly single species studies and although these are useful for identifying differential sensitivities between species, they do not directly address responses and interactions at the community level under natural environmental conditions. Assessing the impacts in situ at the community level and over an extended period of time is an essential step towards predicting ecosystem level impacts. By using the novel technology of heated settlement panels, we will assess the effects of in situ elevated warming on benthic early community development. These British Antarctic Survey (BAS) custom-made panels heat the surface and a thin layer of overlying water to 1ºC or 2ºC above ambient temperatures, thus mimicking oceanic warming predictions for 2050. Panels were deployed at three different sites near to the BAS Rothera Research station, Antarctica for a period of 18 months. The main coloniser across all treatments was the spirorbid worm *Romanchella perieri.* After being returned to the laboratory, upper thermal limit (UTL) experiments were used to identify if the recruited spirorbids had acclimated to the different temperatures. Alongside this a pilot next generation sequencing (NGS) study to characterise the heat shock proteins in this species and evaluate the heat shock response under the different warming regimes.

Analysis of genomes of *Cryobacterium* spp. from Antarctica

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Cryobacterium spp. have been isolated and described by several researchers (Inoue and Komagata, 1976; Reddy *et al.*, 2010; Bajerski *et al.*¸2011). Nevertheless, information pertaining to their genomes and thermal stress-related genes is sparse. Recently, two cold-adapted *Cryobacterium* spp., strains SO1 and SO2 have been isolated from Antarctic snow samples. This project was undertaken to analyze genomes of *Cryobacterium* spp. strains SO1 and SO2 to determine genes that they harbor. Genomes of *Cryobacterium* spp. strains SO1 and SO2 were sequenced using the Illumina HiSeq sequencer, assembled and annotated. Total of 3,633,608 and 3,117,314 reads of SO1 and SO2 genomic DNA were obtained respectively. *Cryobacterium* spp., strains, SO1 and SO2 have DNA G+C contents of 67.6% and 68.4% respectively. They are assembled into 259 and 115 contigs with estimated coverage of 101 and 85 times respectively. Genomes of strains SO1 and SO2 contained 3,665 and 3,799 putative protein coding sequences respectively. Several proteins that facilitated bacteria to adapt to thermal- stress were found. Among them were molecular chaperones, heat-shock proteins, cold-shock proteins, low temperature requirement protein A, and antifreeze protein. Several interesting genes were also found in the genomes of the two Antarctic bacteria.

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The physiological response of plants living in a sub-Antarctic environment to environmental conditions: Looking at diurnal patterns on a seasonal scale.

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Remote sensing creates an opportunity to measure real time physiological responses of plants to changes in environmental conditions. The Photochemical Reflectance Index (PRI) has been shown to be a valuable indicator of photosynthetic rates as well as a proxy for other ecophysiological traits such as the xanthophyll cycle. The xanthophyll cycle acts as a photprotection mechanism within photosystem (PS) and influences photosynthetic activity. In sito PRI measurements were taken at a fine temporal resolution (1 minute measurement frequency) of various plant species together with a variety of environmental variables on Marion Island. The hyper oceanic environments create a unique climate on Marion that is highly influenced by frontal systems. Freezing temperatures and high winds occur therefor throughout the year. The PRI response of four vascular and two bryophyte species (two cushion plants, two gramminoid species and two tuft moss species) suggest that the photosynthetic efficiency of these plants follow irradiance patterns however is highly influenced by wind speeds. Based on the PRI data it is clear that the plants found on Marion Island do not follow an expected diurnal pattern, where the lowest PRI coincides with the highest vapour pressure deficit (VPD) of the day. There is a strong correlation between Fv/Fm' and PRI measurements for all species, which confirms that PRI is suitable as an index of photochemical efficiency for photosystem Ⅱ (PSⅡ). The Fv/Fm' of the different species follow similar patterns throughout the day (0.4< Fv/Fm' >0.7), however the diurnal PRI values of the species differ significantly from each other on the same days, with the mosses having the lowest PRI readings. The PRI values for the different species follows different patterns throughout the seasons, with the gramminoids increasing their PRI in warmer months and the cushion plants and mosses decreasing theirs. This suggests that the different growth forms and functional types have physiologically different responses to environmental variables on different time scales. The low light environment on Marion Island is hypothesized as one of the major limiting factors for plant production. This study, however, shows that wind as well as other environmental factors plays a major role in influencing photosynthetic efficiency on Marion Island. Due to the high temporal resolution measurements the PRI measured in this study, we get a better understanding of photosynthetic efficiency and physiological changes in response to fluctuating environmental conditions on Marion Island.

Reproductive characteristics and occurrence of planktonic larvae of Echinoderm in Admiralty Bay, King George Island, Antarctica

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Polar regions are of great scientific and economic importance due to the abundance of natural resources. The Antarctic ecosystem is characterized by a primary production observed predominantly during a short period corresponding to the Antarctic summer. Due to these environmental conditions, a series of reproductive and life cycle adaptations of Antarctic invertebrates exists. Therefore, the aim of this study was to describe reproductive characteristics of benthic species and the presence of planktonic larvae of echinoderms in Admiralty Bay, Antarctica. Adults were collected with a Van Veen grab sampler in different sectors of Admiralty Bay during the summer period. In the laboratory, the animals were acclimatized in aquariums with aeration, seawater with salinity 33 and temperature varying from -0.5 to 1.7°C.

The species were dissected and the extract of the gonads examined in the optical microscope. The size of the oocytes, sexual pattern (dioecious or hermaphrodite), gonadal maturation and larval development (external or internal) were evaluated. The Zooplankton samples were collected from five points in shallow areas at Admiralty Bay in December 2009 and February 2010. These samples were collected in three replicates in all stations from five minutes oblique tows at 2knots from the sea bottom (30m) to the water surface. A conical net with a 150µm mesh size and 60cm diameter equipped with a flowmeter was used. Samples were preserved in 4% buffered formaldehyde.

The echinoderms larvae were identified and quantified, subsequently the values have been corrected to a standard $100m^3$ (Freire et al. 2006). Seven species were observed in 4 class: Echinoidea – *Sterechinus neumayeri, Abatus nimrodi and Ctenocidaris* aff*. pierri*; Asteroidea - *Odontaster validus, Notasterias armata*; Ophiuroidea – *Ophionotus victoriae*; Crinoidea - *Promachocrinus kerguelensis*. Adult echinoderms had mature gonads and oocytes that varied from 145 a 2100µm in diameter, with 4 species with external development and 3 species with internal development. *Odontaster validus*, *S. neumayeri* and *Ophionotus victoriae* being the most common species in Martel Inlet - Admiralty Bay (Nonato et al. 2000). Eighty five zooplankton samples were collected, of which 41 (48.24%) contained echinoderms larvae.

The average density of larvae were 7.21 (±20.08) larvae.$100m^{-3}$ in December 2009 and 4.75 (±60.55) larvae.$100m^{-3}$ in February 2010. Freire et al. (2006) observed the same pattern, with higher density in early summers of 2000/2001 and 2001/2002.

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Unknown distinctive Fe-redox cycling bacteria beneath the Greenland Ice Sheet: the case of NGRIP bedrock water

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The objective was to recover bacterial life existing beneath the Greenland Ice Sheet (GIS) using the sequencing of bacterial 16S rRNA genes recovered in the NGRIP ice core sample originating from bedrock water containing numerous reddish mineral inclusions. The sample was the moon-shaped ice segment (Bag15) from the 3045m depth. The 'red' part of the segment was cut off, strictly decontaminated and treated under 'clean room' conditions. The cell concentrations failed to estimate by flow fluorocytometry and fluorescent microscopy due to particle autofluorescence. The SEM studies of particles resulted in finding of Fe and Fe oxide everywhere.

The comprehensive DNA analyses included the PCR amplification/sequencing of different regions 16S rRNA genes of bacteria (v3-v5, v4-v8, v4-v6, v4) and archaea (v1-v5 и v3-v5). Archaea were not detected while bacteria gave a signal for all 4 gene regions tested. Of them two regions (v4 and v4-v8) gave only contaminant phylotypes while regions v4-v6 and v3-v5 allowed to recover 4 bacterial phylotypes all passing our contaminant criteria including the Contaminant Library (300 bacterial phylotypes). These 4 non-contaminant phylotypes were pulling out from 15 phylotypes in total.

The only v4-v6 region phylotype showed the conspecificity with the type culture of *Rhodoferax saidenbachensis* of *Beta-proteobacteria* (*Comamonadaceae*) (Kaden et al., 2014) and identity with the Antarctic strain of *Albidiferax* (*Rhodoferax*) sp (Peeters et al., 2011). The phylogenetic assessment of this phylotype showed its reliable clustering with the type culture of *Rhodoferax ferrireducens*, which can reduce Fe(III) (Finneran et al., 2003).

The sequencing of v3-v5 region resulted in discovery of 3 unknown bacterial phylotypes (<80% similarity with known taxa). The 1st phylotype assigning to *Planctomycetes* showed <98% similarity with DNA clones involved in Fe-phyllosilicate redox cycling in sediments (Converse et al., 2015). The 2nd phylotype assigning to *Parcubacteria* showed the family level similarity (<92%) with one soil DNA clone (Dunaj et al., 2012). Its phylogenetic assessment demonstrated reliable clustering with single DNA clones originating from the Fe-ions stratified Lake Pavin (Busigny et al., 2016) and iron-rich snow (Kojima et al., 2009). The 3rd phylotype remained unidentified and unclassified. The only closest DNA clone (91% - family level similarity) originated from pyroclastic surface (containing iron) following a volcano eruption (Zeglin et al., 2016).

Thus, 4 revealed phylotypes could testify for unknown bacterial Fe redox cycling chemolithotrophic communities existing beneath the GIS which are distinct from those thriving beneath Antarctic Ice Sheet (*Beta-proteobacteria* of *Gallionellaceae* (Bulat et al., 2016)).

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New terrestrial Mars analog sites in continental Antarctica for investigating potential habitats on the planet Mars

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Astrobiological investigations were performed in the Transantarctic Mountains. The study sites are located in the Northern Helliwell Hills, Sothern Helliwell Hills (Boggs Valley) and in the Morozumi Range in North Victoria Land (~71.73°S/161.38°E) and were visited in the framework of the 11th German Antarctic North Victoria Land Expedition (GANOVEX XI) during the austral summer of 2015/2016. The local bedrock consists mostly of sedimentary rocks (sandstones) of the Beacon Supergroup and mafic igneous intrusions (Ferrar Dolerites). Within these rocks a variety of micro-niches such as fissures, cracks and some structural micro-cavities within the fine-grained sedimentary rocks are colonized by a diversity of microorganisms. These micro-niches are protecting the organisms against extreme desiccation and UV-irradiation. Through comparison to the surface of the planet Mars these geologically and geomorphologically well-defined macro- and micro-habitats can be classified as Mars-analogs, particularly due to the presence of liquid water at an air temperature below zero and the presence of perchlorates. A test series on collected and isolated microorganisms from these field sites has been started to check their ability to survive or even to live under simulated Mars-like conditions both in the laboratories and in space (de Vera et al. 2014). Investigations were performed in Low Earth Orbit with microorganisms collected and isolated during previous field studies such as done during the GANOVEX X expedition (2009/10). They were tested for 1.5 years on the International Space Station in the frame of the ESA/DLR-space experiment BIOMEX (BIOlogy and Mars EXperiment, 2014-2016, de Vera et al. 2012)) to additionally highlight how important the collaboration between Polar Research and Space Research is as a prerequisite to investigating the habitability of Mars and the ability of instruments to detect life in a very extreme environment. An outlook will also be presented for a new ESA-space experiment which is planned to unify work from Polar research, Ocean/Deep Sea research and Space research to study the habitability of the icy ocean moons of Jupiter and Saturn and to support future ESA or NASA space missions to the outer Solar System.

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Cold environments dwelling microorganisms and their use in human activities

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The discovery of microorganisms living in cold environments was a real challenge of understanding the mechanisms of survival at low temperature and in the same time for theoretical biology. At molecular level, the spatial configuration of their structural and functional molecules, showed important differences when compared with its mesophilic analogues. There are many cold environments and some cold during the entire year, some cold only in certain periods. The ocean cold layers (Foreman et al. 2004) , the sea ice, snow and ice (Garcia- Echauri et al., 2011;Prabagaran et al., 2007) the glaciers, the permafrost, (Vorobyov et al, 1997;Rivkina 1998). the cold desserts (Bakermans et al., 2014), are main cold environments. In addition, there are the so called cold man made environments (Park et al. 2008).Some isolates showed properties which are important for biotechnologies, medicine, and other fields of activity They could release cold active enzymes which can be used in food industry in order to apply to products sensible to normal or high temperature and in textile industry and molecular biology (Sarmiento 2015).Other strains can produce antibiotics (Lo Giudice et al 2007), production of PUFA used for human consumption and inhibition of ice crystals formation (Alcaino et al. 2015).

They can be use in bio mining (Ovalle 1987) and in bioremediation degrading the oil from water and soil and oil derivatives (Brakstad, 2008), polychlorophenols (Langwaldt et al, 2008)., aromatic compounds (Parilli et al., 2010), and acid mine drainage (Kaksonen et., al., 2008). Many other uses can be found, and is necessary a dedicated intensive research for finding new strains with possible new aplications.

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Evolution on ice: Molecular adaptation to temperature in Antarctic sponge species

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Animals in the Antarctic seas have adapted to some of the most challenging conditions found anywhere on Earth. Temperatures generally ranging between 0 and -1.8°C and a food supply which fluctuates widely from summer to winter render their survival difficult. Nevertheless, sponge species have found the means to live and thrive in such conditions. We aim to find the molecular mechanisms that have evolved to allow this, utilising next generation sequencing and comparative analyses.

Sponges of the genera *Axinella*, *Mycale* and *Phorbas* have been selected as model systems, due to their wide distribution and prevalence in these habitats (Dayton et al, 1974). We have generated a range of genomic and transcriptomic resources from warm and cold water-derived samples, and are using comparative techniques to investigate molecular adaptation in these, building on previous physiological and structural work in sponges (e.g. Riesgo et al 2015, Morley et al 2016). These are deep and well assembled (e.g. *Phorbas areolatus* transcriptome, 146,359 contigs, N50 1,050 bp, 93,500,065 total bp, *Phorbas sp. nov.* transcriptome 148,693/988 bp/93,330,104 bp), and as such represent an excellent basis for future work in all these species.

These novel genomic resources will be of wide utility to the community in a range of contexts. Further, a number of specific pathways have been targeted for investigation, including those related to energy metabolism/storage, vitellogenesis and skeletal synthesis, which have been implicated as adaptive in a range of organisms (Riesgo et al 2015, Hu et al 2016). We have also begun to use hypothesis-free methods to assay for gene duplication, upregulation and signatures of positive selection to identify novel genes with a potential role in cold adaptation.

This work will allow us to understand the mechanisms by which sponge species can adapt to vastly different climatic conditions. By comparing the molecular repertoire of several species of demosponge we will be able to determine exact mechanisms of evolution to these conditions, and discern whether the adaptive strategies of these species to cold conditions are convergent, are based on ancestrally shared traits, or differ widely, allowing us to speculate more broadly about the evolution of cold-dwelling species.

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BIOMEX: Resistance of Cryomyces antarcticus grown on Mars and lunar analogues exposed to real space and simulated Mars-like conditions on the ISS

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One of the main scientific challenges for our time is to answer the question whether life ever existed, or still exists on Mars or on other planets or satellites. The investigation of the origin of life on Earth, its persistence on the planet since it appeared, and the search for evidence of life on other planets sheds light on the conditions that permit life. Astrobiologists strive to understand the limits of habitability and to define the requirements for metabolic activity and reproduction in planetary environments, as well as to have the definition of significantly distinguishable biosignatures, i.e. molecules indicating the presence of putative extinct or even extant life, to support future exploration mission. In that contest, the BIOlogy and Mars EXperiment (BIOMEX) is part of the ESA space mission EXPOSE-R2 in Low Earth Orbit (LEO). BIOMEX aims to test the endurance of selected extremophiles, as well as the resistance and stability of biomolecules, under space and Mars-like conditions (de Vera et al., 2012). To mimic real planetary conditions, microorganisms were grown on lunar regolith analogue rocks like anorthosite and on two Mars regolith analogue mixtures, namely Phyllosilicatic Mars Regolith Simulant (P-MRS) and Sulfatic Mars Regolith Simulant (S-MRS); the latter reflect two evolutionary epochs with environmental changes on Mars, i.e. early and present Mars (Böttger et al., 2012). The Antarctic cryptoendolithic black fungus *Cryomyces antarcticus* CCFEE 515, already survived in real space and simulated Mars-like conditions in space (Onofri et al., 2012; 2015), was selected for the experiment. Colonies, grown on Martian and Lunar simulant regolith pellets, were dried and exposed for 1.5 years to LEO space and simulated Mars-like conditions outside the International Space Station (ISS). Here the results of survival, metabolic activity, DNA integrity, and ultrastructural damage of *C. antarcticus* after exposure to real space and simulated Mars-like conditions on the ISS in the frame of BIOMEX project are presented.

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Parental care and demography of a spawning population of Neopagetopsis ionah from the Weddell Sea

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Parental care in notothenioid fish represents a common life history strategy, and is possibly more widespread than previously thought. Four out of five notothenioid families exhibit some kind of parental care, with egg or nest guarding activities aiming to minimize risks of egg predation and therefore increase offspring survival rate. On the other hand, parental care could have potential detrimental effects on parents, as guarding fish have fewer or no chance to feed and thereby risk prolonged starvation. Parental care has been well documented in several icefish, usually with males guarding eggs (Kock et al. 2006). In this study we report for the first time parental care behaviour observed in a spawning population of the icefish *Neopagetopsis ionah* from the south-eastern Weddell Sea. Based on bottom trawling catch and underwater images data, we describe the reproductive traits and demography of this species. Adult specimens represented a spawning population with similar body size (between 43-55cm) and age (between 4-5 years), determined by otolith reading. Individual fecundity, estimated directly from gonads (between 733-1810 eggs/female) or from eggs on nests (between 148-1600 eggs/nest), was relatively low. Batches consisted of eggs as large as 6.5mm, the largest among notothenioid. Sexual dimorphism was present in unpaired fins, with males showing longer and wider first dorsal fin rays than females, and a white horizontal stripe on the anal fin. Finally, we documented for the first time a massive post-spawning mortality in notothenioid fish, through images and catches data of dead specimens in the nesting area.

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Strategies of controlled anabiosis I: Desiccation transcriptomes of two Antarctic lichen photobionts

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Terrestrial vegetation of continental Antarctica is dominated by poikilohydrous bryophytes and lichens. Lichens are characterized by a symbiotic association of a fungus (mycobiont) and a photosynthetic partner (photobiont). Frequent dehydration is a common feature in the lichen life cycle which presupposes the fundamental life strategy of desiccation tolerance. Dehydration of the thallus causes a state of anabiosis. Upon rehydration, metabolic activity is rapidly achieved. For successful colonization of Antarctic terrestrial habitats described by harsh environmental conditions, desiccation tolerance is a key prerequisite for the lichen symbiosis. In the anabiotic state, adverse environmental conditions such as extremes of temperature, pressure and radiation (even UV-C) are tolerated. The potential of desiccation tolerance and revitalization of the lichen symbiosis constitutes lichens as relevant organisms for astrobiological exposure experiments under extreme conditions. Desiccation combined with vacuum and radiation treatment as experienced in the lower earth orbit could be tolerated due to the poikilohydric nature of lichens. Photosynthesis and growth of lichen photobionts could be restored after space exposure. Knowledge on the essential mechanisms supporting desiccation tolerance of lichen photobionts and hence on their contribution to the symbiosis' performance is scarce and largely based on research of the physiological processes. Especially the genetic level of desiccation tolerance of Antarctic lichen photobionts is unknown. In the present study, transcriptome analysis of two photobionts, originating from an Antarctic endemic and a cosmopolitan lichen, has been carried out. The transcriptome response to desiccation as well as the unstressed transcriptomes of the two organisms studied differed significantly, reflecting their differences in stress physiology. Mechanisms of protein and membrane protection as well as a controlled metabolic shutdown are considered major factors of desiccation tolerance. Factors such as ERD and LEA proteins, as well as carbohydrates and amino acids were identified, suggesting an ancient conservation of adaptation to dry conditions. The knowledge achieved by these results provides a solid understanding on the genetic level of the lichen symbiosis considering adaptation to severe environments.

On the reproduction of Antarctic demosponges from the orders Dendroceratida, Poecilosclerida, and Haplosclerida (Porifera)

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Sponges comprise a dominant element of the Antarctic benthic communities, posing both high diversity (> 300 species) and large population densities (McClintock et al. 2005, Campos et al. 2007). Despite that, reproduction events in Antarctic sponges have been rarely studied (Burton et al. 1934, Sarà et al. 2002, Riesgo et al. 2015). In the study here presented, we surveyed 6 species of the orders Dendroceratida (Dendrilla *antarctica*), Poecilosclerida (*Phorbas areolatus, Kirkpatrickia variolosa,* and *Isodyctia kerguelenensis*), and Haplosclerida (*Hemigellius pilosus* and *Haliclona penicillata*) seeking for reproductive elements. Samples were collected by SCUBA on rocky outcrops at 15 m depth in Deception Island (62°59'31.20" S, 60°33'5.07" W, South Shetland Islands) during the Austral Summer season in 2011 and 2013, and they were preserved and processed for light and transmission electron microscopy.

All species contained only female reproductive elements and brooded their embryos within the mesohyl. In general, their reproductive features were similar to those in their counterparts of other latitudes (Ereskovsky 2010), although several characters were observed for the first time in some species, such as bifurcate follicle cells in *P. areolatus*, embryonic gigantism in *I. kerguelenensis*, and spongin fibers within the embryos of *D. antarctica*. Our study contributes to the scarce knowledge of reproduction in benthic Antarctic invertebrates and provides the grounds for the study of their specific adaptations to the environment to understand their ecological and biological resilience.

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Research on Utilization of Various Types of Energy Applied in Antarctica Research Stations

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Based on comparison of advantages and disadvantages of with various types of energy applied in Antarctic Stations, suggestions are proposed to select proper energy systems for stations of different scale, functions, and geological positions. Energy is of crucial importance for heating, cooking, lighting, transportation, operation & maintenance in Antarctica.

Normally, energy is classified into three types, namely, fossil energy (oil, diesel, gasoline, natural gas, etc.), renewable energy (solar\wind\ geothermal\ocean energy) and nuclear power. Among them, petroleum, solar and wind energy are the most popular ones in Antarctica.

Based on analysis and comparison of petroleum, solar and wind energy in aspects of utilization efficiency, life cycle cost, emission quantity, construction difficulty, and impact on biology environment, conclusions are made as follows:

1. Electricity is the most convenient and widely used energy. However, as secondary energy, it can only be generated from other primary energy.
2. Petroleum is the most cost effective energy with defects of oxynitride and carbon dioxide emission, high transportation cost and leakage risk.
3. Solar and wind are green energy without pollution emission, but transformation ratio is low, initial investment is high. In consideration of infrasound effect caused by wind turbine and light pollution caused by solar panel, solar and wind energy also cause environmental risk.
4. Hydrogen, ocean, nuclear and fuel cell energy are future resources of energy waiting for exploration.

The operation and maintenance of scientific stations in Antarctica is highly replied on energy which during its transformation, environmental damages are caused more or less. Therefore, proper energy forms shall be selected in prudent manner to meet the needs of energy consumption and minimize negative effects to the surrounding environment.

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Diversity of phototrophic bacteria in terrestrial samples from the Sør Rondane Mountains, East Antarctica

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Although Cyanobacteria are generally considered the most important phototrophic primary producers and diazotrophs in Antarctic ecosystems, they appear to be scarce in some high-altitude Antarctic locations. Other organisms can therefore be hypothesized to take over their role in these systems. Furthermore, given the limited supply of organic matter, in oligotrophic surface samples, bacteria may use sunlight as an alternative energy source. To test these hypotheses, we investigated the diversity of phototrophs and nitrogen fixing microorganisms in exposed soils from the Sør Rondane Mountains, East Antarctica. An Illumina sequencing approach was used to analyze the bacterial community composition and the diversity and abundance of key genes involved in phototrophy and nitrogen fixation.

Analysis of *pufM* genes, encoding a subunit of photoreaction center 2 found in anoxygenic phototrophic bacteria, revealed a broad diversity, dominated by *Roseobacter*- and *Loktanella*-like sequences. *BchL* and *chlL* genes, involved in (bacterio)chlorophyll synthesis, showed a high relative abundance of either cyanobacterial or green algal trebouxiophyceael chlL reads, depending on the sample, while most *bchX* sequences belonged to previously unidentified phylotypes. Rhodopsin-containing phototrophic bacteria could not be detected in the samples. Our results, while suggesting that Cyanobacteria and green algae are the main phototrophic groups, show that light-harvesting bacteria including aerobic anoxygenic photoheterotrophs are nevertheless very diverse in microbial communities in Antarctic soils.
Nostocales Cyanobacteria, present in greatly varying numbers as assessed by Illumina sequencing of 16S rRNA and *nifH* gene fragments, appear to be the main nitrogen fixers in these habitats.

We also set up a cultivation campaign for culturable aerobic phototrophic bacteria present in the same samples collected in the proximity of the Belgian Princess Elisabeth Station. Approximately 1,000 isolates were obtained and identified by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry and partial 16S rRNA gene sequence analysis. Over half of the isolates grouped among known aerobic anoxygenic phototrophic taxa, particularly with Sphingomonadaceae, *Methylobacterium* and *Brevundimonas*. A total of 330 isolates were tested for presence of key phototrophy genes. While rhodopsin genes were not detected, multiple isolates possessed key genes of the bacteriochlorophyll synthesis pathway. Laboratory growth experiments revealed that light indeed benefits the growth of several of these isolates, whereas others demonstrated better growth in the dark.

Unravelling the secret of the resistance of desert strains of *Chroococcidiopsis* to desiccation and radiation

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Chroococcidiopsis is a unicellular cyanobacterial genus that is growing in extreme dry conditions, either in low or high temperatures. At the lower end of the spectrum, they live as cryptoendoliths in rocks of the Mc Murdo Dry Valleys in Antarctica where they were discovered by Imre Friedmann, while at the higher end, they grow as hypoliths/endoliths in hot deserts, e.g. Negev, Gobi, Atacama (Friedman, 1980).

The capacity of desert strains of *Chroococcidiopsis* to stabilize their sub-cellular organization is so efficient that, when dried, they can cope with simulated space and Martian conditions (Billi et al 2011 ; Baquè et al. 2013a) as well as with high doses of ionizing and UV radiations (Verseux et al. 2017 ; Baqué et al. 2013b).

Since it is known for radiation/desiccation tolerant bacteria that the capability to avoid protein oxidation is critical to cope with such stressors (Frederickson et al. 2008; Daly et al. 2007), the present study investigates the protein oxidation after prolonged desiccation, irradiation with gamma-rays up to 25kGy and treatment with hydrogen peroxide in a selection of desert *Chroococcidiopsis* isolates, including 2 Antarctic strains: CCMEE134 and CMEE171 isolated from Beacon Valley and University Valley, respectively (Mc Murdo Dry Valleys).

A tight correlation was observed between the desiccation and radiation tolerance of the investigated desert strains and the absence of oxidative damage to proteins. The efficiency of the antioxidant systems of the desert strains of *Chroococcidiopsis* was highlighted also by the lack of protein carbonylation until treatment with 1M of oxygen peroxide. The phylogenetic analysis of the investigated 11 desert strains of *Chroococcidiopsis* is reported.

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This work is dedicated to the memory of Roseli Ocampo-Friedmann and E. Imre Friedmann who pioneered the research on *Chroococcidiopsis* and life in extreme environments.

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Preliminary Genomic Analysis of *Plectus murrayi*

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Plectus murrayi is one of the dominant invertebrates of the McMurdo Dry Valley (MCM) terrestrial ecosystems. Its unique physiology, phylogenetic position within the Nematoda, and ability to be cultured on artificial media make *P. murrayi* an ideal model for exploring evolutionary responses to extreme environmental selection. In order to better understand mechanisms of environmental stress tolerance, we sequenced the whole genome of *P. murrayi*. We hypothesized that persistence in an extreme environment could result in evolutionary changes that constrain genome architecture, including genome decay. We collected *P. murrayi* from laboratory cultures and directly from soil samples for whole genome and transcriptome sequencing. A preliminary sequencing analysis resulted in finding significantly fewer protein-coding genes than expected. *P. murrayi* also has shorter introns and exons, and few transposable elements. Such reductions could be evidence of genome decay and intron retention, reflecting an evolutionary response to environmental stress. We discuss these findings in the context of the evolution of life history traits and stress tolerance (freezing and desiccation).

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Single-Molecule Sequencing of Antarctic Paleomats

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Antarctica is uniquely positioned to investigate fundamental questions about the persistence of microbial life. The McMurdo Dry Valleys are located in an arid ice-free area that is exposed to severe katabatic winds, extremely cold air temperatures, and seasonally high UV irradiation followed by unabated darkness. Ice-covered lakes along valley floors are thought to be the remnants of larger glacial lakes that once occupied the Dry Valleys. Within these paleolakes are desiccated microbial mats that are thousands of years old. Such paleomats hold insights not only into adaptations of life to past Antarctic conditions, but if cells within them are viable, they also represent an important system for study of long-term cell survival. Dormancy has long been considered a dominant strategy for microbial survival in harsh conditions, enabling cells to endure extended periods of harsh conditions due to lower reaction rates for many physiological processes, reduced cell membrane fluidity, and changes in intracellular pH. However, true dormancy may be problematic, as the lack of DNA repair allows genome damage to accumulate. To investigate whether cells within the Dry Valleys paleomats (i) are potentially viable, (ii) maintain a low level of metabolic activity aimed at DNA repair, and (iii) carry metabolic and molecular adaptations required to cope with Antarctic conditions over millennia, we utilized two advanced DNA sequencing technologies from Oxford Nanopore Technologies and Pacific Biosciences. Both systems target native DNA, thus eliminating PCR bias, and are capable of sequencing long contiguous strands of DNA (>5kb), which can help distinguish free-floating ancient DNA in the environment, typically 100-500bp in length, from high molecular weight DNA from intact cells. Sequencing long DNA fragments allows for more accurate genome reconstructions and the ability to identify evidence of DNA damage and repair. Bioinformatic analysis is ongoing, but initial findings suggest that Antarctic paleomats do still harbour intact, likely viable, cells over tens of thousands of years.

Community level physiological profiles and extracellular enzymatic activities in the Circumpolar Deep Water (CDW) of the Ross Sea

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In the Ross Sea, warm Circumpolar Deep Water (CDW) intrudes onto the continental shelf preferably on the western sector and flows into the ice shelf cavities, affecting the ice shelf melting rates. In fact, the intrusion of the warm CDW onto the Antarctic shelf area is one of the recognized drivers of ice shelf melting. Moreover, this water mass is the primary source of heat, salt, nutrients and iron (Fe) onto the Antarctic continental shelves playing an important role on the shelf physical and biological processes.

An oceanographic cruise was performed in the framework of the CELEBeR (CDW effects on glacial melting and on bulk of Fe in the Western Ross Sea) project (funded by Italian National Research Programme in Antarctica) in January - February 2017 aboard of R/V Italica, addressed to study microbial community level physiological profiles (by Biolog ecoplate) and extracellular enzymatic activities (EEA) of leucine-aminopeptidase, beta-glucosidase and alkaline phosphatase in the intruding CDW of the Western Ross Sea. The investigated areas covered: a) the Antarctic continental shelf break area near Cape Adare (North Victoria Land); b) the coastal area near the edge of the Mariner and Aviator glaciers; c) the Drygalski Ice Tongue and the nearby Terra Nova Bay polynya.

The functional diversity (catabolic potential) was assessed using the Average Well Color Development (AWCD). Moreover, Richness (R) and Shannon–Weaver index (H), analysis of variance (ANOVA) and principal component analysis (PCA) were used to depict the differences of the microbial functional diversity in the studied areas. Differences in potential metabolic pathways were detected in the different sampling areas.

The measured enzymatic activity rates suggested the potential ability of the microbial community to decompose proteins, carbohydrates and organic phosphates. Different levels of EEA were measured as a function of the CDW proximity - or not - to the glaciers and the trophism of the investigated area.

Identity of plant and biocrust species modulates soil functioning in Maritime Antarctic

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Maritime Antarctic hosts well developed dense cryptogamic covers integrated by several bryophyte and lichen species growing in combination with the only two autochthonous vascular plants *Deschampsia antarctica* and *Colobanthus quitensis*. These mosaic communities generate different microsites which relative coverage (i.e. in terms of species dominance and composition) is highly sensitive to changes in climate. Understanding the relative importance of different microsites in driving soil functioning and nutrient fertility is thus of paramount importance to predict functional responses to climate change in Antarctic ecosystems. Herein, we have studied the effects of four lichen species (*Leptogium puberulum*, *Stereocaulon alpinum*, *Sphaerophorus globosus* and *Cladonia* sp.; the first two being N-fixers), a N-fixing moss (*Sanionia uncinata*) and a vascular plant (*D. antarctica*) on soil microbial communities and associated ecosystem functions in Livingston Island (South Shetland Islands). Bare soil (i.e. devoid of cryptogams and vascular plants) was used as control. Diversity (T-RFLP) and abundance (via quantitative PCR) of fungi and bacteria and of functional genes (ammonia-oxidizing bacteria and archaea and denitrifying prokaryotes) were analysed under each of these microsites. Several soil functions linked to C, N and P availability were also measured. Results showed that species identity had strong influence on soil functioning. In general, presence of vegetation increased, in most of cases, the abundance of the microbial groups studied, and of N and C availability, regarding bare soil, but soil microbes and functions were highly responsive to microsite species identity. The diversity of functional genes did not show sharp differences between microsites, but dominant species differed between vegetation species and bare soil. The responses of potential net N mineralization rates were highly species-specific. These differences in functionality between microsites suggest that any changes in microsite composition in maritime Antarctic soils resulted from climate change will strongly influence soil microbial communities and associated ecosystem functions.

Benthic boundary fluxes of NH_4^+ in relation to sea-ice cover in the eastern Weddell Sea

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Remineralization is a key function of benthic ecosystems. It is affected by climate change through changing extent and duration of sea-ice cover, which in turn influences primary production and therefore organic material reaching the benthos [1]. In the austral summer 2015/16, benthic remineralization rates of NH_4^+ were determined in different regions in the eastern Weddell Sea [2]. We tested for the relation of NH_4^+ fluxes across the sediment-water interface to long-term and short-term ice cover (sea-ice concentration data of summer seasons between 2007 and 2016 obtained from http://www.meereisportal.de), primary production (fluorescence at fluorescence maximum in the water column measured with the CTD served as a proxy) and enhanced food input (addition of *Chaetocystis* sp.). The fluxes across the sediment-water interface were measured in whole-core incubations under controlled temperature and light conditions [3] for a duration of 36 to 144h. While most of the stations showed similar fluxes varying between -14.18 and 6.13µmol $m^{-2}d^{-1}$, the most northern station showed high positive values between 37.08 and 74.24µmol $m^{-2}d^{-1}$. Its divergence to all other sites can be explained by the lower sea-ice concentration over the years and is likely influenced by its geographical distance compared to the other stations. Maximum fluorescence correlated negatively with the sea-ice cover at the sampling date (P = -0.962), but there was no correlation with remineralization fluxes. Fluxes proved to be strongly related to long-term ice conditions (P = -0.577) rather than to short-term variability. Addition of food did not increase NH_4^+ fluxes significantly during our experiments. An increase in remineralization rates as a response to higher food input might be observed after a more pronounced time lag. Overall, our results indicate a sensitivity of benthic systems to long-term climate-related changes.

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Unravelling the responses of shallow soft sediment assemblages to rapid glacier retreat in an Antarctic fjord: Carbon and nitrogen cycling

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At the northern tip of the Western Antarctic Peninsula lies Potter Cove (PC), a fjord-like small embayment (about 3 km^2), influenced by the dynamics of the Fourcade Glacier. Since the 1950s, this glacier has been actively retreating, releasing the underlying soft sediments from the ice, exposing them to glacier calving disturbances (e.g. brash ice and ice scouring), increasing discharge of sediment-laden melt waters and to wave action. Several contrasting shallow (<20m) benthic habitat types are present within the bay. Although bathymetric and granulometric characteristics are relatively similar within the cove, the sediment-inhabiting fauna community composition is very patchy and variable, ranging from colonist to medium-developed benthic assemblages as a result of the locally altered conditions.

Efficient carbon cycling is especially crucial in this very productive bay. The large annual primary producer biomass (mainly benthic microalgae and large macroalgae) needs to be recycled to the basic nutrients. Since benthic communities are - through their feeding and burrowing activities - strongly involved in the degradation of organic matter, it can be expected that the gradient in development of benthic communities in Potter Cove will be somehow reflected in the local patterns in carbon and nitrogen cycling.

In 2015-2016, we had the unique opportunity to measure carbon and nitrogen cycling *in situ* over a seasonal cycle (summer, winter *under ice* measurements, and spring). To this aim, skilled divers deployed a set of benthic chambers on the sediment and measured fluxes of oxygen, inorganic carbon and dissolved inorganic nitrogen species at the sediment-water interface. At the same time, the sediment was sampled to assess environmental variables and benthic assemblage structure. Preliminary results show that despite the low water temperatures (0-2°C), benthic carbon and nitrogen cycling rates were similar to those of temperate regions, which highlights the productivity of the area. Carbon cycling in winter was remarkably lower than in spring and summer, which probably relates to a lower activity and/or biomass of the benthos. The most recent ice-free site, also most frequently disturbed by the glacier calving, was characterized by the least developed communities and lowest carbon cycling rates.

This seasonal set of carbon and nitrogen cycling measurements along a gradient of benthic assemblage statuses in Potter Cove will provide an example dataset for direct and indirect effects of glacier retreat on benthic ecosystem functioning, representing a unique study in the Western Antarctic Peninsula region.

Glass sponge pump rates and their role in biogeochemical cycles in the Weddell Sea, Antarctica

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Glass sponges (Porifera, Hexactinellida) are an important part of epibenthic communities in the shelf areas of Antarctica. They can grow to considerable sizes of up to 2m height and form vast sponge beds which provide habitat for various other animals. Despite continuous research on Antarctic benthic community structure and distribution and the obvious dominance of glass sponges in some shelf communities, very little is known about the physiology of these sessile filter feeders and their role in biogeochemical cycles. While past studies hypothesized that they have a significant impact on carbon and silicon cycling, this had so far not been investigated in situ.

During a recent expedition with RV Polarstern to the south-eastern Weddell Sea in 2015/16, we conducted a first in-situ study of pump rates and metabolism in Antarctic glass sponges. Using a remotely operated vehicle (ROV), we investigated 27 sponges of various sizes (15-65cm height) belonging to several common species (*Rossella sp.* and *Anoxycalyx joubini*) at four stations between 210m and 420m water depth.

We applied a fluorescent dye at the outside wall of the sponges to measure their pump rates and found 63% of them to be actively pumping. Furthermore, we sampled the exhalant current and the corresponding ambient water of 22 individuals with a new custom-made water sampling system. The samples were analysed for dissolved silicon, ammonium and picoplankton and the differences between ambient water and exhalant current were calculated for each sponge. In addition to that, we measured oxygen consumption in 10 sponges using an oxygen optode.

Here, we relate the measured pump rates to sponge size, and present biomass-specific fluxes of carbon, nitrogen, and silicon, as well as clearance and respiration rates for these important foundation species. Extrapolation of our findings to larger spatial scales will help to better estimate the role of Antarctic glass sponges on carbon and silicon cycling.

Feeding strategies of four dominant copepod species in Prydz Bay, Antarctica: Insights from a combined fatty acids and stable isotopes approach

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Feeding strategies and dietary preferences of four dominant copepod species (*Calanoides acutus*, *Calanus propinquus*, *Metridia gerlachei* and *Rhincalanus gigas*) sampled during late austral summer in Prydz Bay, Antarctica, were investigated using fatty acid and stable isotope signatures. The results show that the contribution of diatoms, dinoflagellates and ciliates to the hypothesized food sources (phytoplankton and particulate organic matter) were higher in the inner bay regions than in the oceanic regions of Prydz Bay. Regional differences in composition and abundance of food sources were also reflected in the fatty acid biomarkers and stable isotope values. In the inner bay region, there were nearly twofold higher total fatty acid contents, higher contributions of fatty acids of dinoflagellate origin and higher $\delta^{13}C$ and $\delta^{15}N$ values compared to oceanic region. Fatty acids and stable isotopes biomarkers in copepod species roughly mirrored the spatial patterns in food sources. As found in primary producers, concentrations of dinoflagellate fatty acids, $\delta^{13}C$ and $\delta^{15}N$ values were higher in copepods from the inner bay region. Moreover, fatty acids and stable isotopic values of copepods show some inter-species differences. *C. acutus* and *C. propinquus* show little regional differences in total fatty acid contents while *M. gerlachei* from inner bay region shows higher fatty acids values. *C. acutus* and *C. propinquus* had higher compositions of long chain fatty acids 20:1n-9, 22:1n-9 and 22:1n-1, while DHA was higher in *M. gerlachei*. $\delta^{15}N$ values indicates that the trophic level of *C. acutus* was higher than other copepod species. While the higher fatty acid ratios DHA/EPA and 18:1n-9/18:1n-7 in *M. gerlachei* indicates that this species fed more opportunistically and preferred a carnivorous diet. Insights from the combined fatty acids and stable isotopes approaches suggested dominant copepods in Prydz Bay, Antarctica have flexible feeding strategies in response to food sources during late austral summer.

Iron bioavailability to iron-limited Southern Ocean phytoplankton: from the lab to the field

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Exopolymeric substances (EPS) were shown to enhance iron solubility and its bioavailability to Southern Ocean phytoplankton cultures. Here we will present a dual approach to see how EPS affect iron bioavailability in the field. First, we will present results from a recent expeditions where the impact of bacterial EPS was investigated on natural phytoplankton community from the Drake Passage and the West Antarctic Peninsula. EPS, isolated from these locations were purified. We will present their role on iron chemistry and bioavailability using two iron-limited strains that are relevant to the Southern Ocean: The bacillariophyceae *Pseudo-nitzschia subcurvata* and the prymnesiophyceae *Phaeocystis antarctica*. Results confirm previous data and suggest that EPS are critical for enhancing iron bioavailability in iron-limited areas. Our results will be discussed in the framework of iron limitation across the Southern Ocean and its consequences for carbon fixation and export

Benthic oxygen fluxes in coastal waters off King George Island

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The mass transport across the benthic-pelagic interface is an important quantity for the understanding ecosystem functioning and its effect on biogeochemical cycles. Continuous measurements of benthic exchange fluxes are necessary to assess benthic community response under variable physical forcing and stressors. This can be realized by applying non-invasive flux measurements such as the Eddy Covariance (EC) technique – a common method in atmospheric sciences that recently has been introduced to aquatic sciences. We investigated the benthic consumption and production of oxygen in shallow euphotic waters at Potter Cove, (King George Island, Antarctica) - a site strongly affected by increased turbidity and sedimentation from glacier meltwater runoff. Continuous oxygen flux measurements over day-night cycles allowed estimating ecosystem respiration (at night) and net ecosystem production (at day). The investigated sites differed with respect to water column turbidity, water depth, sea bed substrate, and benthic community. Current velocity and wave motion had minor effect on oxygen fluxes, whereas significantly different oxygen consumption rates were found at locations with different benthic communities. As this EC study is the first of its kind in Antarctic waters we will discuss both, the method itself and the interpretation of the measured oxygen fluxes.

Distribution of biogenic silica and organic carbon in sediment of the "Filchner- Rønne Outflow System" in the southern Weddell Sea.

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Organic carbon (OC), biogenic silica (bSi) and grain size were measured in 16 sediment cores from the continental shelf and slope and the inner trough of the remote Filchner- Rønne Outflow System (FROS) to identify potential organic matter hotspots which may help analyzing the distribution of benthic communities in the area. Sediment sampling was carried out with a multicorer, which enables the collection of the sediment water inter-phase with rather small disturbance. The results present here correspond to the inventories of the upper 5 cm sediment column, the section that contains the most recently deposited material and also exposed to the most intense trophic activity of benthic organisms. The highest OC values were found in samples from the continental slope of the eastern flank of the Filchner Trough, whereas the highest bSi concentrations corresponded to samples from the continental shelf of the same flank. The lowest values for both parameters were associated to the continental shelf and slope of the western flank, whereas samples from the axis of the trough showed intermediate values despite their higher water depth. No significant relationship among biogenic variables and fine sediment (combined fraction of silt and clay) were found; however, samples with the coarser sediment coincided with the highest OC contents and contrastingly, the highest bSi and fine sediment contents were measured in the same samples. Preliminary results showed that the spatial distribution of macrobenthos abundances (ind m-2) match better with OC concentrations, particularly at the shelf break, than with bSi.

Role of the biotic habitat for benthic biogeochemical fluxes and function in the Weddell Sea

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Seafloor habitats provide a number of functions, including secondary productivity and remineralisation of organic matter. On a global scale, the relation between such ecosystem functions and biodiversity is assumed to be positive [1], albeit with differences among habitats and studies. Extending the pure biodiversity–function approach by including the influence of environmental parameters, we tested the effect of different habitat parameters on biogeochemical fluxes in two Southern Ocean benthic shelf systems, the north-western Weddell Sea, characterized by above-average warming of surface waters and sea-ice reduction, and the south-eastern Weddell Sea, generally representing a stable high-Antarctic marine environment that is not (yet) affected by climate change. We performed replicated experiments at 13 sites during two Polarstern expeditions in 2013 and 2016, using ex-situ sediment core incubations [2] to investigate benthic boundary fluxes (oxygen, silicic acid, nitrate, phosphate, ammonium) and their relation to macrofaunal and environmental parameters (Chl a, sea-ice extent. As an example, oxygen fluxes were generally higher in the north-western Weddell Sea (2 to 7 mmol $m^{-2}d^{-1}$) than in the south-eastern Weddell Sea (1 to 3 mmol $m^{-2}d^{-1}$), and this pattern is correlated with differences in sediment pigment concentration and ice-cover patterns. We discuss the importance of different ecosystem compartments in the biotic habitat (macrofaunal diversity, sediment pigments) for benthic boundary fluxes, clarifying their role for the marine biogeochemical function.

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Adaptation and shifting of the phytoplankton community in the Indian Ocean sector of the Southern Ocean

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The phytoplankton pigment indices were used to characterize the spatial succession of the community composition in the frontal regions of the subtropical front (STF), sub-Antarctic front (SAF), and polar front (PF) in the Indian Ocean sector of the Southern Ocean during austral summer 2013. Diagnostic indices revealed that the flagellates were dominant in STF (51%) and progressively declined toward SAF (39%) and PF (11%). Similarly, the prokaryotes were highest in STF (43%) and decreased to SAF (32%) and PF (28%). In contrast, the diatoms were gradually increased from STF (6%) to SAF (29%) and PF (61%). The variability of flagellates and diatoms from the STF to PF is attributed to the variability of photosynthetically available radiation (PAR), sea surface temperature (SST), and sea surface wind speed (SSW). During time series observation in austral summer (1998-2014) the diatoms contribution to the Chlorophyll *a* (Chl *a*) biomass was ≥80% at the PF. On the other hand, the chlorophytes to Chl *a* biomass showed a contrary distribution pattern ≥70% of at the STF and gradually decreased towards the PF, mainly attributed to the temperate adaptation. The maximum PAR was observed at the STF and it progressively decreased to the PF through the SAF. However the trend of diatoms increased at the STF and decreased at the SAF and the PF, conversely the trend of chlorophytes was increased at the STF, SAF and PF. The result shows the communities are shifting in the Indian Ocean sector of the Southern Ocean frontal ecosystem. The in-situ pigment indices were then compared to the NASA Ocean Biogeochemical model that shows the similar patterns of frontal community distribution except their magnitude. Similarly, the satellite retrieved phytoplankton biomass (Chl *a*) was checked for its consistency after comparing with the in-situ observations. The result suggests that the conjunctive analysis of in-situ, satellite, and model archive is suitable to study the impact of climate variability on the biogeochemical cycle and the structure of marine ecosystems.

The response of nitrifying communities to disturbance in the McMurdo Dry Valleys

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The McMurdo Dry Valleys (MDVs) are polar deserts containing the largest ice-free area of the Antarctic continent. This region is extremely dry, cold and oligotrophic where only simple biological communities are able to establish and persist[1]. These communities entail a fundamental role: they drive the biogeochemical cycling of Carbon (C) and Nitrogen (N) throughout the system. While the biogeographical patterns and composition of MDVs microbiome has been very well described, information concerning the functional attributes of these communities is still sparse. Nitrogen (N) is a crucial element for life, however its content in the MDVs soils can be highly variable and often below our detection limits. Major inputs of N into the MDVs are performed by N-fixating organisms, such as cyanobacteria and diazotrphs[2], however, after being fixed N needs to remain in the system in bio-available forms. Nitrification is an aerobic chemoautotrophic process that recycles and maintains N forms within the system. Specific environmental gradients influence the distribution and abundance of different groups of nitrifying organisms, which can in turn influence the nitrification process and N recycling in the MDVs[3].

We designed a manipulative experiment to test the effect of specific environmental disturbances specific environmental disturbances in the nitrification process using bulk soils from two physicochemical distinct Dry Valleys (Beacon and Miers Valleys). We applied five different treatments during 68 days, mimicking low and high concentrations of ammonia, high conductivity and high concentrations of organic matter and copper in the soils. Samples were incubated at -4°C and sampled after 24 hours, 28 days, and 68 days for analysis of 16S rDNA and rRNA amplicons and N-inorganic nutrients concentrations. The analysis of nitrifying communities based on 16S rDNA transcripts suggests that there is a higher potential for nitrification in Miers Valley soils than in Beacon soils. Copper and organic carbon augmentations were correlated with an increased proportion of ammonia-oxidizing archaea over ammonia-oxidizing bacteria. This could indicate the presence of functional resilience in archaeal ammonia oxidizing communities from the MDVs. In Beacon Valley soils, increased conductivity was correlated with an increase in the relative abundance of ammonia-oxidizing archaea, reflecting what has been previously described *in situ*[4] and indicates better adaptation of this group to stronger environmental stressors.

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Unravelling the responses of shallow soft sediment assemblages to rapid glacier retreat in an Antarctic fjord: assemblage structure and trophic interactions

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The West Antarctic Peninsula (WAP) is one of the fastest warming regions on Earth and it is characterized by the presence of a high number of fjords, known to be hotspots of marine biodiversity. Recent observations on the WAP have documented the rapid retreat of many tidewater glaciers whose related calving events lead to more frequent iceberg scouring in the shallow waters, coupled to increased fresh water input and higher sediment loads. All these disturbances are known to affect the marine assemblages in the shallow coastal regions. At the same time, ice retreat may free areas of the marine realm which can in time see the establishment of new local benthic assemblages via colonization and successional processes. We investigated three size classes of the soft sediment benthos (microbenthos, meiofauna and macrofauna) at three sites within Potter Cove (King George Island, WAP) which differed in the glacier retreat-related disturbance regimes and had different ice-free age status. We carried a two-fold investigation integrating assemblage structure observations (e.g. standing stocks) to the more functional aspects of the biota such as the trophic relationships within the assemblages. Our results revealed the presence of a patchy distribution of highly divergent benthic assemblages within a relatively small area (about 1 km2). The three benthic size classes appeared to respond in different ways to the disturbances, suggesting that the capacity to adapt and colonize habitats is dependent on both body size and specific life traits. In a similar fashion, the isotopic niches (an extrapolation of the ecological niche into the isotopic biplot space formed by the δ13C and δ15N natural signatures of the organisms) of the assemblages were locally shaped by the different degrees of glacier retreat-related disturbance. Wider isotopic niche widths were found at the site that had an intermediate ice-free age, whereas they were comparable for the older and the newly ice-free sites. In general ice scour and glacial impact appeared to play a two-fold role within the Cove: i) either stimulating trophic diversity by allowing continuous re-colonization of meiofaunal species or, ii) over time driving the benthic assemblages into a more compact trophic structure with increased connectedness and resource recycling. Finally, we predict that, under continued deglaciation, more diverse, but less patchy, benthic assemblages will become established in areas free from glacier-related disturbance, with a general trend leading to the homogenization of the diversity/trophic pool to be found at these shallow depths.

Snapshots of soft sediment benthos influenced by glacier retreat in an Antarctic fjord: assemblage structure, functioning and biogeochemical cycling

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The West Antarctic Peninsula (WAP) is one of the fastest warming regions on Earth. Recent observations on the WAP have documented the rapid retreat of many tidewater glaciers and the warming of mean air temperatures. This resulted in increased iceberg scouring, local snow and permafrost melting and related freshening events, and higher sediment loads to coastal waters. All these disturbances are known to affect the marine assemblages. At the same time, new ice-free areas are appearing from beneath the ice and represent new habitats for the establishment of benthic assemblages via colonization and succession processes. Potter Cove (King George Island) is a fjord at the northern tip of the WAP, and it is among one of the hot spots of biodiversity of the Antarctic shelf. Benthic biomasses in the cove are extremely high and comparable to those of temperate regions. The structure, functioning and carbon and nitrogen cycling potential of these communities was the focus of a three-fold study which started in 2010 and finished end of 2016. We investigated three size classes (microbenthos, meiofauna and macrofauna) of the soft sediment assemblage of Potter Cove at three sites which differed in the glacier retreat-related disturbance regimes and had different ice-free age status. We focused on (i) standing stocks, (ii) trophic relationships and (iii) in situ biogeochemical cycling, the latter by means of in situ deployment of benthic chambers during summer, winter under ice measurements, and spring. Soft sediment communities have been only poorly studied in the Antarctic. This widely comprehensive and interdisciplinary investigation is unique in its kind and the data and observations gathered during this research represent a baseline in the understanding of the role of Antarctic soft sediment communities in the local, regional and global marine system.

Physiological responses of the Antarctic diatom species *Chaetoceros debilis* to different concentrations of iron and manganese

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In many regions of the Southern Ocean, surface concentrations of the trace metals iron and manganese are very low. These elements are required for numerous metabolic pathways in phytoplankton cells and an insufficient supply can lead to reduced growth and alterations in photophysiology. However, little is known about the effects of manganese limitation alone on Antarctic phytoplankton species and its interaction with iron limitation. Therefore, this study focused on the effects of manganese and iron limitation alone as well as their combination on growth, elemental composition and photophysiology of the bloom-forming Antarctic diatom Chaetoceros debilis. Our experimental treatments consisted of four combinations of the two trace metals with two iron-limited treatments and two iron-rich treatments with and without manganese addition, respectively. Limitation by iron alone lowered carbon fixation and photochemical efficiency whereas manganese limitation alone resulted additionally in reduced growth. Highest values for growth, carbon fixation and photochemical efficiency were only observed after addition of both trace metals. These findings suggest that C. debilis is co-limited under low iron and manganese concentrations. Gaining more inside on the interplay of various trace metals and their potential co-limitation are valuable to better understand the spatial distribution of phytoplankton key species in the present and the future Southern Ocean.

Environment dependent distribution of glacier and subglacial microbial communities from King George Island (NW Antarctica)

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The impact of environmental geochemistry on the bacterial and fungal communities from glacier ice and subglacial streams was investigated on various locations of King George Island, NW Antarctica. Subglacial stream samples (42) and ice samples (63) from glacier transects of Barton Peninsula, Weaver Peninsula and Potter Cove areas were collected during ROICE field trips (February 2015 and February 2016) at King Sejong Station KOPRI (South Korea). Cultured microbiota was obtained by cultivation on 1 x R2B and 1:50 diluted media at 4°C and 15°C, leading to isolation of 102 bacterial colonies from glacier ice and 88 colonies from subglacial streams. Scanning Electron Microscopy analysis of both microbial communities and isolated colonies revealed the presence of cocci, bacilli and filamentous microorganisms, the dominant morphotype varying with the sample location. The identified bacterial strains based on 16S rRNA gene sequence belonged to Proteobacteria, Firmicutes, Bacteroidetes and Actinobacteria phyla, with a high represention of Gammaproteobacteria, the majority being homologous to cold environments bacteria.

Physicochemical and geochemical parameters of melted ice samples showed significantly lower pH, TDS and TOC values of glacier ice relative to those of the subglacier water, suggesting the enrichment of the latter one with geochemical compounds at the interface glacier/forefield with expected impact on its microcosm. All glacier ice samples were rather homogenous, belonging to Na-HCO3 type, with a higher Ca content in the vecinity of subglacier streams, while the stream water was more heterogenous, corresponding to Na-Ca-HCO3 and Na-Cl types. Trace elements analysis revealed the presence of high concentrations of Al, Fe and Sr, in particular in the subglacial stream water.

Genomic DNA was isolated in triplicate from all ice and stream samples, and the bacterial and fungal diversity determined by 16S rRNA and ITS2 partial gene sequencing, respectively, is currently under way using a MiSeq Illumina platform, to unravel the microbial community structure and correlation with the geochemistry of the glacier ice transects and subglacial streams from Kings George Island area, Maritime Antarctica.

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Assessing drivers of coastal phytoplankton productivity in northern Marguerite Bay, Antarctica

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The coastal ocean of the climatically-sensitive west Antarctic Peninsula is experiencing changes in the physical and (photo)chemical properties that strongly affect the phytoplankton. Consequently, a shift from diatoms, pivotal in the Antarctic food web, to more mobile and smaller flagellates has been observed. We employ a combination of field measurements and modeling to discern and quantify the influences of variability in physical, (photo)chemical and biological parameters on gross primary production (GPP) in northern Marguerite Bay. Field data of high-temporal resolution (November 2013 – March 2014) collected at a long-term monitoring site here were combined with estimates of GPP derived from photosynthesis-irradiance incubations and modeled using classical and Random Forest models (RF). Measurements of GPP varied greatly throughout the season, and averaged 1764.3 mg C m-2 d-1. A maximum of 6907.7 mg C m-2 d-1 was reached after the melting of sea ice and the likely release of diatoms concentrated therein. A non-assumptive RF with all possibly relevant parameters (MRFmax) showed that variability in GPP was best explained by light availability and chlorophyll a followed by physical (temperature, mixed layer depth and salinity) and chemical (phosphate, total nitrogen and silicate) water column properties. The predictive power from the relative abundances of diatoms, cryptophytes and haptophytes (as determined by pigment fingerprinting) to GPP was minimal. However, the variability in GPP due to changes in species composition was most likely underestimated due to the contrasting strategies of these phytoplankton groups as we observed significant negative relations between GPP and the relative abundance of flagellates groups. Our reduced model (MRFmin) showed how light availability, chlorophyll a and total nitrogen concentrations can be used to obtain the best estimate of GPP (R2 = 0.93). The resulting estimates from our classical and MRFmin models suggest summer GPP to have been between 214.5 g C m-2 and 176.1 g C m-2. Through the employment of a modeling technique without any assumptions apart from a representative sampling strategy, we showed and estimated how GPP in this climatically sensitive and changing region can best be predicted and described.

Carbon cycling potentials of Antarctic cryoconite hole microbial communities

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Cryoconite holes are pockets of nutrient-rich melt water and sediment on the glacier surface that are believed to be hot-spots of microbial diversity and activity, but are among the least studied ecosystems. Here, we describe the microbial communities associated with cryoconite ecosystems from three different regions of East Antarctica (Dronning Maud Land, Amery Ice Shelf and Larsemann Hills) and their potential role in carbon cycling in these ecosystems. Microbial cell numbers in the cryoconite hole samples ranged from 0.07 × 104 to 9.57 × 104 cells ml-1. Retrieved isolates (n=266) belonged to the phyla Proteobacteria, Bacteroidetes, Firmicutes, Actinobacteria and Basidiomycota. Isolated microbes represented 17 bacterial and 4 yeast genera. The cryoconite holes contained significant concentrations of organic carbon (25-500µgL-1), of which, 21–64% was found to be bio-available providing a source of carbon to resident microbial communities. Microcosm experiments show that the microbial communities have good potential to metabolise organic substrates such as lactate, acetate, formate, propionate, oxalate and succinate present in the cryoconite hole water. Amylase, lipase, protease, β-galactosidase, cellulase, and lignin modifying enzyme activities detected in a significant fraction (94%, n=264) of the isolated microbes support the above findings. Therefore, study of the microbial communities and activity within cryoconite hole ecosystems, is important for a better understanding of biogeochemical processes associated with supraglacial environments.

Marine microbial siderophores: Types, sources and role in carbon biogeochemistry

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Iron is one of the important trace elements required for growth of all marine organisms and plays an important role in ocean biogeochemical processes and global climate. Since bioavailability of iron as ferric iron is critical in photosynthetic pathway, marine surface primary production in open-ocean, especially in High Nutrient Low Chlorophyll (HNLC) regimes, is considered to be largely limited by dissolved iron concentrations. In order to sequester trace amounts of bioavailable iron, microbes including heterotrophic bacteria, fungi and some cyanobacteria produce organic ligands called Siderophores. In-vitro siderophore production has been reported from marine bacteria and few cyanobacteria, which can be intracellular as well as extracellular, either attached with cell surface or free from cell surface. These microbes use iron directly from siderophores while marine phytoplankton take up iron either from siderophore producing bacteria or by specialized mechanism like the ferrireductase pathway. Siderophore producing marine bacteria can increase the bioavilability of iron to phytoplankton population or can compete for bioavailable iron, thereby influencing phytoplankton growth. Moreover, reduction in bioavailability of iron can lead to bloom termination, thereby affecting the biological pump efficiency. In an increasingly changing marine environment (increased acidification), the bioavailability of iron to primary producers may get affected due to changes in dissolved iron concentrations and binding efficiency of siderophores. Coupled with altered phytoplankton composition, changes in iron affinity of siderophores may affect iron uptake by phytoplankton, food-web dynamics and associated biogeochemical processes. Nevertheless, very little is known about the role of siderophores and siderophore producing bacteria in phytoplankton growth and primary production. This poster gives an overview of our present knowledge on marine siderophores, its distribution and siderophore producing bacteria in marine environment, discusses its role in bacteria-phytoplankton interactions and its impact on marine carbon biogeochemical process.

Deep chlorophyll maximum and primary productivity in Indian Ocean sector of the Southern Ocean: Case study in the Subtropical and Polar Front during austral summer 2011

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To understand the implications of deep chlorophyll maximum (DCM) on primary productivity (PP), 3-hourly observations (over 72h) were carried out at the Polar Front (PF) and the Subtropical Front (STF) of the Indian Ocean sector of Southern Ocean during the austral summer (February) 2011. Pronounced vertical variations in hydrographic parameters (temperature, salinity, density, dissolved oxygen) were observed between the fronts, whereas temporal (diurnal) variations of these parameters within the fronts were minimal during the study period. At the PF, a well-defined temperature minimum layer (TML), which is the winter residue of Antarctic Surface Water (AASW), was observed between 50 and 320m. The DCM observed at the PF (~75m) was more prominent than that at the STF and coincided with the upper boundary of the TML. The elevated chlorophyll a (Chl a) concentration in DCM is believed to result from the proliferation of the low-light adapted phytoplankton (shade flora). Due to the presence of a strong DCM the average column-integrated Chl a was nearly two times higher at the PF than at the STF yielding ~1.4 times higher column integrated PP (IPP) at the PF (211mgC m-2 d-1) compared to the STF (152mgC m-2 d-1). Higher Chl a and productivity at the PF was attributed to the dominance of diatoms as indicated from diagnostic pigment analysis by high performance liquid chromatography (HPLC). Owing to their higher sinking rate, the diatoms with sequestered CO2, would generate substantial export production/flux, thereby making the PF region as a potential sink for atmospheric CO2.

Could the break-down of DMS-mediated feedbacks lead to an ecological regime shift in the Southern Ocean?

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Dimethyl sulphide (DMS) plays an important role in ocean biogeochemistry and the climate system. It links the oceanic and atmospheric components of the global sulphur cycle, drives ocean-climate feedbacks (Charlson et al, 1987) and may also influence pelagic ecosystem structure and function (Savoca & Nevitt, 2014). It is produced by some phytoplankton species in response to oxidative stress and also to grazing. Many higher predators in the Southern Ocean have a demonstrated attraction to DMS, and use it to navigate to productive patches in the ocean (eg: Nevitt et al., 1995, Wright et al., 2011). This enhances predator ability to locate their zooplankton prey, and thereby releases phytoplankton from a major source of mortality. By producing DMS, phytoplankton may therefore promote their own blooms which in turn could result in more energy entering the food chain.

Despite the potential importance of DMS in structuring pelagic ecosystems in the Southern Ocean, uncertainties remain as to feedback mechanisms and their importance in maintaining ecosystem function and stability. This is because the strength of non-trophic interactions is difficult to measure in the field, and difficult to capture in food web models.

We have applied a network modelling approach to investigate the importance of DMS-mediated feedbacks in structuring pelagic ecosystems, and for the stability of the ecosystem as a whole. In particular, this model can help inform our understanding of the likelihood that a break-down of DMS-mediated interactions would result in an ecological regime shift in Southern Ocean pelagic ecosystems We simulated climate change impacts on a suite of model structures to test the sensitivity of predicted outcomes to uncertainties in feedback structure.

In this presentation we report on the importance of DMS-mediated interactions in stabilising Southern Ocean ecosystems, and the likelihood that a regime shift will occur as a result of a breakdown of these feedbacks. We will also discuss interactions of critical importance for the stability of the system with the aim of directing future data collection.

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Seasonal concentrations of dimethylsulphide (DMS), dimethylsulphoniopropionate (DMSP) and dimethylsulphoxide (DMSO) in relation to algal seasonal succession in Ryder Bay, Antarctica

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Changes in temperature and weather patterns are reducing the sea ice extent along the West Antarctic Peninsula, and subsequently the nutrient availability. These changes can significantly alter the growth patterns of marine microbial communities growing within sea ice and the water column below. These communities have been identified as significant producers of organic sulphur compounds, likely as an osmoprotectant within the often rapidly changing salinity, temperature and nutrient environment of sea ice: changes to the sea-ice community can subsequently affect the cycling of organic sulphur within the microbial food web. Through reduced production of the volatile organic sulphur compound dimethylsulphide (DMS) by these algae, the flux of sulphur to the atmosphere will also be affected. This study presents the results from a five-year time-series (2012-2017) studying seawater concentrations of DMS, dimethylsulphoniopropionate (DMSP) and dimethylsulphoxide (DMSO) along with the phytoplankton community dynamics alongside the Rothera oceanographic and biological Time Series (RaTS) measurements by the British Antarctic Survey, and assessed the changes in terms of community composition and physico-chemical properties of the region.

During each season, a number of significant bloom events were detected between November to April, with Chl-a reaching concentrations over 25µg L-1. Assessment of phytoplankton community structure using CHEMTAX analysis showed succession of the community: from cryptophytes, prasinophytes and Phaeocystis haptophytes in the early summer, to large diatom species dominating later in the season as the water column increasingly stratified. Concentrations of particulate DMSP were often correlated to Chl-a, and showed concentrations at times exceeding 300nmol L-1 when haptophytes and dinoflagellates were abundant; DMS and DMSO concentrations were regularly identified as being uncoupled to DMSP and Chl-a, with concentrations exceeding 50nmol L-1. High concentrations of these compounds were, however, related to melting sea ice, and were associated with release from the ice-algal community. As the first DMS results measured as part of the RaTS dataset, these measurements give a baseline on which to establish the relationships between DMS, primary production and sea ice melt, which can be expanded in future southern summer seasons.

Monitoring the prokaryotic and viral abundances and the microbial activities in two coastal sites of Terra Nova Bay (Antarctica)

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Studies in coastal areas of Terra Nova Bay (TNB) highlighted the sudden variability of planktonic biomass with ecological implications on the heterotrophic microbial community and the fate of the organic substance on a seasonal scale.

With the aim to monitoring the evolution of the prokaryotic and viral abundance and the hydrolysis of organic matter, in the frame of the CEFA project (Italian PNRA) two fixed stations (Faranda Field - FF; Michaud Pier - MP), were repeatedly sampled.

In FF, a sea ice covered station, the prokaryotic and viral abundances were monitored from the 9th of November 2015 to the 19th of January 2016 with Image Analysis (IA) and Cytofluorimetry (FC). Starting from the 4th of January 2016 the potential enzymatic activities on proteins, carbohydrates and organic phosphates were determined. Moreover, the MP station was monitored from the 12th of January to the 8th of February 2016.

The prokaryotic abundance in FF station varied in the ranges 0.73-3.38 and 0.26-1.85cellsx105ml-1 by IA and FC, respectively. Cells with high nucleic acid content (HNA) accounted from 32 to 84% of the total FC cells. Virus like particles by FC ranged between 8.08 and 22.3VPLx105ml-1 and V1 group accounted for the 64-94% of the total.

The main activity in all samples taken from FF station (under ice) was the phosphatase with the highest values at the beginning of the sampling and showing a decreasing trend when the station was defrosted. This enzyme can be produced in surface water by both bacteria and phytoplankton. The glucosidase activity, showed lower values than phosphatase with a similar trend. The peptidase activities instead increased in the sampling at the end of January in correspondence of the ice absence.

In the MP station, the prokaryotic abundance varied in the ranges 1.00-12.3 and 1.03-4.07cellsx105ml-1 by IA and FC, respectively. Cells with high nucleic acid content (HNA) accounted from 47 to 84% of the total FC cells. Virus like particles by FC resulted to be below the detection limits. High variability of enzymatic activities was observed with time in this station. Generally phosphatase prevailed on other activities with the maximum values on the 13rd and 22nd of January; thereafter it decreased with the ice melting. β-glucosidase, showed peaks on January 16th and from 24th to 29th of January (bay covered by ice), then it decreased. The amino-peptidase showed variable values with peaks on the 12th and 17th of January.

Theme 3
New insights through multi-disciplinary research

Where does the methane entrapped in Antarctic sea ice come from?

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Methane (CH4) atmospheric concentrations have increased by a factor of 2.5 since the beginning of the Industrial Era, mainly because of anthropogenic activities. However, between 1999 and 2006, CH4 growth rate declined to a near-zero level, suggesting that an equilibrium had been reached. But, from 2007 on, atmospheric concentrations underwent a renewed growth, implying major ongoing changes in the CH4 global budget (Nisbet et al., 2016). These changes challenge our understanding on the contribution of existing sources, and in particular natural sources.

Sea ice can strongly affect emissions of CH4 from the ocean, but the precise mechanisms are not well understood. Sea ice has long been considered as an inert and impermeable barrier, but recent studies have highlighted the existence of gas fluxes at the atmosphere-sea ice and sea ice-seawater interfaces (Kort et al., 2012; He et al., 2013; Zhou et al., 2014; Sapart et al., 2016). However, these fluxes are to date poorly understood and quantified. To improve future climate projections, we aim to investigate the control exerted by sea ice on the CH4 atmospheric budget.

To unravel the impacts of the Antarctic sea ice physical environment on biogeochemical cycles, the AWECS (Antarctic Winter Ecosystem Climate Study) expedition was conducted between the 8th of June and the 12th of August 2013 in the Weddell Sea. Such an expedition provides a rare opportunity to obtain insights on the behaviour of sea ice during winter. Ice cores specifically dedicated to the investigation of gas dynamics were collected at ten different stations.

In order to determine CH4 formation and removal pathways in sea ice, we used concentration and stable isotope analysis, which can help to distinguish different processes. Here, we present and discuss our first results of the isotopic composition of CH4 ($\delta^{13}C$ and δD) on sea ice cores from the Weddell Sea and the Ross Ice Shelf. This new dataset will help to determine the origin of the CH4 entrapped in Antarctic sea ice and its potential impact on the current and future atmospheric CH4 budget.

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N_2O production and cycling within Antarctic sea ice

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Nitrous oxide (N2O) is a potent greenhouse gas that has a lifetime of 114 years in the atmosphere and a global warming potential 300 time higher than that of CO2. However there are still large uncertainties and gaps in the understanding of the N2O cycle in polar oceans and particularly associated to sea ice. Sources and sinks of N2O are therefore poorly quantified. To date, only one study by Randall et al. 2012 present N2O measurements in sea ice. They pointed out that sea ice formation and melt has the potential to generate sea-air or air-sea fluxes of N2O, respectively. The main processes (except the transport processes) involved in the N2O cycle within the aquatic environment are nitrification and denitrification. Recent observations of significant nitrification in Antarctic sea ice shed a new light on nitrogen cycle within sea ice. It has been suggested that nitrification supplies up to 70% of nitrate assimilated within Antarctic spring sea ice. Corollary, production of N2O, a by-product of nitrification, can potentially be significant. Our recent studies in Antarctic land fast ice in McMurdo Sound, confirmed this suggestion, where N2O release to the atmosphere was estimated to reach 4µmol.m-2.yr-1. But this assessment is probably an underestimation since it only accounts for dissolved N2O while a significant amount of N2O is likely to occur in the gaseous form like N2, O2 and Ar. We will then address the new tools to measure the bulk concentration of N2O (dissolved and gaseous) in sea ice, and the production of N2O by sympagic microorganisms - what process is dominant and how much N2O is produced - based on the first time series of N2O measurement in sea ice. The determination of the isotopic composition of N2O using cavity enhanced laser absorption spectroscopy technique (Off-axis ICOS) will allow us to determine the origin of these processes.

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Under-shelf ice sampling by ROV reveals specimens of ice-associated crustaceans

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Images taken by seal-borne cameras at the Drescher Inlet (Riiser-Larsen Ice Shelf) in 2004 led to the discovery of an unknown cryo-benthic community being attached head-down to the underside of the floating ice shelf at depths of around 130-150m (Watanabe et al. 2006). Resolution and exposure of the images did not allow distinct identification of species considered as likely isopods or cnidarians, and no information could be gained on the composition, size, dimension and density of the faunal aggregation.

In order to re-assess the earlier findings, an Ocean Modules V8Sii Remotely Operated Vehicle (ROV) was launched through an artificial ice hole in the vicinity of the shelf ice cliff. The ROV provided high resolution and scalable video footage of the shelf-ice associated fauna. A custom-made ROV-mounted dredge was used to collect samples for further identification and DNA-analysis.

A total of thirty specimens (15 adults, 15 juveniles) were sampled between 60 and 80m water depth. Additionally, 2 hours of high resolution digital video footage could be taken during two ROV transects at depths between 80m and 100m (along the vertical shelf ice wall and beneath the floating shelf ice). According to our standard ROV procedure, concurrent hydrographic (depth, temperature, salinity, pH, fluorescence, and oxygen) and three-dimensional dive data (depth, roll, pitch, orientation, and position) were recorded.

Acoustic distance measurements and lens geometry of parallax free optics allowed to determine the strip width (0.5 – 2.0m) and cumulative length (122m) of the transect covering a total area of 133 square meters within the footage.

The continuous scenes of video recordings were converted into single frame sequences and the number of individuals on the images was determined by visual counts. Tagging each individual with a marker and automatic registration of number and coordinates, prevented double counts and allowed for further distribution analyses. In total, 3,280 adults as well as 10,368 juveniles could be identified, leading to initial abundance estimates of 25 adults and 190 juveniles per square meter.
The video footage shows large numbers of probably one single species of isopods. Significant size differences and clustering of the dense aggregations imply a specific association of adults and juvenile life stages, and the successful retrieval of samples provided material for further taxonomic and genetic investigations.

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New insights in Antarctic fast ice biogeochemistry, the role of biofilm

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Antarctic fast ice is known for its high biomass levels at the ocean/ice interface where particulate organic carbon (POC) concentrations can easily exceed 2mmol C l-1 during spring bloom. Coinciding with these high POC levels, high concentrations of nitrate and phosphate were observed during three different fieldwork campaigns in the East Antarctic. At Davis Station, Dumont D'Urville Station and Scott Base, bulk concentrations for nitrate were up to 10-times higher than observed in the underlying seawater suggesting a strong remineralisation and nitrification in the ice. However a long time series at Scott Base showed that the accumulation of inorganic nutrients in the bottom ice started early in the growth season while biomass was still growing. This goes against the classic view of nutrients being consumed during the growth season and regenerated after the height of the bloom. Regardless of the high nitrate levels available in the ice, increasing total nitrogen concentrations also suggest still more nitrogen from the underlying seawater was brought into the ice. A qualitative NPZD-model was elaborated and used to understand these observations. Implementation of a second nutrient pool proved essential in successfully modelling and reproducing the field observations. A biofilm could act as a water retaining barrier and result in chemical gradients in the brine channels and create microenvironments. It can also explain other interesting observations for carbon and phosphate that will be discussed in more detail during the conference.

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Wintertime DMSP production in Antarctic landfast ice

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Ryder Bay is situated at the southern end of the Western Antarctic Peninsula (WAP) – the fastest warming oceanic region on earth – with a recorded increase in winter temperature of 6°C since 1950. Sea ice cover at the WAP shows a general declining trend. The consequences of this decline for biogeochemical processes are poorly understood.

The marginal sea-ice zone is one of largest sources of the climate-active gas dimethylsulphide (DMS). DMS is produced from the enzymatic cleavage of dimethylsulphoniopropionate (DMSP), which is an osmolyte and cryoprotectant in ice algae. The release of DMS occurs mainly during springtime when the ice melts, but may also happen during brine drainage and when gap-layer communities form and mix with melting snow. How the different sea-ice communities and their associated DMSP content build-up and break-down over winter and spring is largely unknown due to a lack of data.

Here we present the development of DMSP in sea ice of Ryder Bay, during two winter seasons: 2014 and 2016. Ice cores were taken as soon as ice was accessible and continued until spring. Over winter only total and dissolved DMS(P) was taken, together with HPLC pigments for algal biomass analyses and classification. In addition to standard bottom sections, dedicated ice-core sections that represented the different ice types were sampled. In spring, ice cores were fully analyzed for DMS, DMSP and DMSO. In addition, stable isotopes were used to calculate conversion rates within the sulphur cycle. Bottom-ice concentrations of DMSP reached values between 2 and 10µM, but also communities at the snow-ice interface produced µM-levels of DMSP. In layers with high biomass, especially DMSP was quickly consumed of which approximately 20% ended up in DMS. Other important pathways were uptake by organisms and demethylation.

Food web in the marginal ice zone: material flow from sea ice through to myctophid fish

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The seasonal prevalence of the sea ice zone is a critical element in the Southern Ocean ecosystem structure and dynamics. Sea ice formed in coastal polynyas in autumn and winter is transported northward and covers a vast area of the Southern Ocean. This ice contains a large variety of sea ice biota (SIB), such as ice algae, protozoans, and crustacean larvae. The SIB is released as the sea ice melts from the ice edge in spring and summer. Although a flood of SIB biomass is released into the water column, there is little information on the pathway and dynamics of the SIB released into the Southern Ocean. The sea ice changes that occur with climate change should affect the Southern Ocean ecosystem via this pathway. We have been investigating the flow of materials derived from SIB through to the Southern Ocean ecosystem after its release into the water column. In a series of studies, we found the nursery grounds of the Antarctic myctophid fish Electrona antarctica, which is an important component of the oceanic food web, in the waters influenced by sea ice. This paper introduces a study of 1) the dynamics of SIB inferred from the flora of floating sea ice (ice algae) and the water column at the ice edge and 2) detritus containing diatoms found in the stomachs of E. antarctica larvae. The origin of the diatoms is discussed. A comparison of the numbers of algal cells in sea ice and the water column indicated that more than 90% of the cells of the dominant diatom species were removed from the surface mixed layer. Most of the algal cells were thought to sink into deeper waters or to be grazed by zooplankton close to the sea ice. Detritus served as a food item for early stage larvae of E. antarctica, and some of the diatom species in the detritus were usually dominant in the SIB assemblage, suggesting that the E. antarctica larvae feed on SIB indirectly, eating the faecal pellets of zooplankton or sinking aggregates. Finally we will also introduce our current observations in seasonally sea ice zone in austral summer, 2016-2017.

Antarctic sea ice trophic status

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The sea ice ecosystem is characterized by steep gradients in temperature, salinity, light and nutrient availability. Despite these challenging environmental conditions, sea ice provides a dynamic habitat for diverse communities of microorganisms. These communities include a wide variety of organisms from different taxonomic groups such as algae, bacteria, heterotrophic protists, fungi as well as viruses. In the frame of the YROSIAE project (Year-Round survey of Ocean-Sea-Ice-Atmosphere Exchanges), carried out at Cape Evans in McMurdo Sound (Antarctica) from Nov. 2011 to Dec. 2012, ice cores, seawater, and brine material were collected at regular time intervals. Physical properties (salinity, temperature, texture) and biogeochemical parameters (pCO2, dissolved inorganic carbon, total alkalinity, chlorophyll-a, macro-nutrients) were analysed. We used dissolved inorganic carbon (DIC) and chlorophyll-a (chl-a) as proxies of net community production and autotrophic biomass, respectively. A high spatial and temporal variability in ice algal biomass and DIC were observed. From spring, very high chl-a concentrations ($>2400 \mu g.L^{-1}$) were observed at the bottom of the ice, a common feature of land fast ice in the McMurdo Sound. This suggests high primary production. Strikingly, at the same time, nutrients at the bottom of the ice increased significantly suggesting high remineralisation. In the middle of the ice column, evolution of DIC was marked by a succession of autotrophic and heterotrophic phases. The overall increase of DIC suggests that the ice interior was rather heterotroph. Such sea ice system should expel CO2. Yet, strong under-saturation in CO2 and DIC depletion appeared at the ice surface, suggesting that sea ice was taking up CO2 from the atmosphere. On the whole, land fast sea ice in McMurdo Sound appears as a puzzling ecosystem. It is able to support elevated growth of autotrophic organisms at the bottom, in parallel to high remineralization, while the top of the ice appears to be rather heterotrophic but still able to pump CO2 from the atmosphere.

Seasonal development of microalgal composition and production in Antarctic landfast ice

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Microalgal composition and production was studied in sea ice in Ryder Bay, Antarctica. Ryder Bay is situated at the southern end of the Western Antarctic Peninsula (WAP); the fastest warming oceanic region on earth, with a recorded increase in winter temperature of 6 °C since 1950. Coinciding with the warming of shelf water the amount of sea ice that is formed over winter shows a general declining trend. The consequences of this decline for biogeochemical processes are poorly understood.

Sea ice was sampled over the period of ice formation in August until ice melt in December 2014. Microalgal composition was studied by means of their pigment signature and microscopy; production capacity was studied by fluorescence analyses. Over the course of 5 months, biomass increased in the bottom layers and reached a maximum concentration of more than 700 µg Chl.a l-1 in December. Early in the season, a mixed algal community inhabited the bottom layer. From November onwards, diatoms dominated the bottom community, with Nitzschia, Fragillariopsis and Berkeley sp. as the main species. The maximum electron transfer rate (ETR) as determined by PAM-fluorescence at the bottom gradually increased over spring from 3 to 30. At the same time, the slope of ETR versus irradiance alfa increased. The value for light saturation (Ik) hardly changed and measured ca. 150µmol photons m-2 s-1. Data from all layers will be presented and the potential consequences of sea-ice decline for biogeochemistry at the WAP will be discussed.

Comparison between lipid and fatty acid composition of the sea ice and water column in early spring in East Antarctica with implications to krill condition

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To understand the sea ice community complex, we need to also understand the availability of key and essential nutrients to consumers. Baseline biochemical data are therefore required in order to gauge any impact the reduction of sea ice will have on the sea ice community. Here we compare lipid class, fatty acid and sterol content and composition of sea ice and water column samples collected during early spring in East Antarctica during the Sea Ice Physics and Ecosystem eXperiments (SIPEX II 2012) expedition (110-130E). The availability of key essential omega-3 long-chain (≥C20) polyunsaturated fatty acids, including - 20:5□3, eicosapentaenoic acid, EPA and 22:6□□3, docosahexaenoic acid, DHA- the major constituents of cell membranes, were found to be severely limited during late winter and early spring, particularly in the under ice water samples. The ramifications for sea ice obligate organisms such as larval krill are discussed.

How critical is sea ice for the overwinter survival of Antarctic krill?

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Sea ice is commonly thought to be critical for the overwinter survival of Antarctic krill (Euphausia superba). This view is predicated on the idea that sea ice provides nutritional resources during periods of limited daylight and reduced phytoplankton production, but we collected data during four austral winters that do not fit with this hypothesis. We tested the hypothesis that nutritional condition of post-larval and larval krill would fluctuate with environmental conditions indexed by sea-ice coverage. We analyzed stable isotopes, lipid content, and fatty acid profiles to indirectly examine the diets of post-larval and larval krill collected over four consecutive winters (2013 – 2016) with varying environmental conditions in the northern Antarctic Peninsula (nAP). Post-larval and larval krill appeared to employ distinct feeding strategies, as inferred by stable isotopes (δ13C and δ15N) and fatty acid profiles. Relative trophic positions and diets of post-larval krill were consistent among years despite inter-annual differences in sea-ice coverage and water-column chlorophyll-a, while relative trophic positions and diets of larval krill showed more inter-annual variability. Although post-larval diets were consistent, lipid content fluctuated among years, while larval krill lipid content was relatively more stable among years despite a more variable diet. Fatty acid biomarkers used to infer degrees of carnivory and herbivory also indicated more inter-annual variability in the diets of larvae. Inter-annual changes in relative trophic position, lipid content, and feeding strategies were not related to annual changes in sea-ice coverage or chlorophyll-a. The lack of meaningful relationships among sea ice, chlorophyll, and diet for both post-larval and larval krill suggest that these environmental factors may not be as influential on krill winter feeding behavior and body condition in the nAP as previous studies have implied. Because inferred levels of carnivory and herbivory each year were not driven by sea-ice coverage, we suggest that nutritional resources derived from ice may not necessarily confer a nutritional advantage on krill over those derived from open water.

Acid-base physiology of the Antarctic sea urchin *Sterechinus neumayeri*: differences according to environmental conditions?

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Increasing atmospheric carbon dioxide concentration alters the chemistry of the oceans towards more acidic conditions. Polar oceans are particularly affected due to their low temperature, low carbonate content and mixing patterns, for instance upwellings. Tolerance to ocean acidification (OA) in metazoans is first linked to acid–base regulation capacities of the extracellular fluids. It has also been suggested to depend on the environmental history of the organism. Organisms living in variable environments would be more adapted or acclimated to changes in sea water pH. To address these questions, we investigated the response of the Antarctic regular euechinoid Sterechinus neumayeri from shallow populations in Adélie Land (Ile des Pétrels) and the Antarctic Peninsula (King George Island), the former region having stable conditions while the second is showing a fast rate of warming due to global change and seasonnally variable conditions. The sea urchins were submitted to a 14-days acidification experiment carried out, respectively, in Dumont d'Urville and Carlini bases in the frame of the vERSO BELSPO and REVOLTA IPEV projects. Two (8.0, 7.7) or three (8.0, 7.7, 7.4) seawater pH-T were tested. The pH, total alkalinity and dissolved inorganic carbon of the coelomic fluid, the main extracellular compartment, were measured, allowing to characterize the acid-base status and its response to a short term acidification.

Acid-base physiology of Antarctic and Sub-antarctic sea urchins and their resilience to ocean acidification

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Increasing atmospheric carbon dioxide concentration alters the chemistry of the oceans towards more acidic conditions. Polar oceans are particularly affected due to their low temperature, low carbonate content and mixing patterns, for instance upwellings. Echinodermata were hypothesized to be at risk due to their high-magnesium calcite skeleton. However, tolerance to ocean acidification (OA) in metazoans is first linked to acid–base regulation capacities of the extracellular fluids. No information on this was available for Antarctic echinoderms and inference from temperate and tropical studies needed support. We investigated the acid–base status of 9 species of sea urchins (3 cidaroids, 2 regular euechinoids and 5 irregular brooding euechinoids) collected in the frame of the ANTXXIX/3 Polarstern campaign, the vERSO BELSPO project and the REVOLTA and PROTEKER IPEV projects. It appears that Antarctic regular euechinoids are equipped with similar acid–base regulation systems as tropical and temperate regular euechinoids and are able to compensate their extracellular pH (pHe) when facing OA by increasing the extracellular bicarbonate concentration. Cidaroids have an acid–base status similar to that of tropical cidaroids, characterized by very low pHe. Therefore, Antarctic cidaroids will most probably not be affected by decreasing seawater pH, the pH drop linked to OA being negligible in comparison with their naturally low pHe. Irregular euechinoids regulate their pHe when facing OA through an unknown mechanism. The pH of sea water in the brooding chambers depends on the pH of the surrounding sea water and is further reduced in presence of calcified juveniles. This suggests that these juveniles will endure worse acidification conditions and might be possibly at risk. Combining these results with the resilience of Antarctic euechinoid larvae suggests that most of these organisms might not be the expected victims of ocean acidification although the impact on brooded juveniles of irregular euechinoids should be further investigated

Is the Sub-antarctic sea urchin *Abatus cordatus* threatened by ocean acidification?

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Increasing atmospheric carbon dioxide concentration alters the chemistry of the oceans towards more acidic conditions. Polar oceans are particularly affected due to their low temperature, low carbonate content and mixing patterns, for instance upwellings. Brooding Echinodermata were hypothesized to be at risk due to their high-magnesium calcite skeleton and brooding habits. We investigated the acid–base status of the Sub-antarctic irregular brooding euechinoid *Abatus cordatus* during a 13-days acidification experiment carried out in Port-aux-Français, Kerguelen Islands, in the frame of the vERSO BELSPO and PROTEKER IPEV projects. Four seawater pH-T were tested (8.3, 8.0, 7.7, 7.4) At the time scale of the experiment, *A.cordatus* regulates the pH of the coelomic fluid, the main extracellular compartment but this is not linked to an accumulation of bicarbonate as it is the case in regular euechinoids. The pH of sea water in the brooding chambers depends on the pH of the surrounding sea water but is lower than the latter by 0.3 to 0.6 pH units and it is further reduced in presence of calcified juveniles. This suggests that adult *A.cordatus* might be resilient to near-future ocean acidification. However juveniles will endure worse acidification conditions and might be possibly at risk. The impact on brooded juveniles of irregular euechinoids should be further investigated.

Effects of ocean acidification on the physiology and biochemistry of adult Antarctic krill

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Ocean acidification is caused by sequestration of atmospheric CO_2 into ocean surface waters, a process that increases ocean pCO_2 and decreases ocean pH. Present day levels of atmospheric CO_2 have reached 400ppm, and are predicted to rise as high as 2000ppm by the year 2300, equating to a decrease in ocean pH of up to 0.7 pH units. Organisms from Polar regions are particularly vulnerable to ocean acidification, due to the increased rate of CO_2 sequestration in colder seawater. Antarctic krill were reared for 11 months in a flow-through seawater system at the Australian Antarctic Division's Krill Aquarium in Tasmania, under five pCO_2 levels (400, 1000, 1500, 2000 and 5000ppm,). We examined the effects of decreased seawater pH on the lipid and fatty acid composition, respiration rate, growth, survival, intermoult period, haemolymph pH and maturity of adult Antarctic krill. Krill showed resilience in the measured physiological and biochemical parameters to the full range of elevated pCO_2

levels, although survival rates were decreased in the highest pCO_2 treatment (5000ppm, pH7.1). Our research suggests that the adult life stages of Antarctic krill have the capacity to tolerate levels of near-future acidification, when elevated pCO_2 is assessed as a single stressor. This research may also aid krill fisheries in assessing whether the composition of krill lipids and fatty acids may be altered in an acidified Southern Ocean.

Physiological response of *Phaeocystis antarctica* (Prymnesiophyceae) to iron limitation and ocean acidification

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In 30-50% of the world's oceans consist of high nutrient low chlorophyll regions, where, rather than macronutrients, the scarcity of certain trace metals (TM) such as iron (Fe) govern primary production and/or plankton species composition. The steadily rising atmospheric CO_2 concentrations will disproportionally affect Southern Ocean ecosystems. While discrete effects of Fe limitation or ocean acidification (OA) on phytoplankton physiology have been investigated, few studies have examined their interactive effects and there is debate on how OA will affect Fe availability. Here we present a laboratory experiment, in which the ecological important SO species *Phaeocystis antarctica* was grown in low TM Antarctic water (Fe<0.64 nM), with (+Fe, 4 nM) and without (-Fe) the addition of Fe, under a pCO_2 of 35 and 900 Pa. -Fe yielded a 10% reduction of cell diameter and decreases in cellular growth rate (35%) and carbon contents (50%), resulting in half of the particular organic carbon (POC) production compared to cultures grown under +Fe conditions. Interestingly, while the cellular TM quotas were expected and found to be significantly lower in -Fe cells, this trend was also observed for other important TMs. Conversely, OA did not result in smaller cells, and while growth rates increased ~10% in both the +Fe and -Fe cultures a 10% decrease in POC resulted in no net change in POC production. With the exception of zinc, OA also resulted in a decrease of all cellular TMs. OA did not significantly affect Fe chemistry or concentrations of naturally occurring ligands and humic acid-like (HA-like) substances. Rather *P. antarctica* was found to produce HA-like substances, resulting in an OA-dependent increase in -Fe cultures but a decline in the +Fe cultures. These results demonstrate that effects due to Fe limitation are generally more prevalent than those due to OA and to a greater physiological extent. Instead of OA changing Fe chemistry and thus impacting the biology, the physiological response of *P. antarctica* to OA changes the chemistry. This may provide a competitive edge for Fe acquisition over other phytoplankton and thus shape species succession in Fe limited regions. Finally, this study addresses the complicated nature of TM limitation and OA interactions, acclimations strategies of *P. antarctica* to both, and highlights the importance of such species specific, mechanistic investigations in order to model the intricate, multiparameter effects of climate change.

antFOCE (Antarctic Free Ocean CO2 Enrichment) – An ocean acidification experiment under sea ice

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Free ocean CO_2 enrichment systems (FOCE) were developed to address the need for research on community level responses to ocean acidification in natural habitats over periods of weeks to months. The antFOCE project was the first polar FOCE experiment and was run at Casey Station, East Antarctica, over 12 weeks in early 2015.

The experimental design consisted of 2 acidified chambers (offset at 0.4 pH below ambient, to approximate a business-as-usual CO_2 emissions scenario), 2 control chambers (at ambient pH) and 2 open plots (no chamber). Chambers were 2 m long x 0.5 X 0.5 m and were deployed on sediments in 14 m of water under 2.6 m of sea ice. The chambers were enclosed but drew in surrounding water, which was mixed with CO_2 enriched seawater in a controlled process allowing pH equilibrium, but also natural variation. Seawater flowed unidirectionally through the chambers, exposing the benthic communities within to lower pH but otherwise unmodified seawater. The aims included: 1) Characterising physical and chemical environmental changes in water and sediments; 2) Examining community responses including sediment bacteria, microphytobenthos, meiofauna, and macrofauna, and hard substrata biofilms and macrofaunal communities; 3) Examining the response of key ecosystem processes including bioturbation and sediment nitrification; 4) Examining the response of some calcifying species such as bryozoans and spirorbid polychaetes.

The deployment and running of this highly complex experiment in such an extreme environment presented many challenges which required innovative solutions to overcome. The system performed to its specifications, maintaining an approximate 0.4 pH offset over an 8 week period. There were occasional power failures and other technical difficulties during which the pH reverted to background for short intervals during the experiment, increasing the variability of the pH treatment. The aragonite saturation state (Ω_{arag}) fluctuated between 0.7 and 0.8 but also reverted to background (approx 1.7) during system outages. An overview of the experiment, its deployment and some results will be presented, including effects of lower pH on the photosynthetic activity of Antarctic microphytobenthos, on microbial communities, on sediment meiofaunal and macrofaunal communities, effects on bioturbation and other findings. While it is too early to gain a full understanding of the effects of a 0.4 pH reduction, results indicate a potentially large range of changes in this Antarctic ecosystem from ocean acidification.

Biodiversity at the shallow waters of Deception Island, an active Antarctic volcano

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Deception Island, located at the southernmost end of the South Shetland Archipelago, is an active volcano with a flooded caldera, named Port Foster's bay. After the last eruption in 1970, notable benthic recolonization was reported within this Bay (Retamal et al. 1982, Barnes et al. 2008), being echinoderms the dominant epifauna (the ophiuroid *Ophionotus victoriae*, the echinoid *Sterechinus neumayeri*, and the asteroid *Odontaster validus*; Angulo-Preckler et al. 2017), together with many detritivore species. Here, we describe the biodiversity of shallow subtidal areas of 'Foster's Bay (down to 25 m), including algal and faunal communities, from our studies at the island during the last 8 years. Due to the different sampling efforts done among localities and cruises, species were qualitatively scored as presence/absence. A total of ca. 120 species belonging to 16 phyla were found, many of them never cited for the island before. Our data also show a richer species composition than previously reported for some particular groups, such as algae and porifera, with a dramatic increase in overall biodiversity towards the entrance of the bay. We suggest that recolonization from external waters may not be the only reason for this pattern. In fact, the intense sediment flux rates and substrate instability that affect most areas within Port Foster's Bay are considered determinant disturbances conditioning the composition of benthic community assemblages. These processes are likely favoring the flourishment of detritivore communities at the most internal locations of the bay, while filter-feeding communities are only found next to the entrance, where rocky areas exist. This study describes the current status of the marine benthic communities in this peculiar volcanic Antarctic island, providing a remarkably extended species inventory from previous reports. All this information should also be considered when managing the impact of increasing tourism in the island.

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Introduced rabbits and extreme weather events: a dangerous combination for the reproductive output of three sympatric albatrosses

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Invasive species present a major conservation threat globally and nowhere are their impacts more pronounced than in island ecosystems. Understanding the demographic responses of native island populations to invasive species, especially under climate stress, is vital for their conservation. Subantarctic islands are currently experiencing climate-driven changes to wind patterns, rainfall and surface air temperatures, which have driven ecosystem shifts and threatened native species. The implications of invasive species and climate change for native species are often difficult to disentangle as both long-term demographic and invasive species population data are required but are rarely simultaneously available. Using 20 years of mark-recapture data from three sympatric species of albatross (black-browed *Thalassarche melanophris*, grey-headed *T. chrystostoma*, and light-mantled albatross *Phoebetria palpebrata*) on subantarctic Macquarie Island, we quantified the influence of invasive European rabbits (*Oryctolagus cuniculus*) and extreme weather patterns on breeding probability and success. Temporal variability in rabbit density explained 20-76% of the variability in breeding probability, with severe declines observed during periods of highest rabbit numbers. For black-browed albatross, the combination of extreme rainfall and high rabbit density dramatically reduced breeding success. Breeding probability and success of black-browed, grey-headed and light-mantled albatross have already responded positively to the recent successful eradication of rabbits from the island, highlighting the value of active management of island ecosystems.

New insights into the temporal and spatial impacts of the Larsen AB ice shelf collapse on sponge assemblages

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Regional warming in the western sector of the Antarctic has been observed since the 1950s. In 1995, this warming led to the collapse of the Larsen A ice-shelf, followed by the Larsen B ice shelf in 2002. Research expeditions in 2007, 2011, and 2013 were conducted by a multi-disciplinary team to track and monitor the ecological and oceanographic changes in this region (Gutt et al. 2010).

Our project assesses how sponge assemblages have responded to ice-shelf collapse in the Larsen AB region. Sponges play a key role in Southern Ocean benthic communities, important both for biomass and as a habitat for many other organisms in the Antarctic. We utilise taxonomy, ROV imagery, and environmental data to understand sponge response to ice-shelf collapse. Pioneer and depth traits are applied to determine changes in the ecological succession of sponge assemblages and connectivity with the shelf and deep-sea.

Our project highlights the importance of hexactinellids as pioneers and colonisers in this region. Utilising the powerful combination of ROV imagery and taxonomic identification, we have observed an unprecedented doubling and tripling respectively of hexactinellid sponge biomass and abundance at Larsen A (Fillinger et al. 2013). Our results explore how sponges are one of the ecological 'winners' of the Larsen ice-shelf collapse.

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Changes in the distribution of food at the seafloor and predicted consequences for benthic biodiversity after a major glacier calving event

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Many Antarctic seafloor communities heavily rely on food that derives from primary productivity in surface waters and is exported to depth. Disturbances or changes in the flow of surface production to the seafloor are therefore thought to have major influence on the abundance and composition of those communities. Ice-shelf collapses or glacier calvings are events that can trigger drastic changes in patterns of surface primary productivity. Here, we quantify the influence of the calving of the Mertz Glacier Tongue in 2010 on the availability of surface-derived food for seafloor communities and predict how these communities might change as a result. We use a statistical framework that combines remotely sensed surface productivity and seafloor currents from oceanographic models with particle-tracking to quantify the spatial distribution of surface-derived food before and after the calving of the Glacier Tongue. We show that the calving event has dramatically influenced the oceanographic setting of the region by shortening the ice-free season, changing spatial patterns of surface productivity and altering seafloor currents. Our findings suggest that the combination of these changes will alter the spatial distribution of food availability at the seafloor particularly on the Mertz Bank, while other areas such as the Adélie Bank seem to be less affected. We further quantify how the abundance of seafloor suspension feeders is likely to change in the future as a result of the changing environmental conditions. Dramatic changes in the icescape around Antarctica are likely more common events in the future because of climate change. Our findings help to better understand how these changes might influence the distribution of biodiversity on the seafloor and can help to better evaluate the effectiveness and representativeness of current and future Marine Protected Areas.

Impact of extreme climatic events on seabirds in the Southern Ocean

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More extreme climatic events (ECEs) is one of the most visible impacts of global warming in our society and increasingly the focus of the general public, policy makers, climatologists and also biologists. Van de Pol et al. (in press) argue that a mechanistic understanding of the biological response will prove to be crucial to comprehend how extreme climatic events impact biological systems. Here, we present two mechanistic approaches using demographic modelling to understand the effect of ECE on the population dynamics of two seabirds species: the Southern Fulmar (Jenouvrier et al. 2015) and the Black-Browed Albatross (Pardo et al, submitted). The Southern Fulmar is an ice-dependent seabird foraging near the ice edge. During an extreme unfavorable year (when sea ice area is reduced and distance between ice edge and colony is high), observed foraging trips were greater in distance and duration. As a result, adults brought less food to their chicks, which fledged in the poorest body condition. During such unfavourable years, breeding success was extremely low and population growth rate was greatly reduced. Finally, changes in the frequency of extreme events may strongly impact persistence of Southern Fulmar populations. The black-browed albatross breeds in subantarctic islands, and its vital rates varied in response to changes in Sea Surface Temperature (SST) in their foraging zones during the breeding season. Young and old individuals were more sensitive to SST (Pardo et al. 2013). Here we assess the impact of changes in mean and variability of a SST distribution, as well as the effects of frequency and magnitude of warm SST ECE on the stochastic population growth rate and stable age structure. A local sensitivity analysis showed the stochastic population growth rate was positively affected by a change in mean but negatively by a change in standard deviation. Larger environmental mean increased the occurrence of SST close to the optimal value that buffered the negative effect of increasing variability and ECE. The 'climate safety margin' and the specific shape of the response function for a species thus determine how ECE affect the stochastic population growth rate. Effects on the age distribution were contrasted but all led to a younger population, with potentially important conservation implications for black-browed albatrosses.

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Plankton response to salinity changes in the WAP: Application of a 1D physical-biological model

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Glacier melting rate in the Western Antarctic Peninsula (WAP) has increased over the past 50 years, promoting freshwater input into the water column, especially in shallow coastal environments. Freshwater is likely impacting on the structure and function of coastal food webs. Experimental studies in the WAP have demonstrated an association between salinity changes and the dominance of certain phytoplankton groups in coastal ecosystems of the WAP: a microcosm study performed in Potter Cove (Isla 25 de Mayo/King George Is.) with a natural marine phytoplankton assemblage exposed to low salinity conditions (30 psu) showed a replacement of big centric diatoms by small pennate ones. Here we study phytoplankton and zooplankton responses to salinity fluctuations in a turbulent environment applying a coupled physical-biological model. We used a one-dimensional water column model (General Ocean Turbulence Model) coupled to a simple biological model with two phytoplankton groups (large and small) and two zooplankton groups (microzooplankton and mesozooplankton) simulating plankton dynamics. The model was modified to take into account the osmotic stress: classes of phytoplankton had different optimum salinity habitat. Forcing of the model was done with local meteorological data, and temperature and salinity profiles of 2009-10 and 2010-11 summer seasons from Potter Cove. Outcomes of the model show distinct phytoplankton responses between seasons, where dominance in the phytoplankton community differs due to salinity variation. In 2009-10, when salinity presented a relatively constant value of 34 psu, simulations resulted in lower concentrations of small phytoplankton and higher concentrations of large phytoplankton. On the other hand, in season 2010-11 when surface salinity fluctuated between 30 and 34 psu, small cells were the dominant group. Interestingly, if both phytoplankton groups are considered, the dynamics of the phytoplankton community is similar, with low concentrations in spring (Oct-Nov) and high concentrations in summer (Dec-Feb). Microzooplankton dynamics was tightly coupled with phytoplankton behavior, showing a strong prey-predator relationship. Our results of plankton response to salinity variation in Potter Cove suggest that phytoplankton responds to a threshold in salinity, upon which the community structure varies between two dominant groups. Ongoing changes in environmental conditions, such as larger freshwater inputs, might lead to a marked and irreversible shift in the plankton assemblage of coastal areas in the WAP.

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Extreme events: Solitons shape Antarctic hexactinellid sponge communities

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Non-linear solitary internal waves (or solitons) are generated where strong tidal flows interact with topography in stratified waters. Here we report on gargantuan solitons (>200m amplitude) in the Antarctic peninsula region likely resulting from the interaction of tidal flows with the ice shelf. Mixing of surface production and resuspension of bedload material may enhance microbial processes in the benthic boundary layer and favour growth conditions for hexactinellid sponges. Soliton-enhanced sponge growth and dispersal of propagules may have helped to boost the growth of hexactinellid sponges following the collapse of the Larsen A ice shelf. Sponges knocked over in the direction of current jets (>1m/s) testify to the importance of rare events in shaping Antarctic megafaunal communities.

Past penguin colony responses to explosive volcanism and climate change on the Antarctic Peninsula

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Warming and reductions in land- and sea-ice in some parts of the Antarctica Peninsula (AP) in recent decades are having a negative impact some penguin species (e.g., Adélie) by altering access routes to breeding sites and shifting the location of northern AP shelf-edge krill spawning grounds. Meanwhile, populations of gentoo penguins, which are generalist, inshore predators and prefer to breed in ice-free areas, have remained stable or increased.

Over the last 30 years, the largest breeding population of gentoo penguins in Antarctica on Ardley Island, north-western AP, has increased by c. +300% to more than 5,000 breeding pairs. Intriguingly, genetic, sub-fossil and biogeochemical studies have shown that species-specific population trends across the AP in recent decades are different from those of previous warm-periods, but also that the response of gentoo penguins to warming has been consistently positive (Clucas et al., 2014; Emslie et al., 2014). To test this hypothesis further, we used biogeochemical analysis of penguin guano in lake sediments to track past changes in penguin colony size on Ardley Island over the last 8,500 years. We then compared this data with *in-situ* sub-fossil records of penguin presence and records of past climate, sea-ice extent and volcanic activity from across the Antarctic Peninsula. Results show that after deglaciation, c. 8,500 years ago, the first sustained penguin colony was established on Ardley Island c. 6,700 years ago, pre-dating previous sub-fossil evidence of Peninsula-wide occupation by c. 1,000 years. The Ardley Lake penguin colony experienced five population maxima during the mid-late Holocene, responding most positively c. 4,000-3,000 years ago during a well-defined regionally-warmer phase of the late Holocene.

However, we find no statistically-consistent relationships with local-regional atmospheric and ocean temperatures or sea-ice conditions for the mid to late Holocene as a whole. This is because three of the five phases of penguin colony expansion were abruptly ended by the deposition of volcanic ash from large volcanic eruptions from nearby Deception Island. Sustainable post-eruption colony recovery took, on average, 400-800 years, but was particularly slow following the most disruptive phase of volcanic activity that began c. 5,500 years ago. We are currently investigating whether biomarker and environmental DNA analysis of lacustrine sediments provides a reliable archive of past penguin presence and if past changes in penguin species distribution can be reconstructed (e.g., Fernandez-Carazo et al., 2013).

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On the impact of different UAV models on Antarctic wildlife

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The impact of unmanned aerial vehicles (UAVs), of which numerous applications in different scientific and commercial fields have led to an enormous increase in numbers in recent years worldwide as well as in polar regions, has been a highly discussed topic during the last year. The protection of the pristine wildlife of the Antarctic from such impact seems particularly important and calls for detailed knowledge about the strength of disturbances by UAVs. Our previous studies (Ruemmler et al. 2015) as well as those of others (Korczak-Abshire et al. 2016) led us to first insights into the reaction of Adèlie and gentoo penguins (*Pygoscelis adeliae/ P. papua*) to UAV surveys. Those first results suggest, amongst other things, that the reaction differs between various types of UAVs (differing in engine, size, shape and others), but seems to be detectable only in low flight altitudes below 100m and still smaller than the disturbance assumed to be caused by field workers on the grounds within the colony. In the field season 2016/17, we started to extent these results by measuring physiological data during UAV surveys as well as human fieldwork and thereby building a basis for comparing the magnitude of both sources of disturbance. All field work was carried out on Fildes peninsula and Ardley Island (King George Island, Antarctic Peninsula). The gathering of physiological data was accomplished by equipping penguin nests with artificial eggs containing an acoustic heart beat recording system (Arnold et al. 2011). Additionally, video recordings have been made to analyse the according behaviour of the individuals. Trials have been carried out using three different UAV models (one octocopter, one quadrocopter and a fixed-wing-UAV) flying in altitudes of 100 to 20m to examine the impact of different flight characteristics and heights. In addition to penguins, experiments have been conducted on other wildlife species occurring on Fildes peninsula. Southern giant petrels (*Macronectes giganteus*) have been observed regarding their behavioural and physiological reaction to UAVs. For kelp gulls (*Larus dominicanus*), south polar – and brown skuas (*Catharacta maccormicki/Catharacta antarctica lonnbergii*) and Antarctic fur seals (*Arctocephalus gazella*) the behaviour was analysed. The data from field season 2016/17 is now being analysed and the results of the analyses will be presented.

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Loss of benthic biodiversity and biomass at a shallow coastal site in Antarctica due to increased ice scour

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Antarctic marine biodiversity can be rich and the average benthic biomass can be higher than that of similar habitats and depths in temperate and sub tropical communities. The shallow waters around the western Antarctic Peninsula (WAP) have warmed rapidly, with some shallow water temperatures increasing by 1˚C since 1951. Rapid change has led to: increased air temperature, increased water temperature, increased wind speeds and increased precipitation which all contribute to loss of sea ice, ice shelf collapse and glacial retreat ultimately increasing ice scour in the Southern Ocean. This is increasing the disturbance of benthic communities due to iceberg scour, which is causing concerns over future pattern of biodiversity. There is a need to determine the current status of Antarctic benthic marine biodiversity and predict its likely response to environmental change. The aim of this study was to assess the abundance and biomass of marine invertebrates on hard substrata at Rothera point, WAP and compare with an earlier benthic survey conducted in 1998. The abundance and biomass (wet mass) of benthic taxa were measured along three transects, at three depths (6,12 and 20m) that corresponded with the 1998 survey. The greatest change was found at 12m were there was a significant reduction in faunal density, biological diversity, species richness and faunal biomass since 1998. With increasing climate driven iceberg scouring in future many shallow water polar communities could be held at early successional stages by chronic ice scour.

Ocean colour remote sensing in the Antarctic waters: Effect of phytoplankton pigment composition and packaging

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The Antarctic waters are known to be optically unique and the standard empirical ocean color algorithms applied to these waters may not address the regional bio-optical characteristics. The present work focuses on the performance of current empirical algorithms and a regionally optimised algorithm for retrieval of chlorophyll-*a* (Chl-*a*) concentration from Aqua- Moderate Resolution Imaging Spectroradiometer (Aqua-MODIS) and Sea-viewing Wide Field-of-view Sensor (SeaWiFS) for Antarctic waters. Analysis indicated that empirical algorithms used for retrieval of Chl-*a* concentration from Aqua-MODIS and SeaWiFS underestimate by a factor varying from 2 to 2.9, resulting in underestimation when *in situ* Chl-*a* exceeds ~0.3 mg m^{-3}. In order to account for these uncertainties, the present study was carried out to understand the effect of phytoplankton pigment composition and pigment packaging on remote sensing reflectance [$R_{rs}(\lambda)$], based on the analysis of phytoplankton specific absorption coefficient [$a_{ph}^*(\lambda)$]. The spatial variation of phytoplankton groups analyzed using diagnostics pigments (DP) indicated a shifting in phytoplankton community structure from offshore to coastal Antarctic, with a significant increasing trend for diatoms and decreasing trend for haptophytes population. Diatom dominated population exhibited lower $a_{ph}^*(\lambda)$ in 405-510nm region (with relative flattening in 443-489nm) compared to $a_{ph}^*(\lambda)$ spectra of haptophytes dominated populations that peaked near 443nm. The flattening of $a_{ph}^*(\lambda)$ spectra for diatom dominated population was attributed to its larger cell size which leads to pigment packaging (intracellular shading) which in turn results in higher $R_{rs}(\lambda)$. The relationship between pigment composition (normalized by Chl-*a*) and blue/green absorption band ratios [$a_{ph}^*(443)$/ $a_{ph}^*(555)$ and $a_{ph}^*(489)$/ $a_{ph}^*(555)$] corresponding to Aqua-MODIS and SeaWiFS bands showed in-phase associations with most of the pigments such as 19'-hexanoyloxyfucoxanthin, 19'-butanoyloxyfucoxanthin, peridinin, and zeaxanthin. In contrast, out-of-phase relationship observed between blue/green absorption ratios and fucoxanthin, indicated apparent deviations from general pigment retrieval algorithms which assumes that blue/green ratios vary in a systematic way with Chl-*a*. Nearly 72.9% of the variance in $a_{ph}(443)/a_{ph}(555)$ could be explained by the proportion of fucoxanthin/Chl-*a*, and for bands $a_{ph}(489)/a_{ph}(555)$ the variance explained was ~68%. The out-of-phase relationship suggests that the increasing trend of fucoxanthin pigments towards Antarctic coast was associated with decreasing trend of blue/green absorption ratios, which in turn results higher $R_{rs}(\lambda)$. In conclusion, an increase in $R_{rs}(\lambda)$ leads to underestimation of Chl-*a* concentration from Aqua-MODIS and SeaWiFS in the Antarctic waters. Besides, the possible sources of uncertainties in atmospheric correction scheme will be addressed.

Classifying symbiotic relationships within Vulnerable Marine Ecosystems using DNA and compound specific stable isotope analysis: Octocorals and Polynoidae of the South Orkney Island, Southern Ocean

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In 2016 the State of the Antarctic Ecosystem (SO-AntEco) research cruise led by British Antarctic Survey sampled the benthic fauna within and around the South Orkney Island Southern Shelf marine protected area (SOISS MPA). Most of the sites sampled contained an abundance of species indicative of vulnerable marine ecosystems, also known as VME taxa. These VME taxa assigned by CCAMLR are easily damaged and slow to recover from physical disturbance (CCAMLR, 2009). Furthermore many VME taxa including cold water corals provide substrata for other organisms and act as host species for other fauna living on them such as polychaete worms.

This project investigates the relationship between polynoid polychaetes and their host corals. A total of 88 individual polynoid symbionts from two morphotypes were collected either directly from coral hosts or, were deemed to have fallen off corals during sample collection using an Agassiz trawl over a depth range of 500 to 1500m. We use short sequences of DNA to identify the number of polynoid species present on VME corals and describe their connectivity within the sampled region. After which, we will use compound specific stable isotope analysis to determine the trophic traits of these species, using their trophic position within the food web to help us classify the type of symbiotic relationship between the two species. These data will contribute to the growing number of multidisciplinary investigations into the diversity, connectivity and functionality of species within the SOISS MPA which are essential for future data driven marine management of this region.

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DueSouth: A tool for sharing Southern Ocean plans

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The remoteness of Antarctica and the Southern Ocean and the consequent cost of conducting science in this region imposes tight constraints on researchers' capacity to collect the data they need. Berths on ships are limited and any nation's ships can only visit a tiny fraction of the polar region in any given year. These limits to field resources mean that international and interdisciplinary collaboration is even more critical than in other parts of the world. To date, however, there has not been a truly international place for voyage coordinators and scientists to share their plans and therefore create opportunities for collaborations.

DueSouth is a database of upcoming expeditions to the Southern Ocean and it holds information about the ships, voyage plans, and the scientific projects being conducted onboard. The information in the database is contributed by individual scientists and national cruise coordinators as well as through digital transfers with related databases. In time, DueSouth will also provide a record of historic data gathering efforts in the Southern Ocean that can be used to improve planning for ongoing systematic observation in this remote region.

In this presentation we will introduce DueSouth and report our progress in establishing DueSouth as a centralised list of upcoming scientific work in the Southern Ocean and the challenges we have encountered to date.

Krill distribution in Palmer Deep Canyon on the West Antarctic Peninsula

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Shifts between diurnal and semi-diurnal tidal regimes influence the nearshore distribution of Antarctic krill near Palmer Station on the West Antarctic Peninsula. Integrated krill biomass increases significantly during diurnal tides (Bernard and Steinberg, 2013). This is supported by changes seen in Adélie penguin foraging location also in response tidal cycle, during semidiurnal tides the penguins traveled further from the colony to forage than during diurnal tides where they remained nearshore (Oliver et al., 2013). These spatial differences in foraging were hypothesized to be due to changes in prey availability, specifically Antarctic krill a primary food source for the Adélie penguins, between tidal regimes. While there is a clear pattern associated with krill distribution and tidal regime nearshore, less is know about what drives krill distribution further offshore. We expected that offshore, in Palmer Deep Canyon a similar pattern of increased krill abundance would occur during diurnal tides. Two acoustic Doppler current profilers (ADCP) each mounted on an autonomous underwater vehicle (AUV) were used to sample Palmer Deep. Relative acoustic backscatter was used as a proxy to identify presence-absence of krill and the likelihood of finding krill during semidiurnal and diurnal tides was computed. Changes between diurnal and semi-diurnal tidal regime did not increase krill abundance offshore in Palmer Deep as it did nearshore. The results did show increased krill presence is associated with a shallow mix layer depth, likely due to higher chlorophyll concentrations (Carvalho et al., 2016). In contrast to the high concentrations of krill in the nearshore environment during diurnal tides, these results suggest that offshore in Palmer Deep Canyon the availability of phytoplankton may be a stronger driver of krill distribution than tidal regime.

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Moving from "your model vs. my model" to "our model": A case study in building open access databases for collaborative model development.

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Until recently, Antarctic penguin data have been scattered across government reports, peer reviewed journals, and reference books, with some data remaining unpublished years after collection. As a result, and consistent with the existing paradigm in the biological sciences, researchers construct models based on individually-curated datasets and data structures. This disconnect between underlying datasets, and differences in the way models are developed, leads to different modelling outcomes and inconsistent inference about the biological processes under study. Without a common data structure for development, these divergent models are difficult to reconcile, and may not reflect biologically relevant differences in the models themselves. One of the best ways to alleviate this issue is to build a common platform of data that facilitates a community-based modelling approach (i.e. where models are created or shared in a web framework that allows transparent critique and evaluation of model outcomes). The Mapping Application for Penguin Populations and Projected Dynamics (MAPPPD) brings together a wide array of penguin census data for the four penguins that breed regularly in Antarctica (Adélie; *Pygoscelis adeliae, Chinstrap; P. antarcticus,* Gentoo: *P. papua*, and Emperor; *Aptenodytes forsterii*) and places it in the public sphere. Currently, the database contains 3,176 census records from 101 sources, covering 660 sites around the continent.

The mapping application itself is found at www.penguinmap.com/mapppd and requires no log in. All census data are downloadable with appropriate sources, citations and metadata attached and can be queried a number of ways. We have also created a baseline population model for *Pygoscelis adeliae*, which predicts population size (i.e. number of breeding pairs) for each colony and each year from 1982 to the present. We envision this initial model as the "seed" for a suite of community-derived models that will allow for ensemble model predictions and rigorous comparisons across models for each of these four species. All code for generation of the models will be hosted on GitHub, which opens up our platform as a potential for community model construction. We will discuss the opportunities and challenges for community-based models within our framework, and present suggestions on ways of moving forward using methods taken from the data science community.

INTEGRATING SOUTHERN OCEAN ECOSYSTEM SCIENCE: Highlights of the SCAR co-sponsored the Integrating Climate and Ecosystem Dynamics in the Southern Ocean (ICED) programme.

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Southern Ocean ecosystems provide globally important ecosystem services: maintaining biodiversity, influencing biogeochemical cycles and in supporting fisheries they affect global food security. They are also being affected by rapid climate driven changes, with impacts being observed at every trophic level in the ecosystem. Understanding the impacts of change in these ecosystems requires integrated (end-to-end) ecosystem analyses at regional and circumpolar scales. Developing those analyses has been the focus of the Integrating Climate and Ecosystem Dynamics in the Southern Ocean (ICED) programme. This 10 year programme has three major scientific objectives: 1) understand how climate processes affect ecosystem structure and dynamics, 2) understand how ecosystem structure and dynamics interact with biogeochemical cycles, and 3) determine how ecosystem structure and dynamics should be incorporated into management approaches for sustainable exploitation. These are being achieved through three key activities; circumpolar data synthesis and mining, field coordination and modelling. Here we highlight major current ICED activities focused on particularly on the development of multidisciplinary coordination, end-to-end analyses and models, and scenarios and projections of the impacts of future change.

Breeding-foraging tactics in Adélie penguins: A quantitative approach

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The mechanisms that can explain population responses to environmental variability via phenotypic plasticity responses of behavioural traits are not well understood yet, but they are key in assessing the on-going and future capacities of these populations to cope with global changes.

For instance, long-lived species like the Adélie penguin (*Pygoscelis Adeliae*) have developed well adapted foraging-breeding tactics that represent a trade-off between individual survival and reproduction success. However these tactics depend not only on individual quality, but also on environmental constraints.

We present a quantitative dynamical model for foraging-breeding tactics of Adélie penguin couples that take into account both individual and environmental variability.

The dynamics is given as a set of nonlinear stochastic equations in which all parameters can be interpreted in terms of ecological or physical measurable variables, and can be calibrated with exiting data from our own database.

This database has been built during 10 years of monitoring of a colony of Adélie penguins (ca. 250 couples) in Adélie Land. Most of the penguins from our colony are tagged with sub-cutaneous RFID microchips that trigger signals at antennas located at the entry points of the colony, allowing us to record every passage into and from the colony to the sea. The gateways are also equipped with an automatic weighing system, so that at each passage we can also measure the mass of the individual, which is linked to the body condition.

The stochastic differential description of the model at the individual level makes it very convenient to simulate Individual Based Models under different scenarios, and it may provide new insights in forecasting the impact of changing environmental conditions in animal populations.

An integrated approach for regionally resolved circumpolar assessment of Southern Ocean habitat status and trends

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Decision-making for ecosystem management in marine environments requires regular assessment of ecosystem status and trends (Constable 2011, Nymand-Larsen et al. 2014). A key component of ecosystem assessment is understanding and quantifying change in marine habitats and habitat components – i.e. habitat assessment (United Nations 2015). Assessments need to be conducted at scales that are meaningful for management, for example the scale at which fisheries are managed or scales that are pertinent for marine spatial planning. The ultimate goal of assessment is to quantify the quality, availability and change of habitats and habitat components within each spatial unit. In order to do this, it is necessary to translate observations of change in the physical environment into biologically meaningful measures of habitat that account for seasonality, extreme values, and patterns of spatial and temporal variability. In considering the requirements for a spatially resolved approach to habitat assessment, key questions to consider include: What constitutes habitat for different kinds of species? Among available data sources, what variables correspond to components of these habitats? How can variability in these habitat components be characterised? Are there key thresholds in habitat components (in terms of the mean or extreme values) that define what areas constitute suitable habitat for key taxa?

Here we describe work through the Antarctic Climate & Ecosystems Cooperative Research Centre and the Australian Antarctic Division to develop a quantitative framework for integrated, regionally resolved assessment of Southern Ocean habitat, and summarise the first assessment using that framework. We use time series of remotely sensed sea surface temperature, sea ice concentration (and derived values of sea ice season duration) and chlorophyll-a to consider patterns of variability in physical features and how these relate to optimum ranges and absolute tolerances for key species. We describe some of the challenges and solutions related to data extraction, statistical summaries and visualisations in our habitat assessment. We also discuss how this framework could be used in a full ecosystem assessment for the Southern Ocean or indeed for other large-scale ocean environments. This work is leading towards an international conference in Hobart in 2018 on Marine Ecosystem Assessment for the Southern Ocean (www.measo2018.aq), which aims to consolidate results from various groups into a circumpolar ecosystem assessment and to help set the stage for ecosystem research priorities from 2020 to 2025.

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The Register for Antarctic Marine Species, and the Register of Antarctic Species: Going beyond the Sea

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The Register of Antarctic Marine species (RAMS) is an authoritative taxonomic list of species occurring in the Antarctic marine environment The register was launched in 2004, as part of the SCAR-MarBIN project and forms an important contribution to the last International Polar Year.

To support and encourage scientific research on biodiversity and ecosystem functioning, Europe recently launched LifeWatch within the European Strategy Forum on Research Infrastructures (ESFRI). Within this framework a central taxonomic backbone (TB) will be created to facilitate the standardization of species data and the integration of the distributed biodiversity facilities.

In this framework RAMS will enter a new phase, getting an additional portal the Register of Antarctic Species (RAS) that will allow creating authoritative taxonomic list of terrestrial Antarctic and sub-Antarctic species. But also a wider list of species information services (taxonomy access services, a taxonomic editing environment, species occurrence services and catalogue services) and integrates different component databases and data systems. Next to taxonomic information (taxonomic databases, species registers and nomenclators), the Lifewatch TB will also include biogeographical data (species observations), ecological data (traits), genomic data and links to the available literature.

Here we provide an overview of the most important new features and how Antarctic researcher can use them and can contribute to them.

Methods to assess the performance of ocean models for use as forcing in end-to-end ecosystem models

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Ecosystems are fundamentally dependent on the physical environment (habitat) in which they exist. As such, end-to-end ecosystem models require physical variables as input forcing in order to properly drive ecosystem interactions. For marine ecosystem models, when describing current conditions, this physical forcing may be from observations but is often from physical models that offer greater spatial and temporal coverage, or reanalyses (that combine models and observations). This is especially so in data-sparse regions such as the Southern Ocean. Furthermore, if we wish to use marine ecosystem models to simulate possible future conditions then ocean model output is necessary either as a direct input into the ecosystem model, or to perturb observations of current climate.

Few end-to-end ecosystem models include an ocean model generated specifically for that purpose, usually relying on existing model simulations of the appropriate time and place. While an existing model has the advantage of having already undergone an assessment of its effectiveness, this assessment may not have been focused on suitability for use as input to an ecosystem model. In this presentation we outline a set of criteria that can be used to assess suitability for ocean models to be used as input to ecosystem models in the Southern Ocean. These criteria are: evolution of mixed layer depth, eddy kinetic energy, particle transport in the region of interest, bottom flow on the shelf and shelf break, evolution of water masses within polynyas and conservation of water properties under transformation to polygon structure.

We assess the performance of a circum-Antarctic realisation of the ROMS ocean model (Galton-Fenzi et al 2012, Corney et al in prep) that is being used to drive a configuration of the Atlantis (Fulton et al. 2004, 2011) ecosystem model for the Indian Sector of the Southern Ocean. Crucially, the assessment metrics we propose are focused on those properties that influence the ecosystem response. These metrics differ from those used to assess an ocean model from an oceanographic point of view and thus assessment of the performance of the model may differ.

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Implementing the Atlantis model for East Antarctica

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Managing the impacts of climate change and regional human pressures such as fishing in the Southern Ocean requires robust assessments of the likelihood of different future ecosystem states under plausible scenarios for fisheries and environmental change. End-to-end models that integrate physical, biogeochemical and behavioural processes are fundamental tools for supporting such assessments. We have developed an implementation of the Atlantis end-to-end ecosystem model for East Antarctica, specifically the southern Kerguelen Axis (Prydz Bay and southern Kerguelen Plateau, 50°E to 110°E, from the coast to 55°S). The Kerguelen Axis region is the most important location for primary production in East Antarctica, supports high value toothfish and icefish fisheries (on the northern Kerguelen Plateau), and is an important foraging area for marine mammals and birds.

Atlantis (Fulton et al. 2004, 2011) is a modelling framework that was developed to support management strategy evaluation and includes dynamic, integrated representations of the biophysical system, human use and adaptive management. The Atlantis biophysical submodel is based on a system of irregular spatial polygons or 'boxes' in which ecological components are represented as either biomass pools or age-structured populations. The East Antarctic implementation of Atlantis currently comprises the biophysical submodel with 43 functional groups across the full spectrum of trophic levels (from bacteria to whales), 11 depth layers and 24 polygons (boxes). It also includes seasonal sea ice that provides habitat and nutrient cycling functions. For simplicity, the southern Kerguelen Axis domain does not include subantartic islands and associated breeding colonies for mammals and birds, but does include foraging ranges of these species. This 24-box domain is nested in a larger domain (99 polygons) that covers the entire Indian Sector from 30°E to 175°E (out to 40°S) and the smaller domain is intended in part as a foundation for implementing this large model for the full region. The physical forcing for our Atlantis model is a circumpolar version of the Regional Ocean Modelling System (ROMS).

We present results for current and future climate runs of the model. Given the growing community of Atlantis users and end-to-end modellers, new tools and workflows for visualising and manipulating model inputs and outputs are emerging to support the needs of this community. In this context, we also report on new R tools and workflows we have been using and developing in association with our Atlantis model.

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Modelling the changing role of whales in the Southern Ocean food web

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The aim of this study was to examine the effects of whaling on the Southern Ocean food web using ecosystem modelling of biomass and biogenic iron flows. In the first part of the study, the depletion trajectory and unexploited biomass of Antarctic rorqual populations was reconstructed using annual catches and surplus production models. Unexploited biomass estimates were employed to construct an Ecopath model of the pre-whaling Southern Ocean food web of 1900. The rorqual depletion trajectory was then used in an Ecosim scenario to examine the plausibility of the "krill surplus" hypothesis and other whaling effects on the food web in 1900–2008. Additional Ecosim scenarios reflecting inferred trends in Southern Ocean primary productivity were employed to investigate the interaction of bottom-up and top-down forcing in the food web. These scenarios indicated that while the "krill surplus" hypothesis is a plausible explanation of abundance trends observed in some penguins and pinnipeds in 1950-1975, excess krill biomass was likely eliminated by a rapid decline in primary productivity in 1975–1995. Changes in physical conditions in the Southern Ocean during this period may have eliminated the trophic effects of rorqual depletion, although the mechanism responsible is currently unknown.

The second part of this study used ecosystem models to investigate the role of whales in biological iron cycling in the Southern Ocean. First, another mass-balanced Ecopath model was constructed to represent the post-whaling ecosystem state of 2008. Functional group biomasses ($t.km^{-2}$) were then converted to biogenic Fe pools ($kg.km^{-2}$) using published Fe content ranges to yield Fe-balanced Ecopath models for 1900 and 2008. In both of these, plankton and small nekton contained and consumed the most biogenic Fe in the pelagic realm. Plankton biomass production, particularly in unicellular groups, accounted for the highest annual Fe demand. Microzooplankton contributed most to biological Fe recycling, followed by carnivorous zooplankton and krill. The total mass of Fe recycled matched previous estimates and, under most conditions, could completely meet the Fe demands of bacterioplankton and phytoplankton. The mass of Fe recycled by large baleen whales was reduced tenfold by whaling between 1900 and 2008. However, even in 1900 the contribution of whales to Fe recycling was negligible compared with that of planktonic consumers. These models represent a step forward in examining the role of whales in food web dynamics and biological Fe cycling in the Southern Ocean, highlighting gaps in current knowledge and questions for future research.

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Size based models for understanding Southern Ocean food web structure and energy pathways

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Size-based models are extremely informative for revealing how underlying size-based, individual-level interactions and processes shape marine communities and ecosystems against a complex backdrop of species pattern (Trebilco et al. 2013, Blanchard et al. 2017). Empirical analysis of relationships between individual body size and trophic position at community scales can be particularly illuminating, providing foundational information for both static macroecological and dynamical size spectrum models for understanding energy flows and biomass distributions (Jennings & Blanchard 2004, Trebilco et al. 2016, Scott et al. 2014).

In the Southern Ocean, there is considerable uncertainty regarding major energy pathways, their variation across space and time, and how they shape community and ecosystem structure and function; this is particularly true for mid-trophic levels. A lack of detailed information on the biomass and diets of key mid-trophic-level taxa has been problematic for traditional species-focused approaches. Size-based models present a promising, less data-intensive, alternative avenue for understanding how major energy pathways shape Southern Ocean Communities and ecosystems.

We are developing multi-species dynamical size spectrum models (Scott et al. 2014) for the Southern Ocean, with an initial focus on the Kerguelen Plateau region in the Indian Ocean Sector. We have assembled trait information for zooplankton, fish and higher predators for representation in this framework. In parallel we have collated and analysed available information on the relationship between trophic level and individual body size to enable empirical estimation of mean prey size preference to inform model development, and to explore macroecological expectations for broad scale patterns of community size structure. Here we present an overview of this work and discuss key findings to date.

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Endocrinology of migrating humpback whales: Liquid chromatography tandem mass spectrometry quantitation of steroid hormones in blubber biopsies

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After the Moratorium on commercial whaling in the Southern Ocean, humpback whales (*Megaptera novaeangliae*) migrating along the east coasts of Australia (breeding stock E1 as dentified by the IWC) (IWC 1999) have greatly recovered from the status of "critically endangered" to a situation of "least concern" (Clapman 1999). A poor understanding of humpback whale reproductive physiology and population fecundity, however, prevents robust estimation of the annual growth rate of these populations. Further, there are no available methods to evaluate changes to these parameters as a function of external factors such as Antarctic krill fluctuations (Seyboth 2016) and increasing coastal anthropogenic activity (Weilgart 2007).

The steroid hormone profile of blubber from live humpback whales was measured in this study with the aim of defining baseline concentrations and identifying hormonal biomarkers of physiological status. Steroid concentrations in blubber previously have been used with success to assess the reproductive state (sex steroids) and stress status (corticosteroids) in various whale species (Kellar 2006; Champagne 2017). Nevertheless, blubber hormonal information for live humpback whales is limited to testosterone, a biomarker male fertility (Vu 2007). This study targeted a wide steroid hormone profile consisting of eleven analytes (progesterone, 17-OH-progesterone, testosterone, androstenedione, cortisol, 11-deoxycortisol, 11D-corticosterone cortisone, corticosterone, estrone and estradiol), simultaneously quantified by liquid chromatography tandem mass spectrometry (LC-MS/MS). By analysing steroid hormone suites, interpretation of endocrine status is more thorough than measuring individual hormone signals (Boggs 2016). We tested the hypothesis that this method could lead to the identification of unambiguous endocrine patterns in migrating humpback whales (e.g pregnancy, stress), for which limited supporting information regarding the life-history of the examined individuals can be accessed.

To study the endocrinology of migratory humpback whales, a total of 119 blubber biopsies were obtained from free-ranging random individuals at two different seasons. This strategy provides an insight into two phases of the reproductive season. Whales were targeted during June-July when moving from the polar feeding grounds to the warmer equatorial waters to breed (n=65), and in September-October when the adults and their nursing newborn calves return from equatorial breeding grounds (n=55).

The seasonal endocrine profiles for males and females were discussed and crossed with observational data (i.e. pod number and behaviour, presence of calves). The relationship between these variables was used to investigate the proportion of pregnant cows and their inter-calving period, which are key information to the evaluation of the annual growth rate.

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Facing climate change: Effects of temperature and salinity on fatty acid content in Antarctic plankton

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Marine planktonic communities in Antarctica are increasingly exposed to higher surface temperatures from global ocean warming and to reduced salinities from enhanced glacial melting. We performed a 7-day microcosm experiment on the shores of Potter Bay in King George Island, in which we assessed the effects of an increase (4 ºC) in temperature (T) and a decrease (4 units) in salinity (S) on plankton composition, carbon content, fatty acid (content and composition) and Thiobarbituric Acid Reactive Substances (TBARS) content as a measure of lipid damage from oxidative stress. Triplicate microcosms were exposed to four treatments: ambient T&S (control), ambient T-lower S, higher T-ambient S, and higher T-lower S. Phytoplankton assemblages showed an increase in the relative abundance of diatoms >20 µm in size in the manipulation treatments compared to the control, an increase in smaller diatoms (10-20 µm) only at higher T-ambient S, and a decrease in prasinophytes at higher T-lower S. Carbon content increased significantly in the higher T-ambient S and higher T-lower S treatments, with maximum values after 5 days. A significant increase in the relative abundance of unsaturated fatty acids EPA, C18:4ω3 and C16:1ω7, was measured in all treatments, compared to the control, after only 24 h. However, after 48 h, the increase in abundance of unsaturated fatty acid was only sustained at ambient T-lower S and at higher T-ambient S. The fatty acid composition changes measured under both ambient T-lower S and higher T-ambient S treatments, resulted in an increase in TBARS content by 48 h. However, at higher T-lower S, the increase in the proportion of unsaturated fatty acids was not different than that in the control. This may indicate that at low salinity, elevated temperatures increase enzymatic activity, which decreases the fluidity of cell's membranes, and therefore helps to avoid osmotic stress and the production of reactive oxygen species. Interestingly, although fatty acid composition showed variations for at least 48 h, there was no change in phytoplankton assemblages during this period in any of the manipulation treatments compared to the control. Physiological changes on plankton carbon fixation and fatty acid levels due to these stressors can have serious implications for food-web energy flow and the overall functioning of Antarctic coastal ecosystems.

Development of a regional glycerol dialkyl glycerol tetraether (GDGT) temperature calibration for Antarctic and sub-Antarctic lakes

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Modern-day temperature calibration models based on the relative abundances of Glycerol dialkyl glycerol tetraethers (GDGTs – temperature-sensitive membrane lipids of Archaea and bacteria), in surface sediments have been used to reconstruct past temperatures from marine and terrestrial sedimentary records, but have not been widely applied in high latitude terrestrial lacustrine environments. This is mainly because the presence, type and provenance of GDGT compounds in remains uncertain or unknown in many lacustrine settings, while the performance of GDGT–temperature calibrations at lower temperatures is comparatively poorly understood. To address these issues, we examined surface sediments from 38 Antarctic, sub-Antarctic and Southern Chilean lakes (Foster et al., 2016). First, we quantified which GDGT compounds were present and then investigated modern-day environmental controls on GDGT composition. GDGTs were found in 37 of 38 lakes studied. Branched GDGTs (brGDGTs) were dominant in 36 lakes and multivariate statistical analyses showed that their composition was strongly correlated with mean summer air temperature (MSAT) rather than pH, conductivity or water depth. Second, we developed the first regional brGDGT–temperature calibration for Antarctic and sub-Antarctic lakes based on four brGDGT compounds (GDGT-Ib, GDGT-II, GDGT-III and GDGT-IIIb). The GDGT-IIIb compound had not been included in previous global calibrations, but proved particularly important in cold lacustrine environments. Compared to previous global calibrations (Pearson et al., 2011), our new brGDGT–Antarctic temperature calibration dataset exhibited an improved statistical performance at low temperatures (r^2=0.83, RMSE=1.45◦C, RMSEP-LOO=1.68◦C, n=36 samples). Third, as a proof of concept test for the new Antarctic calibration model, we applied the new Antarctic brGDGT–temperature calibration to strategically-located and well-dated lake sediment records from the Antarctic Peninsula and South Georgia. Downcore temperature reconstructions using the Antarctic brGDGT–temperature calibration proved to be more sensitive to even relatively minor temperature variations compared to existing global calibrations, and each record reproduced known periods of mid-late Holocene warmth. In conclusion, our study highlights the importance of basing palaeotemperature reconstructions on regional GDGT–temperature calibrations for the Polar Regions, where the inclusion of additional location-specific compounds leads to improved model performance.

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Highly branched isoprenoid lipids (HBIs) reveal the impact of ice algae on the functioning and connectivity of Antarctic marine food webs.

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Sea ice algae are an important food source in zooplankton life cycles and consequently also a key source of nutrition for higher trophic levels. Yet little is known about the relative contribution of ice-related versus open-water primary production in Southern Ocean marine ecosystems.

Trophic interaction in the Bellingshausen Sea shelf ecosystem were investigated using stable isotope and highly branched isoprenoid (HBI) lipid analysis at 4 stations in Marguerite Bay. We established the trophic links between the pelagic and benthic ecosystem by measuring carbon and nitrogen stable isotope ratios in suspended and sinking particulate organic matter, sediments and key benthic and pelagic species. There was significant overlap in $\delta^{13}C$ between pelagic and benthic species at 3 of the 4 stations, suggesting close connectivity between the surface and the seabed. At the 4th station, the overlap in carbon isotope signatures was low suggesting little connectivity between benthic and pelagic food chains.

However, HBI analysis enabled us to trace biomarkers produced by sea-ice algae at the surface to the benthos at this outlier station, thus establishing trophic links between the surface and the seabed that stable isotope analysis could not reveal. This ability to discriminate communities predominantly influenced by sea-ice phytoplankton from those influenced by open-water phytoplankton is key to determining the importance of sea-ice algae to the Antarctic food web. In turn, the knowledge of the impact sea-ice algae have on the functioning and connectivity of the Antarctic food web is particularly important as sea-ice cover along the Antarctic Peninsula becomes increasingly variable with a changing climate.

Ecology of the past: Old-growth mosses as potential biological proxies for past Antarctic climate

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Climate changes in temperature, stratospheric ozone levels, wind speed and precipitation have strong implications on the bryophyte-dominated terrestrial vegetation of Antarctica. The reduction in stratospheric ozone substantially impacts wind, precipitation and radiation patterns over the southern continent potentially leading to dramatic shifts in species diversity, location and abundance. Thus, monitoring regional climates is becoming increasingly important. However, there is a substantial need for climate proxies, e.g. biomarkers, given the sparse distribution, limitations and short record of Antarctic meteorological stations. Bryophytes (mosses, liverworts), non-vascular plants that are crucial components to Antarctic terrestrial life, have unique abilities to show rapid and long-term changes in their biochemical signatures and ecophysiology in response to their surrounding environment. Therefore, we aim to develop and use Antarctic mosses as biological proxies for climate around the Antarctic coast. This included analysing pigments (photosynthetic and photoprotective), stable isotopes ($\delta^{13}C$), hormones and sugars of a range of Continental and Maritime mosses that have been dated using the radiocarbon bomb-pulse method. In some East Antarctic moss species, the $\delta^{13}C$ signature in cellulose can be an accurate and preserved way to detect past water environments. Therefore, long-term regional climate records, such as moss water availability and ozone levels, could be locked away as chemical signatures within ancient moss shoots of up to 420 years old. We show, however, that this is likely to be species specific and so we discuss the potential of various moss species, including *Ceratodon purpureus*, *Schistidium antarctici*, *Chorisodontium aciphyllym*, *Polytrichastrum alpinum* and *Bryum pseudotriquetrum*, as biomarkers. In addition, we show how important it is to evaluate the abilities of specific species to record and preserve past local environments in order to determine the scale of which these miniature plants can provide regional climate records. We explain that there are complications and that various species as well as environmental factors need to be considered when using biomarkers in the Antarctic.

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Antarctic coastal embayment as a sentinel site: A case from King George Island and a new program with a proposal for a partnership and database

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Antarctic coastal embayment is an environment where multiple systems interact to elicit responses reflecting overall Antarctic and Southern Ocean changes. These locations are often more easily accessible by established research stations or instrument installations. Atmospheric, oceanographic, sea ice and glacier changes can be more systematically observed in multidisciplinary fashion with corresponding alterations in ecosystem structures and dynamics. Marine observations from a fixed site near King Sejong Station and records from the station log for nearly two decades provide a clue to the trends of sea ice that are related to water column temperature. There also appear to be a pattern in the magnitude and timing of primary production enhancement that is governed by the retreat of sea ice and wind. A new Korean program titled CHAMP 2050 (CHAnges in Coastal Marine Systems of the Antarctic Peninsula: A 2050 Outlook) aims to elucidate driving forces and underlying mechanisms for benthic as well as pelagic ecosystem responses, particularly in the context of glacier retreat and ocean acidification, seeking to generate future scenarios. In this contribution, a case for King George Island situated in the rapidly changing Antarctic Peninsula region is made with a proposal for partnership and data base that can fill the gap in understanding 'along-the-Peninsula' gradient.

Iron concentrations and the stoichiometry of nutrient/micro-nutrient flux of stream waters entering the coastal Southern Ocean

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Primary production in the Southern Ocean is thought to be limited by the micro-nutrient iron (Fe). Numerous investigations over the past decade have attempted to quantify the major sources and chemical speciation of Fe into the Southern Ocean. The potential sources include icebergs, atmospheric deposition, deep-water upwelling, melting glacier and sea ice, and groundwater/ subglacial inflow. Our initial work demonstrated that as glaciers retreat and ice-free areas in Antarctica expand, streams could also be a major source of Fe into the coastal ocean. We have expanded our work, and have examined streams flowing directly into the ocean in both the McMurdo Dry Valley (MDV), and from Livingston Island, South Shetlands. In the MDV's streams, we have measured three physiochemical forms (i.e. acid soluble, that passing 0.4μ filter, and that passing 0.2μ filter) of Fe. Not surprisingly the 0.2μ filtered fraction has the lowest concentration and the acid soluble the highest. In both sets of streams we have compared the stoichiometry of the stream waters (N:P:Si:Fe) to that of phytoplankton, and conclude that these streams provide excess Fe and P, relative to fixed N and Si needed by the plants. Our results support the idea that increased cryospheric loss should increase the flux of Fe into the coastal Southern Ocean, and perhaps be a positive feedback on increasing atmospheric CO_2.

Multi-disciplinary studies of Andvord Bay indicate katabatic wind forcing, pulses of export flux, and high food availability and benthic abundance in inner fjord basins

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The West Antarctic Peninsula (WAP) has extensive, rapidly-warming fjords with tidewater glaciers. Some of these fjords are hotspots of biomass/biodiversity, with high abundances of krill, whales, and benthic megafauna. These spectacular fjords attract >20,000 per year, yet drivers of fjord productivity/biodiversity and their sensitivity to climate warming are poorly understood. Our *FjordEco Project* integrates field and modeling studies in Andvord Bay to evaluate oceanographic processes, glacial inputs, and ecosystem structure in a sub-polar WAP fjord, addressing two overarching questions: (1) What physical, glaciological, biological, and chemical processes interact to enhance fjord productivity and biodiversity? (2) How sensitive are these fjord processes to increased glacial meltwater and sediment inputs expected from climate warming? Fjord physical forcing and ecological responses are being addressed via: (1) Moorings, weather stations, and glacial, seafloor and sea-ice time-lapse cameras in the fjord and the adjacent Gerlache Strait deployed over 15 months; (2) Spring and fall process cruises using shipboard CTD, towed Acrobat system, AUV glider, and phytoplankton/benthic sampling and incubations; (3) Integration of field data into a physical/biological model (ROMS/COBALT) to evaluate drivers of biogeochemical cycles and their sensitivity to enhanced meltwater and sediment inputs.

Our studies across one summer season (Dec2015-Apr2016) indicate little meltwater input and buoyancy-driven flow along the fjord, with subsurface sediment plumes restricted to ~100 m depths near glacial termini. Microstructure measurements indicate very low turbulence levels in Andvord Bay compared to Gerlache Strait. High oxygen levels and weak water-mass differences indicate that inner fjord waters are not strongly isolated below sill depth. Strong katabatic winds (>30m/s) at intervals of weeks-months weaken fjord stratification, apparently setting up temporary "estuarine-like" circulation, with upper waters moving outward, inflow at depth, and weak upwelling in the inner fjord. Primary production is intermittently high throughout the fjord, yielding intense pulses of export flux in the middle basin. Benthic respiration and chl-a concentrations indicate high detrital food availability throughout the fjord in late summer, with the greatest levels in an inner basin near fast-flowing glaciers. Seafloor megafaunal abundance matches the pattern of food availability, while macrofaunal abundance peaks in mid fjord. We hypothesize that macrofauna are more sensitive than megafauna to burial stress in the inner fjord due to lower mobility and body sizes. Our results suggest that climate warming and enhanced meltwater/sediment inputs may fundamentally alter circulation in Andvord Bay and yield differential burial disturbance of rich macrofaunal assemblages in the middle fjord.

Unmanned aircraft systems (UAS) for non-destructive health mapping of polar vegetation: Showcase of East Antarctic moss beds

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Moss beds are one of the few dominant vegetation types that can be found along the Antarctic coastline. Antarctic mosses are very sensitive to environmental conditions impacted by climate change (Robinson et al. 2003). In some areas, moss communities have experienced a strong health decline. As the moss beds are spatially highly fragmented (small dispersed patches) with a relatively small spatial extent, remotely sensed imagery with an ultra-high spatial resolution (<10 cm pixel size) is required for health monitoring. We have developed two health assessment approaches based on airborne optical images collected from Unmanned Aircraft Systems (UAS).

The first approach uses a single UAS equipped with a hyperspectral imaging spectroradiometer (micro-Hyperspec) from which the imagery is processed by a machine-learning support vector regression (SVM) model (Malenovský et al. 2015). SVMs were trained with laboratory spectral measurements of moss stress stages to quantitatively predict total chlorophyll *a+b* content (indicating biochemical changes in moss cells) and effective leaf density (tracking shoot growth and/or acute turf water content). Relative moss vigour, obtained from a combination of the two indicators, corresponded well with independent field measurements. Statistically significant regressions were found with relative abundances of healthy (r^2 = 0.71), stressed (r^2 = 0.50) and moribund moss (r^2 = 0.54) at two study sites near Casey Antarctic Station (ASPA 135 and Robinson's Ridge).

The second approach is based on a combination of data sourced from multiple low-cost sensors mounted on small-size off-the-shelf UAS (Turner et al. 2014). Machine-learning Random Forest Models (RFM) were trained to model the health of the moss beds based on multisource UAS data derivatives, such as spectral reflectance, optical vegetation indices, and terrain properties. RFM outputs allowed us to identify the key inputs that were responsible for explaining health variability and re-train the models. The first results demonstrated how well the RFM can predict moss health in long-term monitoring quadrats inspected regularly at the Robinson's Ridge study site. Results indicate that moss health (expressed as a percentage) can be predicted with an RMSE of around 10%. The RFM was consequently applied to the multisource UAS datasets of the entire moss bed collected in 2011 and then in 2014 in order to investigate temporal health change between the two vegetation seasons.

Although the first approach is universally applicable (site non-specific), the second approach uses inexpensive technology and takes advantage of various data fusion techniques. Both approaches have, however, potential to be adapted to other polar plant communities.

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Cape Adare – A sentinel for change in Antarctica

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Cape Adare stretches some 40km beyond the Antarctic Continent across the Continental Shelf. It is flanked to the east by the northern Ross Sea and to the west by Robertson Bay. The following characteristics make it an ideal monitoring and observation point to understand the impact of warm ocean and climate propagating into Antarctica from the Southern Ocean:

Robertson Bay is some 500m deep and has the potential to record deep-water inflow which is predicted as climate warms and is also indicated as the biggest risk for melting Antarctic ice shelves.
Cape Adare also lies between the Antarctic continental high pressure and the Southern Ocean low pressure
Ridley Beach at the tip of the Peninsula is home to Antarctica's largest Adelie Penguin Colony

In 2015 and 2016 we conducted a pilot survey of the marine and terrestrial ecology and physical setting, with a view to determining what opportunities exist for developing a long term monitoring system. Cape Adare and the Ridley Beach Penguin Colony also offers the advantage of being on the edge of the proposed Ross Sea marine protected area and may represent an opportunity to monitor the associated ecosystem. Our goal is to find a long-term ecological research and monitoring site that:

1. integrates across a range of marine and terrestrial environments,
2. integrates across a range of timescales,
3. allows a time-series to be developed that attributes change in order to inform policy and managements goals,
4. can decipher trend and variability without aliasing the signal, and
5. acts as a sentinel for wider scale processes and connections.

In our recent visits, we were able to begin a penguin monitoring programme through nest monitoring and attaching splash tags to adult birds, collect a range of soil samples across Ridley Beach and Adare Ridge (for nutrient, DNA, isotope, TOC and elemental analysis), install the first ANTOS (Antarctic Nearshore and Terrestrial Observing System) station (two met stations, soil monitoring sensors and a camera). We were also able to identify benthic habitats and communities using a drop camera from the Roberston Bay Sea Ice, conduct plankton tows and sea ice algae, and conduct a series of CTD casts to define the Robertson Bay water column.

Preliminary analysis indicates that Robertson Bay has a stratified water column that is a direct extension of the Southern Ocean and the benthos is indicative of an environment more connected to the southern Ocean than sites further south in the Ross Embayment. The site is also exposed to the regular and strong cyclonic storms that circulate around the Southern Ocean.

Theme 4
Threats and impacts: from the poles to the globe to the poles

Advancing the CCAMLR Feedback Management Plan for the Antarctic Krill Fishery - Data Needs and Next Steps

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Commercial fishing grounds for Antarctic krill (*Euphausia superba*) have a high degree of overlap with foraging ranges for krill-dependent land-based predators. This overlap creates fisheries competition that, combined with the impact of climate change, could weaken ecosystems and compromise breeding and feeding conditions for many Southern Ocean species, particularly as the fishery grows. To address this challenge, the Commission for the Conservation of Antarctic Marine Living Resources (CCAMLR) Scientific Committee has agreed to implement "Feedback Management", which CCAMLR has defined as "a system of managing the krill fishery that uses information on the status of the ecosystem to alter the levels of fishing in order to ensure that the desired state of the ecosystem is sustained" (CCAMLR, 1990). Feedback management will rely on monitoring the status and dynamics of important features of the ecosystem, such as populations of predators and prey. CCAMLR will use those results to increase or decrease annual catch limits in specific areas in order "to ensure that a desired state of the ecosystem is sustained." It is meant to be a flexible system that, when successfully implemented, will evaluate the ecosystem as a whole to determine the amount and segment of the Antarctic krill population can be removed before negative system impacts set in.

CCAMLR is currently implementing the first stage of Feedback Management, and has agreed to progress the development of Feedback Management including the spatial allocation of catch no later than the annual CCAMLR meeting in 2019. Similar to other efforts to move toward ecosystem-based fisheries management, scientific challenges in advancing to stage two of Feedback Management include CCAMLR access to necessary data at the appropriate scale, development and agreement of analytical methods, and communicating a highly technical set of tools to decision makers, who must then agree to make decisions by consensus. To understand the challenges to advancing Feedback Management, we reviewed CCAMLR reports on Feedback Management and consulted with CCAMLR scientists that are highly engaged with Antarctic krill science and management. We provide an overview of the current management framework for Antarctic krill, including background on and the four stages of Feedback Management. We also outline the key scientific components needed to advance Feedback Management. Finally, we provide recommendations on priority next steps for advancing to the next stage of Feedback Management, including outlining how scientists who do not regularly attend CCAMLR scientific committee meetings can engage in the process.

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Antarctic resilience through the creation of a network of marine protected areas - Data challenges and plans beyond the Ross Sea designation

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Following recommendations from the United Nations World Summit on Sustainable Development in 2002, and recognizing the value of marine protected areas (MPAs), the Convention for the Conservation of Antarctic Marine Living Resources (CCAMLR) was the first international body to commit to creating an MPA network. The commitment was based on CCAMLR's mission to protect the life in its waters, as well as the precautionary principle. In 2011, CCAMLR members agreed by consensus to a framework for creating a network of MPAs by adopting Conservation Measure 91-04 and also identified nine planning domains, areas that provide a mechanism in which to plan and report on MPAs (CCAMLR, 2016).

With the establishment of the Ross Sea Region MPA in 2016, CCAMLR has taken the first step needed to create a network of MPAs, which would preserve connectivity and provide resilience for the many unique ecosystems of the Southern Ocean. The next steps towards creating this network include designating the proposed Weddell Sea and East Antarctic MPAs, as well as the forthcoming proposal for an MPA off the Western Antarctic Peninsula. It is likely that CCAMLR members will develop additional MPA proposals to create a truly circumpolar network of protection in the Southern Ocean.

Proposals for MPAs must be developed and supported by the best available science, or rely on the precautionary approach in its absence. In this presentation, we provide an update on the status of the CCAMLR MPAs in their various stages. Next, we provide an overview of the data and analyses that were considered in the creation of the Ross Sea Region MPA. We also outline the key scientific components needed to establish additional MPAs as well as to support the creation of a research and monitoring plan which can detect the effectiveness of the Ross Sea Region MPA. Finally, we outline how scientists who do not regularly attend meetings of the CCAMLR scientific committee or its working groups can share their expertise in the creation of a CCAMLR MPA network.

Facilitating *ex situ* Antarctic conservation: the establishment of an international Antarctic Genetic Archive (AGAr).

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A change in climate throughout the Antarctic continent is now predicted to occur within the next 50-100 years with the projected healing of the ozone hole. A change in biodiversity is certain to progress with this event, most likely resulting in a shift in biological community composition and structure and eventual loss in diversity – especially in the microbial flora. It is imperative that quick action be taken to preserve the Antarctica's unique genetic diversity. Newly developed molecular genetic tools, borrowed from the human forensic sciences, now allow us to acquire and indefinitely maintain samples of DNA at extremely low cost. Hundreds of thousands of samples of DNA can be archived at room temperature with a minimal cost and footprint. Newly developed DNA methods now allow us to comprehensively copy and amplify a small sample of DNA repeatedly producing virtually an unlimited supply when needed.

Through initial support from Antarctica New Zealand and the New Zealand Antarctic Research Institute (NZARI) an international archive of Antarctic genetic diversity has been established at the University of Waikato, New Zealand. The Antarctic Genetic Archive (AGAr) has the ability to receive DNA from all types of environmental samples (soil, filtered water, tissue, plant etc.) and store and manage these samples using available barcoded archive technologies. A centralized database has been designed to capture critical meta-data that will be searchable online.

We have now opened this new repository to all international programs working on aspects of Antarctic environmental research thereby centralizing the archiving, protection, and distribution of Antarctic biodiversity and genetic complexity in perpetuity. It is hoped that the facility will provide full coverage of the continent and research programs underway. We have also developed simple sampling kits designed to capture "samples of opportunity" from expeditions to remote regions where biologists are not present. Field researchers would be provided with preservation kits and instructions prior to going into the field. On return from the ice the kits will be sent directly to the archive for processing. Selected samples would be extracted, amplified and archived by the facility with split samples shipped to the sister facility for replication. Researchers currently with major collections are also encouraged to deposit selected samples for archiving. The archive has been designed specifically to make available unique DNA samples from remote areas of the continent to any Antarctic researchers thereby facilitating extremely difficult comparative studies and reducing the direct and indirect impacts need to revisit already sampled sites.

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Protected areas: Enhancing science and Antarctic governance

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The Antarctic Treaty and its Environmental Protocol and the Convention on the Conservation of Antarctic Marine Living Resources (CAMLR Convention) both contain numerous provisions and principles that aim to protect the long-term health of the Antarctic environment. One tool that both bodies have available is the designation of protected areas. To date, this tool remains underused by both the ATCM and CCAMLR. We will explore the specific ways in which networks of terrestrial and marine protected areas can contribute to the work of the ATCM and CCAMLR, and how such networks can achieve the environmental objectives of the Protocol and the CAMLR Convention. The designation of these networks will ensure that signatories to the Protocol and the CAMLR Convention are meeting their obligations to protect the Antarctic environment in a time of rapid Antarctic environmental change and increasing human presence.

Moreover, both bodies are currently addressing a variety of management challenges and protected areas would contribute to addressing those challenges. For example, a recent analysis determined that CCAMLR did not have sufficient scientific information to ensure that it was meeting the requirements of Article II of the CAMLR Convention (Australia, Chile and the USA 2015), which establishes three principles of conservation to guide management decisions. We will show that by acting as reference areas that can be compared with areas where activities take place, protected areas can reduce these uncertainties in decisionmaking. They may also provide a means of managing human activities in a more comprehensive fashion, which may simplify the work of the ATCM and CCAMLR. Finally, scientific information plays a critical role in the design and implementation of protected areas, but scientists will also benefit from the development of protected area networks. In addition to serving as reference areas that can provide valuable data, they can ensure that scientific research sites are not affected by human activities. By assessing current and emerging impacts to the Antarctic environment and taking into account scientific research priorities, we can design and implement networks of protected areas that will achieve environmental outcomes as well as benefit Antarctic science.

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Spatially distributing fishing to reduce risks of adverse impacts on the Antarctic marine ecosystem by the Antarctic krill fishery: progress and priorities.

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The Commission for the Conservation of Antarctic Marine Living Resources (CCAMLR) manages the expanding Antarctic krill fishery with a series of management measures that relate to precautionary catch limits for krill and a spatial distribution of the catch limits to minimise local ecosystem impacts of the fishery. For the South Atlantic and west Antarctic Peninsula (Area 48), the catch limit is set at a level that cannot be exceeded until a management procedure for the krill fishery is established to effectively distribute the total allowable catch spatially; this is known as the 'trigger level'. Conservation Measure 51-07 provides an interim spatial distribution of the trigger level in the fishery. It was established because the Commission recognised that localised catches up to the trigger level may affect krill predators. They wished to establish a spatial distribution of the trigger level that ensured that krill predators "would not be inadvertently and disproportionately affected by fishing activity". In this paper, we discuss progress in formalising a spatial management procedure for the krill fishery. In particular, we focus on advances in 2016 that used a risk assessment method for distributing the catch, thereby spreading the risk to predators and krill while taking account of the needs of the fishery. We will present the risk assessment method and the analyses undertaken to update the CM 51-07. We will also describe how this method can be readily updated with new spatial information on the dynamics of krill, krill predators and the fishery. In particular, we show how these kinds of data can be used to establish maps of the risks of ecosystem effects of fishing with all available data. We then discuss priorities for gathering and using the best scientific evidence available for maintaining a precautionary ecosystem approach while the Antarctic krill fishery expands.

Developing an international research and monitoring plan for the new Ross Sea region Marine Protected Area

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In 2016, the Commission for the Conservation of Antarctic Marine Living Resources (CCAMLR) adopted the Ross Sea region Marine Protected Area (RSRMPA). The RSRMPA comes into force on 1 December 2017. The conservation measure establishing this protected area requires introduction of a research and monitoring plan to the forthcoming meetings of CCAMLR and its Scientific Committee in October 2017. The purpose of this plan is to identify research and monitoring activities required, over a period of 35y, to 1) achieve a specific set of scientific objectives for the protected area, and 2) deliver scientific knowledge sufficient to advise CCAMLR on whether the MPA is achieving an additional set of conservation objectives. During April 2017, we convened an international workshop, in Rome, to develop a first draft of this plan, to coordinate research activities, and to ensure international agreement on the scope of and priority areas for research in the Ross Sea region. We present the results of the workshop discussions and an outline of the draft Research and Monitoring Plan for this unique, large, open-ocean, and polar marine protected area. We welcome comments and views from colleagues in the Antarctic marine science community and aim to use such comments to improve the draft plan.

Linking Antarctic science with environmental protection policies: Do scientists and policy-makers speak the same language?

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For over half a century, the Scientific Committee on Antarctic Research (SCAR) has supported the Antarctic Treaty System (ATS) in providing evidence-based science to inform managers of environmental issues in the Antarctic. This expert advice has formed the basis for many policies directed towards the protection of the Antarctic environment. A mini-symposium was held in Malaysia, at the 2016 SCAR OSC, aimed to highlight the policy relevance of research carried out by the international Antarctic research community in influencing decisions taken by the policy-makers of the Antarctic Treaty Parties. In this presentation, we will present the highlights from this mini-symposium, with a focus on assessing to what extent the research carried out by Antarctic scientists has made a substantial contribution to the development of regulatory mechanisms through the ATS. Moreover, we will illustrate how such contributions can facilitate discussions on how SCAR researchers can further engage with ATS issues and assist in identifying the most pressing scientific and environmental challenges the ATS should address. While it is no surprise that the ATS and the Protocol on Environmental Protection to the Antarctic Treaty, in particular, are central to Antarctic environmental protection, the policy relevance and value of robust, evidence-based science can be underestimated by policy makers. A need exists for improved two-way communication between Antarctic scientists and policy makers to foster evidence-based decision-making. In many cases, scientists need to work internationally and collaboratively to provide of substantial scientific insights that are of relevance to policy makers, and more needs to be done to ensure that these insights are communicated in an appropriate and efficient manner to policy-makers. The coordination between scientists, science managers, policy makers and funding bodies may need to be enhanced to ensure resources are available to fund policy-relevant science.

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The priorities and science needs of the Antarctic Committee for Environmental Protection

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When celebrating the 25th anniversary of the Protocol on Environmental Protection to the Antarctic Treaty (the Environmental Protocol) in 2016, the Antarctic Treaty Parties pledged to further strengthen their efforts to preserve and protect the Antarctic environment, and reaffirmed the importance of drawing upon the best available scientific advice in the management and protection of Antarctica. The Committee for Environmental Protection (CEP) plays an important role in these ongoing efforts, as the international body established under the Environmental Protocol to advise the Parties on how best to meet their shared objective of comprehensively protecting the Antarctic environment.

To effectively discharge its role the CEP must be well informed about observed and anticipated changes in the state of the Antarctic environment, and the environmental consequences of human activities both within and outside the Antarctic region. This presentation will outline the work of the CEP, and associated science needs. Current high priorities include: understanding and responding to the environmental consequences of climate change in the Antarctic region; addressing the risks to biodiversity associated with non-native species; understanding and managing the environmental impacts of tourism and non-governmental activities; and further developing the Antarctic protected area system.

Increased program engagement and effective response protocols against non-native species: two practical implementation tools to be reinforced in order to prevent biological invasions

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The on-going introduction of non-native species to Antarctica due to expanding human activity presents an increasing threat to biodiversity. Under the Protocol on Environmental Protection to the Antarctic Treaty, all introduced non-native species should be removed from the Antarctic Treaty area. However, little widespread, internationally coordinated or systematic monitoring of non-native species establishment has occurred, but available data suggest that establishment of non-native micro-invertebrates may be greatly underestimated. To help facilitate this we identify areas requiring further research and policy development, such as to reduce anthropogenic transfer of indigenous Antarctic species between distinct biogeographic regions, avoid microbial contamination of pristine areas and limit introduction of non-native marine species. Lastly, a response protocol is proposed for use following the discovery of a potential non-native species within the Antarctica Treaty area, which includes recommendations concerning Parties' initial response and any subsequent eradication or control measures

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Ross Sea Marine Protected Area: Evaluating the conservation value of the world's largest marine reserve

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The UN aims to protect at least 10% of coastal and marine areas by 2020 (Lubchenco & Grorud-Colvert, 2015) and large high-seas MPAs are key to this (Toonen et al., 2013). Very large high-seas MPAs are being established at an increasing rate worldwide, mainly in remote regions (Corrigan & Kershaw, 2008; Devillers et al., 2015; McCauley, 2014), yet many question whether they are: (1) effective (in achieving their stated goals) and (2) efficient (i.e. would traditional fishery management approaches provide equivalent conservation value at lower cost to fisheries) (Kaplan et al., 2010; Roberts & Hilborn, 2013; Caveen et al., 2015).

In December 2017 the world's largest Marine Protected Area (MPA) will come into effect in the Ross Sea region of the Southern Ocean. This provides an unprecedented opportunity to study to what extent high seas MPAs (1) conserve representative ecological structure and function; (2) mitigate threats to ecosystems from fishing; and (3) provide a reference area to better gauge the effects of fishing and climate change.

At over 1.55 million km^2 in size, tracking change and evaluating the conservation value of the Ross Sea MPA is a highly complex, technical and unprecedented challenge. Globally, it is unknown whether, within reasonable logistic and funding constraints, we can detect the effect of a high-seas MPA given the range of biological, spatial and temporal scales involved.

New Zealand research aims to consider whether it is possible to evaluate the performance of the Ross Sea region MPA in ten specific components:

1. physico-chemical environment
2. bio-regions (representative protection)
3. carrying capacity (primary production and energy flow through the microbial system)
4. keystones (krill, silverfish, myctophids, zooplankton)
5. krill predators (Adélie and emperor penguins)
6. toothfish predators (primarily weddell seals)
7. toothfish prey (predation release effects on icefish and macrourids)
8. Antarctic toothfish (changes to spatial distribution)
9. bycatch species (skates and eel cods)
10. vulnerable benthic ecosystems (structure-forming benthic invertebrates)

In particular, oceanographic variability, ecological complexity, highly mobile species and multidecadal trends present daunting challenges to proving or disproving the value of large high-seas marine reserves. We summarise plans for baseline characterisation, the design of long-term (affordable) monitoring, and analysis approaches for assessing the effect of the MPA.

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Scale matters in Antarctic protected areas: ASPAs/ASMAs, and CCAMLR MPAs

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The Antarctic region, encompassing the Antarctic continent and the Southern Ocean, is parceled among various international treaties, each of which was negotiated to reflect a range of political, scientific, nature preservation, and economic drivers.

The consideration of measures on the preservation and conservation of living resources in Antarctica is one of the requirements of the 1959 Antarctic Treaty, subsequently included in related instruments that constitute the Antarctic Treaty System, notably the 1980 Convention on the Conservation of Antarctic Marine Living Resources (CCAMLR Convention) and the 1991 Protocol of Environmental Protection to the Antarctic Treaty (the Protocol). Both instruments include the use of area protection or management as a response to actual or potential impacts from the activities they regulate. However, environmental outcomes from implementing those instruments are often subordinated to a range of drivers, such as ensuring access to sites for logistic development, tourism, or fishing activities.

We examine some key aspects of scale matters in Antarctic area protection using the Driver–Pressure–State–Impact–Response (DPSIR) as framework to structure the analysis. Our analysis is informed in our role as participant observers and stakeholders in Antarctic Treaty System fora for many years, and on an examination of the protected area regimes and related instruments under both the Protocol and the CAMLR Convention. We will look at issues of scale of protected areas relative to the values to be protected and the scale of pressures on these areas; and the interface between different types of protected areas, particularly in the coastal environment. The presentation will examine the existing Antarctic specially protected or managed areas (ASPAs or ASMAs) adopted under the Protocol as well as Marine Protected Areas (MPAs) adopted under the CAMLR Convention, and evaluate their effectiveness considering inter alia current pressures, state of the environment, and potential or known impacts.

We suggest that protected area systems under these regimes should be both expanded (to achieve greater spatial - and temporal - coverage) and better integrated, particularly in coastal areas. In a context of global climate change and expansion of activities and actors in the Antarctic region the effectiveness of the protected area regime needs to be augmented to ensure that the long term conservation and environmental protection objectives of these instruments are achieved. A consideration of scale matters is one necessary step to improve the protected area regime under these related protected area instruments.

This presentation complements a presentation on related topics by the same authors.

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Scientists are Antarctic stakeholders who generally prefer protection over fishing

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U.S. government fishery scientists like myself do not generally think of scientists as stakeholders. We aim to analyze data objectively without making normative statements about our policy preferences and mostly expect the same from our colleagues. The Antarctic Treaty challenges this perspective; Antarctica is a place "dedicated to peace and science." I believe this phrase establishes Antarctic scientists as stakeholders and obligates policy makers to consider scientists' preferences when they also consider those of industry and environmental organizations. As the U.S. Scientific Committee representative to the Commission for the Conservation of Antarctic Marine Living Resources (CCAMLR), I also believe the Treaty obligates me to be familiar with the policy preferences of U.S. scientists who work in Antarctica. Thus, to advise the State Department on the design and establishment of marine protected areas (MPAs) in the Southern Ocean, I held two workshops and "interviewed" several prominent U.S. scientists to understand their preferences for spatial protection. I asked separate groups of scientists to state their objectives for MPAs in the Ross Sea and Antarctic Peninsula regions and, to achieve their objectives, prioritize specific areas for protection within these regions. The scientists I interviewed specified a wide range of objectives for MPAs but mostly preferred protection to fishing. I inferred this conclusion from the overlap of the scientists' spatial prioritizations and locations of recent fishing activity. Spatial priorities for protection were also highest in areas closest to existing, long-term study sites (e.g., near McMurdo and Palmer Stations). The results of my first interview were critically important in negotiations to adopt the new Ross Sea region MPA (RSRMPA). The RSRMPA is unlikely to achieve all of the objectives that U.S. scientists originally hoped, but this MPA also aims to achieve the objectives of other stakeholders (i.e., the fishing industry). Results for the Antarctic Peninsula region suggest that the current system of marine Antarctic Specially Protected and Managed Areas (ASPAs and ASMAs) is unlikely to achieve the protection objectives of U.S. scientists, but it might be possible to achieve a satisfactory outcome for U.S. scientists and the krill fishing industry simultaneously. To date, my experience designing and negotiating MPAs in both regions suggests that scientists' objectives to promote future research may offer a more powerful negotiating position than those that simply aim to protect populations or communities which scientists feel are intrinsically valuable.

A strategy to protect reference sites for future microbiology research in Antarctica

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In addition to iconic animals and birds, Antarctica harbours surprisingly diverse microbial communities that drive important biogeochemical processes in virtually all habitats, including ice-free regions, ice sheets and subglacial habitats. Recent studies have shown that Antarctic microbiomes may have unique compositions and functions, exhibit biogeographic patterns, and include endemic taxa that have survived in refugia since the continent started to glaciate.

Microbial habitats are under constant pressure due to anthropogenic activities, which may introduce non-indigenous microorganisms, via human bodies, clothing, food, cargo, or construction material. New 'entry points' for microbial contamination are a consequence of the increase and diversification of tourism and research stations. Climatic changes might increase the probability of establishment of non-native taxa. The impacts of such introductions are still unknown, but might lead to a loss of the native microbial biodiversity, or its modification.

The technical progress in molecular methodologies has generated very sensitive high-throughput methods. They have the potential to describe the microbial communities with unprecedented detail. However, due to the anthropogenic pressure described above, we may be losing the pristine Antarctic areas that would enable scientists to study the native microbial flora, its functions and properties.

One tool of the Protocol on Environmental Protection of the Antarctic Treaty that could be specifically used to protect microbial habitats is the creation of inviolate areas where a special entry permit is required (inside ASPAs, for example) and quarantine equipment needs to be used. These zones could be set aside for future research and become extremely valuable as after a few decades, they would be unique examples of pristine habitats, representative of the native microbial diversity and processes. Examples of this are ASPA 126, Byers Peninsula, and ASPA 172, Lower Taylor Glacier and Blood Falls.

This option would require discussions and a consensus with scientists of other disciplines to select these regions, and careful management protocols of the sites and their vicinity. In addition, gaps in knowledge should be addressed, like the extent of transportation of microorganisms by natural means (wind, birds...), and the probability of subsequent colonization of new areas by microorganisms coming from other Antarctic regions or from outside Antarctica.

We hope that the dialogue between scientists and policy makers will improve the conservation of Antarctic microbial diversity and safeguard the possibility to study these unique communities in the future by the next generation of scientists, with the most advanced techniques of the time.

Ecosystem functioning at both sides of Drake Passage: comparing sub-Antarctic Tierra del Fuego and maritime Antarctica

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Maritime Antarctica is characterised by mild climatic conditions (vs. continental Antarctica), and is mainly dominated by cryptogamic vegetation. Just 800 kilometres north, at the other side of the Drake Passage, the southern tip of South America (Tierra de Fuego, TdF) abruptly contrasts with this region. TdF has wet-mild sub-Antarctic climate and hosts old, dense, and vast *Nothofagus* forests. This region has recently been reported to hold one of the fastest plant succession and lichen growth rate registered on Earth. In addition, the treeline is located at relatively low elevation (from 0 to 600 m a.s.l.) with sub-Antarctic tundra resembling the plant and cryptogamic communities that can be found in maritime Antarctica. Thus, this relatively short distance separating such dramatically different regions points to these areas as natural experiments for testing climate change effects on maritime Antarctica. Herein, we compare different habitats from sub-Antarctic and Antarctic regions of TdF and Livingston Island (South Shetland Islands, Antarctica). Soils from an altitudinal gradient from 0 to 800 m a.s.l. were collected in Navarino Island (TdF), comprising old *Nothofagus* forest, densely vegetated sub-Antarctic tundra and unvegetated sub-Antarctic tundra. In Livingston Island, soils were collected under vegetated and unvegetated Antarctic tundra. Diversity (T-RFLP) and abundance (via quantitative PCR) of fungi and bacteria and functional genes (nitrifiers and denitrifiers) were analysed. Several soil variables linked to C, N and P availability were measured, as well as the potential activity of seven soil enzymes linked to organic matter decomposition. Results suggest that climate warming and subsequent plant succession in maritime Antarctica may dramatically change soil functionality and microbial community composition. Soil C and N and N mineralization were always higher in old *Nothofagus* forest than in the maritime Antarctic region, which however showed similar levels to the sub-Antarctic tundra. Soil enzyme activities will be also promoted under this scenario, especially those of α and β-glucosidase and phosphatase, which are linked to C and P availability, respectively. Meanwhile, phosphates would be depleted - a common side-effect of ecosystem development. Community composition would show divergent trends. However, only the abundance of fungi and bacteria would increase. Ammonia oxidizers diversity would decrease, while denitrifying prokaryotes would hold similar diversity values. These differences between locations suggest that future warming and plant succession in maritime Antarctic soils will strongly influence soil microbial communities and associated ecosystem functions.

Using spatially dynamic ecosystem models to aid MPA planning in the Western Antarctic Peninsula Region

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Well-designed marine protected areas (MPAs) help preserve biodiversity and contribute to the management of sustainable fisheries. MPAs may be particularly important in environments where sea ice loss is rapidly increasing areas available to fisheries. The Commission for the Conservation of Antarctic Marine Living Resources (CCAMLR) has recognized that establishing MPAs could help achieve its conservation and fisheries management goals. CCAMLR has adopted two MPAs, and has agreed on objectives to be met by future MPAs. Two of these objectives relate to preserving ecosystem processes and functions. Antarctic MPA design processes to date have relied on static maps of biodiversity values and human use patterns to inform boundary selection. One underlying assumption is that if places of high biodiversity value are protected, then the ecosystem process that created the biodiversity would also be protected. We seek to supplement the MPA planning process by explicitly using food web modelling to inform MPA boundary selection. The software package Ecopath with Ecosim (EwE) allows for the development of a time dynamic and spatially explicit food web model that can evaluate the impact of potential MPA boundaries on biomass accumulation, and thus test if suggested boundaries would protect ecosystem processes that contribute to the accumulation of biomass. A mass balanced foodweb model (Ecopath) has been created for the Western Antarctic Peninsula region and temporal dynamic simulations have been performed using Ecosim. When sea ice temporal dynamics are included as forcing functions, the model successfully recreates historic trends in abundance for key monitored species such as penguins, fur seals and krill. We are currently developing a dynamic spatial version of the model (Ecospace). Ecospace can evaluate MPA boundaries created externally to the software, and it can perform spatial optimization algorithms to select boundaries based on underlying foodweb dynamics. Because time dynamic simulations illustrated the importance of the sea ice regime, spatial sea ice dynamics are included in the Ecospace scenario. The aim of this research is to use insights gained from Ecospace analyses to contribute to the discussion on which areas to prioritize for protection in the Western Antarctic Peninsula Region.

The impact of increased hydrologic connectivity on the biogeochemistry of the McMurdo Dry Valleys aquatic ecosystems

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The McMurdo Dry Valleys (MDV) are the largest ice-free area in Antarctica. The hydrologic system in the MDV primarily consists of glacier melt flowing down channelized streams into perennially ice-covered, closed-basin lakes. However, as the climate warms it is predicted that increased glacier melt, along with the melting of buried ice and permafrost will lead to increased hydrologic connectivity within the landscape. This wetting of the previously dry soils will greatly impact the biogeochemistry of the aquatic ecosystem, as the soils are the major reservoir of salts and other soluble materials in the landscape. This trend is already occurring in the Arctic where warming and thawing of sub-surface soil has led to the increased aquatic flux of major elements, and in some cases P and DOC as well. In this presentation we use previously published data to describe how the biogeochemistry of the MDV streams and lakes will change as the connectivity of the landscape is increased through the wetting of the soils, and the flux of liquid water is increased. As the climate warms, the increased hydrologic flux of soluble materials varies with respect to landscape age and position. Our conceptual modeling suggests that the physical characteristics, as well as the biogeochemistry of both the streams and lakes will change from what is currently observed, and thus impact the functioning of these aquatic ecosystems.

Towards an integrated and evidence-based protected area network for terrestrial Antarctica

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In recent years, the number and distribution of Antarctic Specially Protected Areas have received increasing scrutiny. While there is little doubt that most ASPAs protect values that are consistent with those outlined in Annex 5 of the Protocol on Environmental Protection to the Antarctic Treaty, several of the recent assessments have questioned the efficacy of the current set of ASPAs. Shortcomings identified include that these areas are inadequate in terms of size and extent, unrepresentative on a habitat and/or bioregional scale, and that they are at risk from human activities and non-native species.

However, concomitant with this increasing scrutiny, and sometimes critical assessment, is a burgeoning suite of research into the provision of an evidence-base for designation of protected areas. The science underpinning this research is often typified by a strong focus on more holistic approaches to protected area designation, and usually incorporates continental or large scale data and analyses. An overarching aim of much of this research is the designation of a true network of integrated ASPAs that efficiently and effectively provide protection for the values outlined under the Protocol.

Here I provide some empirical examples of these continental scale approaches for terrestrial Antarctica, and outline how they could form the building blocks of the foundation for a more integrated protected area network. I will show how Antarctic habitats can be delineated and potentially used as a proxy for biodiversity, how bio-physical models can provide important insights into vulnerable and unique areas, and how the incorporation of climate change is a critical element of any future designations. I will also highlight recent and developing research that has the potential to contribute to the evidence-base for area protection and conclude with an overview of how such research can influence terrestrial area protection through the instruments of the Antarctic Treaty System.

1D characteristic length scale estimation: an opportunity for timely response to ecological regime shifts

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Ecosystem-based management for the Southern Ocean requires understanding current ecosystem dynamics and the ability to adapt management to changes in those dynamics. An important challenge in designing robust, adaptive management approaches is understanding the likelihood of ecological regime shifts. Regime shifts are of particular concern for ecosystem management because they can be very difficult to reverse, difficult to detect and even more difficult to predict, particularly when data are patchy in time and space as they are for Antarctic ecosystems. In the Southern Ocean for example, if the system dynamics change such that large biomasses of krill are no longer supported, then we would need to adjust catch limits of the krill fishery in order to avoid depleting krill stocks completely. Failure to recognise such changes and continuing to manage the new regime according the dynamics of the previous regime could result in stabilisation of the new, less desirable regime and potentially further deterioration in the ecosystem state (eg: Möllmann et al. 2009).

Current methods for detecting regime shifts rely on having a multitude of concurrent, long time series data (Beaugrand et al. 2002, Rodionov 2004), which is simply not available for Antarctic ecosystems. To address this, we have developed a new method to detect ecological regime shifts from transect data: 1D Characteristic Length Scale (CLS) estimation. This represents a significant increase in capability to detect regime shifts in ecosystems with scarce data, such as Antarctic and other remote ecosystems.

In this presentation we describe how 1D CLS estimation works and give example applications to real ecosystem data. We recommend that transect data be considered as a suitable format for ecosystem Essential Ocean Variables, and that transects be routinely collected in the future so that population level trends can be placed into the context of ecosystem regime dynamics using this method. To that end, we also discuss guidelines for data type and resolution for the use of this method and potential for application to Antarctic ecosystems.

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Observed soil animal community dynamics support predictions of climate change effects in the McMurdo Dry Valleys

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The McMurdo Dry Valleys, the largest ice-free terrestrial region in Antarctica, are valuable sites to study the response of soil biota to climate change, due to their relatively simple communities and the lack of confounding factors such as land use change and plant community dynamics. Based on previous studies in Taylor Valley, certain changes in the Antarctic soil fauna are predicted to occur under impending climate projections: (i) decline in the dominant animal species, the microbial- feeding nematode *Scottnema lindsayae*; (ii) increased abundance of subordinate species; and therefore (iii) increased species diversity and evenness. To test whether such trends have already been occurring in Taylor Valley, and whether they have also been occurring in other Dry Valleys, we studied the soil fauna along environmental gradients, based on elevation transects above the lakes, in three locations: Taylor Valley from 1993 to 2016, Miers Valley from 2011 to 2016, and Garwood Valley from 2012 to 2016.

We found that the expected community changes were detectable in Taylor Valley after 2001-02, with significant decline of *S. lindsayae* paralleled by increases in *Plectus* and rotifers. These trends correspond to an increase in average daily temperatures in the field season (December-January- February) since 2001. Again in Taylor Valley, rotifers and the large nematode *Eudorylaimus* peaked in abundance in the summer of 2008-09, which was characterized by increased moisture due to a large melting event. Species evenness since 2014-15 was higher than it was in the late 1990s, indicating that shifts in community structure are already occurring.

Some of the trends in Taylor Valley were found in the other valleys, but with notable differences: subordinate species abundance increased in Taylor and Miers but remained rare in Garwood Valley, whereas *S. lindsayae* abundance declined in Taylor and Garwood but not in Miers Valley. However, the juvenile proportion of *S. lindsayae* decreased in all three valleys, portending reduced recruitment and subsequent abundance declines in the succeeding years. Overall, our findings support hypotheses that underlie on-going ecological studies in the McMurdo Dry Valleys, but also show considerable spatial variation in some temporal trends. Our data provides a valuable baseline for future experiments and models, especially in the comparably less-studied Miers and Garwood Valleys. Our findings show that tracking soil community dynamics across time in multiple field sites is critical to validate the forecasts of ecological effects of climate change.

How important is carbon storage by southern polar benthos as a negative feedback on climate change?

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Carbon capture and storage by southern polar benthos is potentially the largest negative feedback on climate change. Most feedbacks on global climate change are positive; they exacerbate physical change. The few known strong negative feedbacks, those which reduce physical change, are polar, and include i) broadening existing sinks with sea-ice losses over polar continental shelves, ii) subarctic vegetation growth increases and iii) formation of new sinks where ice shelves collapse. To date, carbon sequestration gains have been recorded around the Antarctic coastal shallows where they are likely to be offset by fjordic losses associated with sedimentation, and open coast losses through increased iceberg scouring. These feedbacks are complicated by additional positive forcing associated with greater heat absorption from albedo change. In contrast there is no albedo change (negligible sea ice losses) over sub-Antarctic shelves, where rising sea temperatures are likely to increase carbon storage by animals.

The continental shelves along polar continent margins and archipelagos are wide, deep and rich in life. Most species known from polar waters live on these shallower shelf regions and it has been observed that they play an increasingly important role in the carbon cycle. Carbon is transported through the system by being fixed in photosynthesis by algae, which are eaten by benthic invertebrates, and then buried when the animal dies. We aim to measure how much carbon is held per unit area of the seabed per year and how this varies in time and space.

Teasing apart biological processes in these important geographic regions is vital to our understanding of global carbon capture. One of the biggest sources of error in this regard is understanding the extent to which these feedbacks are effects of climate forcing on sub-Antarctic and Arctic shelf benthos performance. This type of carbon sequestration, termed blue carbon (associated with natural processes), is likely to increase, so long as sea ice and ice shelf losses continue to be sustained. Our research project, titled Antarctic Seabed Carbon Capture Change (ASCCC) has participated in the Antarctic Circumnavigation Expedition (ACE) in 2016 and 2017 to address the question 'How will regional warming influence how much carbon is captured and stored by life on the seabed around Antarctica and the sub-Antarctic?', from which we plan to estimate increased benthic carbon stored across the southern polar region due to recent ice shelf losses, sea ice losses and temperature increases.

Assessing the potential exposure of migratory animals to disturbance

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While many studies have examined the sensitivity of marine animals to underwater noise an essential component of any risk assessment is the likelihood that individuals of a given population will be exposed to that disturbance. An essential component of risk assessment is identification whether individuals will be exposed to a risk. This requires information on the proportion of the population exposed, for how long, and during what activity (i.e., feeding, migrating, and breeding). Using satellite telemetry data for humpback and blue whales feeding and migratory regions in Antarctica, California, and Bering Sea, we modelled the potential exposure of individuals to an acoustic disturbance. Foraging and transit regions along the tracks were identified and using a switching state space model the time spent foraging in each region calculated. A simulated seismic survey was randomly placed (100 iterations) within the habitat of each of species and the amount of time individual animals were exposed determined. A large disturbance (i.e. 100 km) only exposed 6% of the population of humpback whales in Antarctica and 19% blue whales off California. In contrast, humpback whales in the Bering Sea experienced high exposure with only a 5 km disturbance. This approach can be used to develop a framework for estimating the likelihood that a given animal population would be exposed to disturbance and to develop general risk assessment guidelines. Output from this exposure model can be used to evaluate the potential effect of disturbance on an animals energy budget in terms of energy expended but not acquired and how that would effect on offspring growth and survival.

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A new submarine observatory of the Sub-Antarctic coastal benthos facing climate change in Kerguelen Islands

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In the current context of climate change, variations in sea surface temperature, sea level change, and latitudinal shifts of currents and hydrological fronts are expected to affect marine biodiversity of the Sub-Antarctic Islands located near the Polar Front, such as the Kerguelen Islands, particularly in coastal waters. Characterizing the impact of these changes on sub-Antarctic biota and ecosystems requires recording environmental changes through the establishment of long-term *in situ* monitoring. The IPEV program PROTEKER aims at the establishment of such a submarine observatory consisting in multi-disciplinary research: oceanographic, benthic habitat mapping and inventories, genetic, eco-physiological, and trophic analyses. In addition, the program also aims at providing with scientific criteria the managers in charge of protection and conservation policies (TAF National Nature Reserve). Sampling sites of previous oceanographic programs focused on the Kerguelen Islands were revisited during summer campaigns. Among eighteen coastal sites explored through scuba diving, eight were selected for monitoring, as representative of the Kerguelen sub-Antarctic marine habitats, and were progressively equipped with sensors and settlement plots. ROV observations and beam trawling (50 and 100m) have also been conducted for contextualization. Eight sites in the Morbihan Bay [4], in the North [2] and in the South [2] of the Kerguelen Islands are monitored using photo and video surveys, temperature loggers installed at 5 and 15m depth, and settlement plots at about 10m depth. Temperature data have been recovered yearly since 2011 at some sites. Biodiversity found on settlement plots will be characterized yearly through morphology and DNA techniques. Phylogeographical studies of target taxa within molluscs, crustaceans, echinoderms, and fish are being conducted to improve our knowledge of endemicity and connectivity levels among sub-Antarctic islands. In addition, our knowledge of sub-Antarctic life and of its potential resilience to environmental changes will be improved by trophic analyses and eco-physiological experiments performed in situ. The originality of the PROTEKER observatory consists of (1) the nature of the investigated region [Sub-Antarctic zone], (2) the large spatial scale of the observing system (8 permanent monitored sites with different environmental conditions of open sea, sheltered bays, and fjord), (3) the experiment duration [over 8 years], (4) the dynamic approach to characterize the colonization process, (5) the double approach including taxonomic and metagenomics analyses, (6) the fact that the monitored sites and data in open, interoperable and reusable formats will also be used for other scientific programs, hereby the submarine observatory truly making sense.

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Seafloor Winners and Losers: A Century of Projected Future Southern Ocean Warming

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The waters of the Southern Ocean, along with the rest of the World's oceans, are projected to warm over the coming century. When faced with warming ocean temperatures marine species have been shown to exhibit poleward range shifts (Perry et al., 2005; Sunday et al., 2015), however, for polar organisms it could be said that they are at the end of the line, with limited options in terms of northwards or southwards migration.

Southern Ocean seafloor temperatures for the present and projected future scenarios were derived using 19 models from the CMIP5 coupled climate ensemble for both the historical (1976-2005) and the most extreme future (2070-2099) scenario adopted by the IPCC, RCP8.5. The benthic species occurrence data, for depths shallower than 1,000 m and from south of 40°S, was extracted from the SCAR Biogeographic Atlas of the Southern Ocean (De Broyer et al., 2014) and the Ocean Biogeographic Information System. A total of 57,827 benthic occurrence records were used for the 963 selected species.

Projected temperature changes in the Antarctic and subAntarctic show warming in most regions, especially the West Antarctic Peninsula, the Kerguelen Plateau and parts of the Ross and Weddell Seas. The seafloor south of the Polar Front (PF) is expected to warm by an average of 0.4°C, with a maximum projected increase of 2.15°C. Species currently only found north of the PF are unlikely to be able to cross into Antarctic waters with the seafloor not having warmed sufficiently to compensate for the strong meridional temperature gradient. 66% of all Southern Ocean species are expected to experience a reduction in their current potential suitable temperature habitat (over half of which are only found south of the PF). A projected overall reduction in species numbers in West Antarctica, the South Orkney Islands and South Georgia is due to temperatures reaching a threshold that excludes many cold water specialists but not warming enough for more northerly, non-Antarctic, species to colonise. The Weddell Sea, Ross Sea and parts of East Antarctica show a projected increase in diversity due to a slight increase in temperatures that favours a greater number of Antarctic species without excluding the cold water specialists.

These results show that, even under the most extreme future climate projections, Antarctic seafloor life is facing a potential redistribution rather than wholesale invasion or extinction.

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Something imperceptible but sensible: Genetic sub-population of *Sanionia uncinata* within Antarctic Specially Protected Areas (ASPA) and other ice free access areas in Antarctica and Southern Patagonia

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Antarctic Specially Protected Areas (ASPAs) in Antarctica were created to establish areas with restricted access to protect outstanding environmental, scientific, historic, aesthetic or wilderness values. However, in practice the conservation network of terrestrial biodiversity from a continent-wide perspective has been pointed out to be as ´inadequate, unrepresentative and at risk´ (Shaw et al. 2014), requiring an holistic reconsideration. Thus, genetic studies are getting a growing relevance in assisting policy and procedures for conservation work to address the relationship and dynamics of the biogeographic hierarchies and ecological zoning (Laikre 2010). In this context the work presented here is intended to determine the genetic structure of populations in the cosmopolitan moss *Sanionia uncinata* (Hedw.) Loeske, in several populations of its southernmost distribution (e.g. South Shetland Island, James Ross Island and South-Patagonia), focussing on the current ASPA boundaries versus nearby free access areas analyzing ancestry origin and presence of subpopulation.Results show presence of several sub-populations in and among ASPAs as well as in respect to other free access sites in Antarctica and South-Patagonia, all of them with different levels of polymorphism and heterozygosity. In cases such as Barton and Potter Peninsula, which are formed by ASPA (N°171 and 132, respectively) and free access areas, results show equivalent level of polymorphism inside and outside the ASPA forming two subpopulations. In such cases, from the point of view of the genetic analysis, the effort in conservation is been restricted to one subpopulation and not the complete range of the variants existing within these places. Other cases, such as Suffield Point or Bellingshausen Beach which are free access sites, showed high amount of polymorphism and ancestry in population far away, which are imperceptible for humans and it could give background for conservation plans. Because of the dynamism of the species in the different hierarchies, this work can be useful for decisions makers in the reviewing of management plans as to elaborate an strategic designation of new sites of protection that further reduce bias in conservation efforts.

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Korea's action plan on ecosystem research and conservation of Ross Sea MPA

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The significance of Ross Sea in the Antarctic marine ecosystem has been known to us through various studies, and the MPA (Marine Protected Area) was designated last year by CCAMLR to preserve it. We have already set up an ecosystem monitoring plan based on the Korean Jang Bogo Station (JBS) after several years of planning, and have successfully conducted a preliminary survey to set up summer camps in Cape Hallett last season with New Zealand colleagues. We will set up the semi-permanent camp here in next season to monitor the environmental changes in ecosystem around Adelie penguin colony and study marine environment in the surrounding waters with icebreaker. A new research project will be launched with support of the Ministry of Maritime Affairs and Fisheries from June this year. The goal is to understand the impact of environmental changes on Ross Sea MPA ecosystem structure and the Adelie penguin populations, especially in the Northern Victoria Land. The main focuses will be on ecosystem structure and function of Ross Sea, population ecology of krill-dependent Adelie penguins, and identification of environmental changes affecting ecosystem. It will provide basic data necessary for the management of Ross Sea MPA in the international organizations such as CCAMLR. For this research in Antarctica, we need various infrastructure such as research icebreakers and airplanes, so we are planning to build a cooperation system with various countries including New Zealand, USA, and Italy. We plan to take a leading role in research activities using our research icebreaker 'Araon', air-network based on JBS, and Cape Hallett forward camp. We are also looking forward to the participation of overseas researchers in various fields to further maximize the performance of our research projects.

Toxicity in sediments across the Antarctic continental shelf

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Sediments act as long term sink for hydrophobic pollutants and the assessment of their toxicological quality provides information on the environmental characteristics where they were generated at upper layers of the water column. The toxicity and presence of CYP1A inducers in Antarctic continental shelf sediments were investigated to estimate the potential anthropogenic impact in a remote, presumably pristine area of the world ocean. CYP1A inducers, e.g., polycyclic aromatic hydrocarbons, dioxins and dioxine-like compounds are related to anthropogenic activity. The fish hepatoma cell line PLHC-1 was exposed to organic extracts of 12 samples of the upper 5 mm of the sediment column from four zones to assess and compare among them the a-priori negligible impact of anthropogenic pollution. The regions under investigation were the Drake Passage off the South Shetland Islands and the Bransfield Strait (DP), the NW Weddell Sea (NW), the Filchner shelf at the southernmost Atlantic (SW) and the Austasen shelf at the easternmost Weddell Sea (EW). The regions DP and NW are currently exposed to comparatively higher ship transit, whereas EW and SW undergo less transit and harsh environmental conditions, which require ship ice-breaking capabilities. Preliminary results revealed striking values of sediment toxicity. On the one hand, the DP and NW sediment extracts showed cytotoxicity in PLHC-1 cells and significantly induced the activity 7-ethoxyresorufin O-deethylase (EROD) after 24 h exposure at concentrations comparable to those found in Mediterranean coastal areas, whereas on the other hand, no cytotoxicity and low or no presence of CYP1A inducers were detected in SW and EW samples. These findings strongly suggest that anthropogenic activities are clearly impacting the Antarctic continental shelf threatening the rich and diverse shelf benthic communities, formerly thought as relatively isolated from anthropogenic pollution. The investigation is still open to identify the potential sources of these pollutants and their historical records.

Monitoring the impact of human activities in Admiralty Bay, Antarctica: a stable isotope analysis of the benthic community

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The Brazilian Antarctic Station "Comandante Ferraz" (CF) is located in Admiralty Bay (King George Island), an Antarctic Specially Managed Area (ASMA1). It belongs to the region of the West Antarctic Peninsula, considered one of the most vulnerable to global changes, and the area with more research stations. A joint project, performed from 2002 to 2006, allowed a characterization of the main impacts on the marine environment of Admiralty Bay (Weber and Montone 2006). The influence of sewage and hydrocarbons in the sediment was observed only in the proximity of CF sewage outfall within a distance of 700m. A continuous monitoring program of the marine environment has been established since 2007 - The National Institute of Science and Technology - Antarctic Environmental Research (INCT-APA). In this sense, the trophic interactions throughout the benthic community were analysed by carbon and nitrogen stable isotopes to verify if there was anthropogenic influence off the Antarctic Brazilian Station during the austral summer of 2010. Three areas were chosen at depths between 20 and 30m: in front of the Brazilian Station (CF), under sewage outfall influence, and Ullmann Point (UP) and Refugio 2 (RF), as reference areas. Samples of suspended particulate matter (SPM), macroalgae, sediment and benthic invertebrates were obtained. Benthic invertebrate isotopic values were compared by a General Linear Model. Similar species were compared by ANOVA or *t* Test. Material from the sewage treatment station at CF had a low $\delta^{13}C$ mean value (-27.65±0.17‰), as the sublittoral sediment under its influence (-24.43±1.30‰). Nevertheless, CF community did not differ from the other two reference areas in both $\delta^{13}C$ and $\delta^{15}N$ values. The $\delta^{13}C$ values for the selected species were lower at CF than at UP or RF: *Barrukia cristata*, *Nacella concinna, Paraserolis polita*, *Rhodine antarctica*, *Sterechinus neumayeri,* and *Yoldia eightsii*; however those differences in some cases were not significant. Our results have suggested that the changes on the sewage treatment along the recent years have been reflected on the isotopic data of the benthic community, showing less differences within the areas in contrast with the previous studies done in the summers of 2003 and 2005/2006 (Corbisier et al., 2011).

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Conservation research and management of albatrosses and large petrels: progress and priorities identified by the Agreement on the Conservation of Albatrosses and Petrels

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Seabirds are amongst the most globally-threatened of all birds. Albatrosses and large petrels have extensive at-sea distributions, and face a major threat from incidental mortality (bycatch) in industrial pelagic and demersal longline, trawl or artisanal fisheries, often in both national and international waters. This led to the Agreement on the Conservation of Albatrosses and Petrels (ACAP) which has been ratified by 13 member countries (Parties). Here we outline the aims of ACAP, which are to develop policy, coordinate international cooperation, and support capacity building to improve conservation of the listed species. We review the population trends of, and threats to the 31 ACAP-listed species, progress in addressing those threats since ACAP entered into force in 2004, current conservation research and management priorities, current global trends and the major data gaps for the listed species. There are effective mitigation measures that reduce bycatch, and best-practise advice is available from ACAP and BirdLife International. The talk will describe selected success stories, and review the framework adopted by ACAP for identifying priority fisheries for conservation action where bycatch rates are high, mitigation is not mandatory or does not meet best-practice standards, and levels of implementation and monitoring of compliance are inadequate. Intentional take of seabirds (harvesting), pollution (including plastic ingestion), and threats at breeding colonies affect fewer species than bycatch; however, the impacts of disease and of predation by introduced species are severe for some breeding populations. The talk will describe the recent progress made in controlling or eradicating pests at ACAP breeding sites, the objective criteria used by ACAP to assess terrestrial threats, and the framework for prioritisation of key sites for conservation management. We also identify potential avenues for research that would improve the conservation status of ACAP species and other seabirds, which we encourage members of the audience and the wider research community to pursue.

Natural and anthropogenic content in Skua food remains

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In contrast to various global ecosystems, Antarctic biodiversity is relatively poor in species resulting in rather simple food webs. Among avian species, Skuas represent the top predators in the Antarctic food web. The natural diet of Skuas varies and includes any bird species, small crustaceans and fish as well as carcass. The main focus of this study is to observe the food remains of two Skua species: the brown Skua (*Catharacta antarctica lonnbergi*) and the South Polar Skua (*C. maccormicki*). Where both species occur sympatrically, they have an overlapping prey spectrum, however the brown Skua mainly feeds on penguins whereas the South Polar Skua mostly forage for krill and fish. The study was conducted on Fildes Peninsula on King George Island, Antarctic. The area also represents the logistical center of the Antarctic Peninsula with its six stations, hosting more than 300 persons during summer, and a runway. Though, taking this density of people into account, high amounts of daily waste are produced and some of this waste together with a substantial dimension of marine debris find its way into the Antarctic ecosystem. During nest controls of both, Brown Skua and South Polar Skua, pellets, excrements and all waste, that was introduced by the birds, were sampled in approximate 5m radius around skua nests. Analyses of the food remains revealed comprehensive information of the food spectrum. In addition, examination of otoliths, small ear bones of fish, allows conclusions about the species and size of the consumed marine prey. Moreover, data on chick growth of several consecutive years are to be compared with the diet data. Determinants such as composition of the diet or prey size can be used to draw conclusions about variability of food spectra within or between the breeding seasons which may be reflected in the body condition of the offspring. Skuas as particularly opportunistic feeders tend to use every available food source. Thus, anthropogenic items can often be found in the nesting area as well in the food remains. This includes ingested plastic which may derive from direct intake of station waste or marine debris or on the other hand by plastic in the stomach content of prey species, e.g. storm petrels. The latter indicates a vertical transfer within the food web. Thus, skuas may be used as indicators of human impact in the Antarctic.

Pétrel Island (Terre Adélie) population are in need of active protection following two complete breeding failure over the past 3 years

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In the 2013-14 reproductive season, the 26,000 pairs of Adélie penguins from Pétrel Island, Terre Adélie, failed to fledge their chicks. This catastrophic breeding failure resulted from two factors. First, the season saw an extreme sea-ice extent (the greatest extent recorded in East Antarctica since the beginning of satellite measurements) that forced Adélie parents to cover great distances to reach the open water during the incubation and early chick-rearing phases. The extended absence of parents meant that the partner and/or the chick fasted longer at the nest, increasing the risk of desertion by the partner and the risk of dying of prolonged fast for the chick(s). Second, the season was characterized by unusual precipitations of rain around the turn of the year that killed massively the already weakened young chicks. While we haven't seen yet the consequences of this "zero year" on the demography of the population there, a second complete breeding failure took place in the season 2016-17, leading to the deaths of all the chicks of the 28,000 Adélie pairs that bred in this season. Once more sea-ice extent was the major cause of failure. Sea-ice conditions in 2016-17 were even more drastic than in 2013-14, as sea ice extended as far as 80 km from the colony but over the entire breeding period. Snow precipitations occurred only over 2-3 days in mid-November 2016 and several nests were buried under more than a meter of snow, but the snow falls were immediately followed by almost a week with temperatures continuously above 4°C that sent flows of melting snow through the colony, wiping out nests and eggs. Two "zero years" occurring within three breeding seasons will definitely affect the demographics of the population at Pétrels Island. Furthermore, the situation is not going to improve as long as the B9B giant berg stays anchored in Commonwealth Bay, on the east of the island. The B9B blocks icebergs from the Mertz glacier in front of Pétrel Island. This is a serious threat to the populations of Pétrel Island and a strong incentive for the creation of the D'Urville Sea/Mertz Marine Protected Area. Preventing fishing activities would avoid adding further constraints on the avifauna there, especially since some colonies, 5km on the west (Cap Prud'homme) and 35 km on the east (Cap Bienvenu) of Pétrel Island, seem to fare slightly better and need active protection.

A spatio-temporal review of penguin contaminant loads in Antarctic and sub-Antarctic systems

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Heavy metals and persistent organic pollutants (POPs) have been detected in and around Antarctica for the past several decades, even though there is no production or use of agricultural and industrial pollutants in the area. This region, isolated from the rest of the planet by strong barriers such as the Antarctic Circumpolar Current, receives comparatively limited inputs of pollutants that are transported long distances from industrial centers. Improved understanding of the distribution of anthropogenic impacts on the complex biotic and abiotic environment of the Antarctic system can inform global management policies for agriculture and industry. Penguins serve as a practical biomonitoring tool for this purpose because they (1) do not migrate out of the region, (2) are mesopredators that bioaccumulate lipophilic pollutants, and (3) undergo a unique catastrophic molt during an extended fasting period that provides strong signals of the previous year's contaminant exposure. In this review, we summarize the available literature on contaminant levels in penguins breeding in Antarctica and the sub-Antarctic islands. Most penguin tissues sampled in the reviewed studies include non-destructive collection of feathers, blood, guano and eggshells, with each tissue reflecting exposure over different temporal periods in penguin phenology. Taken collectively, these tissue analyses demonstrate the potential for penguins to provide an index of the contamination loads in the Southern Ocean, however the geographical distribution of these studies and the taxonomic distribution of studied penguin species are incomplete relative to the potential overall distribution of contamination. Our summary highlights the utility of initiating systematic long-term monitoring projects that remain consistent over location, species and — if suitable marking methods can be found — individual birds.

Trace metals in Antarctic Krill Euphausia superba: Does sex matter?

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Although Antarctica is seen as the remote and pristine continent, the levels of contaminants in the Southern Ocean have increased significantly. With this study we aim to better understand the concentration of different trace elements (Hg, As, Cd, Co, Cr, Cu, Fe, Ni, Pb, Se, V, Zn) in one of the most important marine organisms in the Southern Ocean, the Antarctic Krill (*Euphausia superba).* Antarctic Krill is considered to be an important trophic link between primary producers and top predators, but accumulation processes of trace elements in krill and the propagation of these elements through the Antarctic food web are still poorly understood.

Samples of Antarctic krill were collected during the austral summer of 2016 (January-February) around the South Orkney Islands (60º58'S, 045º50' W), in one important Antarctic krill fishing area. The samples were collected using two Rectangular Mid-water Trawls (RMT25 and RMT8). A total of 523 individuals were collected and analysed (182 Males, 175 Females and 166 Sub-adults/juveniles) from 9 different stations (5 on -shelf and 4 off-shelf).

This presentation will specifically evaluate the effect of sex and maturity on trace element content in Antarctic krill in order to test if differences in accumulation between sexes can be explained by the fact that females can use egg-laying as an elimination route for some trace metals, thus leading to lower concentrations than found in males. Sub-adults are expected to have lower concentrations levels as they had less life time to bio-accumulate these elements. Establishing the base levels of trace elements in Antarctic krill is crucial to understanding the pathways of trace metals in Antarctic ecosystems.

The shifting of temporal patterns in the breeding phenology of Adélie and Gentoo penguins

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Pygoscelis penguins are an important part of the Antarctic ecosystem. They are considered as indicators of changes in biotic and abiotic conditions in the environment. One probable response on climatic variances is shifting of temporal patterns in breeding phenology.

A colony of *Pygoscelis* penguins on Ardley Island, south-west of King George Island, has been studied during breeding seasons 2014/15, 2015/16 and 2016/17. About 120 nests of gentoo penguins (*Pygoscelis papua*) and about 30 of Adélie penguins (*Pygoscelis adeliae*) were marked and controlled in an interval of three days. The selected nests are distributed over the whole Island to represent the topographic (altitude, slope, etc.) and biotic (size of nest group, predator activity) variety of the breeding sites.

With these data it was possible to describe breeding phenology, which gives an overview of the breeding behaviour of the entire colony during the season. It was further possible to identify the dates of important breeding events, like the peak of egg laying and the peak of hatching. Furthermore, differences in the breeding phenology between the species could be determined. The breeding chronologies were also compared between the three considered seasons to reveal interseasonal differences.

The breeding phenology of Adélie penguins shows nearly similar temporal pattern in all three seasons. The first chicks hatched around 30th of November. The peak of hatching was around 14th of December in season 2014/15 and 2015/16, only in season 2016/17 the peak already appeared on 8th of December.

In contrast to this relatively stable interseasonal pattern of the Adélie penguins, the gentoo penguins show much higher differences in their temporal breeding pattern between the seasons. The whole breeding process started two weeks earlier during season 2016/17 than in the two other seasons. Related to this, the whole phenology shifted forward by about two weeks. The peak of hatching for example appeared already on the 4th of December, whereas in the other two seasons the peak was located around 18th of December.

A likely reason for the early start of 2016/17 breeding cycle was the average snow height which was much lower than in the two years before. Hence, snow free areas appeared earlier in the season. Obviously the amount of snow during the breeding season has a large impact on the breeding phenology of gentoo penguins, while the impact on Adélie penguins is much lower.

Feathers of *Daption capense* and *Macronectes giganteus* found in breeding colonies: non-invasive method to access cadmium level in Antarctic seabirds

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Cadmium (Cd) is an extremely toxic metal naturally available on the planet, that may have its levels increased by anthropogenic activities. As overexposures may occur even in situations where trace quantities of this element are found, conduct studies in remote and pristine areas - as Antarctic - are important to assess the overall impact of Cd in wildlife (Bargagli, 2008). Seabirds in general present high levels of Cd, which can varies according age, diet, ecosystem use and physiological status (Burger, 1993). They can be exposed to Cd mainly through diet and, in this way, feathers can provide a nonlethal matrix for assessing the exposure of seabirds to these element. *Daption capense* (Dca) feeds mainly on fish and on crustacean (Creet et al. 1994) and *Macronectes giganteus* (Mgi) feeds preferably on fish and on seal carcasses (Raya Rey et al., 2012).

We report Cd concentrations in feathers of Dca and Mgi. Feathers from remains of predation and loose in the ground were collected near breeding areas at Admiralty Bay, King George Island, Antarctica. The samples (Dca n=5; Mgi n=5) were washed to remove external contamination, digested in acid solution and quantified in a Graphite Furnace Atomic Absorption Spectrometer. The concentration ranged from 110 to 590ng.g^{-1} to Dca and 20 to 110ng.g^{-1} to Mgi. Dca presented Cd values significantly higher than Mgi ($t=2,749$ $df=8$; $P=0,0251$). Diet has important influence in trace elements accumulation, antarctic fishes usually have low cadmium levels when compared to cephalopods or crustaceans (Honda et al., 1987; Moreno et al., 1997; Nygard et al. 2001; Anderson et al., 2010), so a diet rich in crustaceans can be supplying cadmium to Dca. Our results are similar to those found in other study with 10 species of procellariiformes from South Georgia, in that authors also found lower levels to Mgi (Anderson et al., 2010).

One negative aspect in the use of samples without the capture of the animals is the lack of information about health and physical characteristics of the individuals that can be affecting Cd accumulation and elimination in these species. Study of contaminants in *Dca* are rather scarce, possibly due to the difficulty of capturing animals that breed on cliffs or rocky slopes. Feathers collected from carcases of this specie can help to fill in the contamination data gap.

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The environmental impacts of wastewater and sewage outfalls in Antarctica: a case study from Davis station, Antarctica

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The treatment and disposal of sewage and wastewater are an ongoing environmental concern in Antarctica. In 2010 an environmental impact assessment of the Davis Station sewage outfall was done to provide information to direct the upgrade of wastewater treatment facilities. The aims were: 1) Determine the properties of wastewater effluent; 2) Assess the hydrodynamic characteristics of the nearshore marine environment; 3) Describe the nature and extent of impacts. In addition we examined the potential impacts of wastewater treated according to the minimum requirements under the Antarctic Treaty (Madrid Protocol), including the examination of likely dispersal and dilution conditions in Antarctic coastal waters.

Wastewater was high in BOD, nutrients, solids and contaminants. Levels of faecal indicator bacteria were typical of untreated human sewage. Wastewater was lethal to local marine invertebrates at dilutions as low as 3%. Thirty sites were surveyed for sediment chemistry, sewage biomarkers, and micro and macrobiological impacts. The marine environment at Davis is heterogeneous with a range of habitat types, sediment properties and physical exposure. Current meters and a coastal discharge model were used to examine hydrodynamic conditions. Hydrodynamic studies indicated that wastewater was generally dispersed in a narrow plume along the coast in the direction of the prevailing winds, however, there was retention of effluent around the discharge point and the wharf. Faecal indicator bacteria and contaminants were detectable in sediments up to 1.5 km from the outfall. The rate of dispersal was insufficient to prevent accumulation of contaminants in local habitats. Histopathological deformities were observed in fish, consistent with exposure to contaminants present in wastewater. There was evidence of impacts on macrobiological communities, and analysis of nitrogen stable isotopes indicated sewage and associated contaminants are making their way into the food chain. Genes encoding for anti-microbial resistance in *E. coli* in seawater, sediment and carried by non-native organisms have been introduced into the Davis marine environment including in a filter feeding mollusc. Based on the results of this study the Australian Antarctic Division is installing a new treatment facility at Davis which will treat wastewater to the standard of drinking water. The results of this study provide evidence that the minimum requirements of the Protocol on Environmental Protection to the Antarctic Treaty are insufficient to prevent environmental degradation and this situation is likely to be common at Antarctic coastal stations.

Cleaning up Antarctica: monitoring ecosystem health 12 years after remediation of an abandoned waste disposal site at Casey Station, Antarctica

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Thala Valley, near Casey station in East Antarctica, was the location of a shoreline landfill/waste disposal site for station refuse including domestic rubbish, construction materials, machinery parts and waste chemicals from 1964 through to the mid 1980s. Some of this waste material ended up in adjacent Brown Bay through the practice of 'sea icing', while the erosion of soil by meltwater flow through the valley and tidal inundation resulted in the input of approximately 10 m^3 of contaminated soil and waste materials to the bay annually. This resulted in contamination of the sediment in Brown Bay with metals such as Cd, Cu, Pb and Zn and petroleum hydrocarbons. Assessment of the contaminated site and the surrounding marine environment demonstrated a causal link between anthropogenic contamination and ecosystem damage (i.e. human impacts).

In 2003-04 the Australian Antarctic Division, guided by obligations to cleanup abandoned work and waste disposal sites in the Madrid Protocol to the Antarctic Treaty, undertook remediation of the Thala Valley site. Frozen waste and contaminated soil were excavated into containers for transportation to Tasmania for chemical treatment (metal fixation) and disposal. A monitoring program was begun to look at both the impacts of the remediation operation as well as the long term health and recovery of the local ecosystem.

Measurement of contaminants in the terrestrial and marine environment (in soil, sediment, and water) has been an integral component of the remediation process at Thala Valley. Chemical monitoring of contaminants during, and 5 and 10 years post the cleanup, in conjunction with biological monitoring of the marine ecosystem, have informed on the fate of contaminants in the benthic environment and the degree of success of the cleanup.

We present an overview of contamination data for Thala Valley and Brown Bay determined pre-, during and post-cleanup of the site, documenting the chemical changes occurring in Brown Bay sediment over this time period. The principal focus is on metals, but also includes data on hydrocarbons and POPs. We review the analytical methodology employed to acquire the data, and touch on potential future developments to improve capability in monitoring contaminants in cold and remote regions.

Persistent organic pollutants in red- and white-blooded High-Antarctic fish

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The Antarctic ecosystem is progressively exposed to anthropogenic persistent organic pollutants (POPs), which are introduced via atmospheric long-range transport and accumulated by global distillation. Particularly Antarctic fish, which appear to possess low endogenous elimination rates for chemicals, are expected to increasingly accumulate POPs in their tissues with ongoing anthropogenic pollution.

In this study, we aimed to determine the pollutant load in muscle of red- and white-blooded (*Trematomus loennbergii* and *Chionodraco hamatus*, respectively) High-Antarctic fish from the ice-free Filchner region in the Weddell Sea. We compared these data to our previous measurements of POPs in Sub-Antarctic icefish from the South Shetland Islands and Antarctic Peninsula.

Using a chemical-analytical method, we determined concentrations of polychlorinated biphenyls (iPCBs, dlPCBs), polybrominated diphenyl ethers (PBDEs), hexachlorobenzene (HCB), hexachlorocyclohexanes (HCHs) and dichlorodiphenyltrichloroethanes (DDTs) and calculated toxic equivalents (TEQs). We found lower levels of PCBs and of selected pesticides, such as HCBs, HCHs and DDTs, in the High-Antarctic compared to the Low-Antarctic fish. In contrast, the PBDEs were higher in the High-Antarctic species. Amongst the two High-Antarctic species analysed in the present study, the red-blooded *T. loennbergii* displayed generally lower contaminant levels (normalized for lipid weight) than the white-blooded *C. hamatus*, apart from the PCBs. The TEQs of the High-Antarctic species were at least 10-times lower than in Low-Antarctic fish. This indicates that toxicity effects by POPs could be lower in High-Antarctic than in Low-Antarctic fish.

Generally, the body burdens of High-Antarctic fish lie about10 to 100-times below those of fish from the Northern hemisphere. Yet, body burdens of Antarctic fish are increasing since the 90s. Particularly the fact that POP concentrations are in a similar in Low- and High-Antarctic notothenioids reflects a global redistribution and increasing transfer of POPs to the Southern Ocean. This could contribute to an increasing bioaccumulation of contaminants in Antarctic fish in the future.

Detection and quantification of unseen human impact on the McMurdo Dry Valley soils: new forensic DNA methods.

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Human presence is ever-increasing in the Antarctic, primarily in forms of tourism and science-driven activities. Under the Antarctic Treaty of 1959 and the Environmental protocol of 1991, there is an obligation to keep the environment in a 'pristine' state. However, the current definition of 'pristine' focuses on visible impact, such as physical (to the landscape and visible biota) and chemical (i.e., release of material) disturbances. The unseen impact in the form of human genetic material and human-associated microorganisms is poorly understood and much less quantified in an Antarctic environment. The McMurdo Dry Valley (MDV) ecosystem is microbe dominated and is comprised of unique microbial communities. Direct experimentation has demonstrated that these microbial communities have the capacity to respond and change to altered environmental conditions. The effects of releasing human DNA and associated microbiota via routine activity have not been investigated in an MDV environment, for instance, whether microbial community composition and functionality is altered and whether there is a change in overall phylogenetic signal. It is necessary to identify whether the release of such materials is an environmental risk.

As part of New Zealand's effort to carry out evidence-based risk assessment for the Dry Valley Ecosystem Resilience project (DryVER), this research will identify whether human trace (i.e. human genetic materials and microbes) persists at detectable levels in an MDV environment and will quantify the remnants of human activity over spatial and temporal scales. Study sites were areas of human activity in the MDVs, including camps and stations from which soil samples were collected. The accumulation of human impact over time and also recovery of a camp after human visitation had ceased was also assessed, by incorporating a range of historical and contemporary campsites. Newly developed genetic tools in conjunction with digital PCR were used to detect human presence at the lowest possible limit, to a single human cell. The data generated from a MDV setting will be used to create metric tools for detecting human genetic and microbiological footprints that will have applications in environmental forensics. The direct outcome of this research will be a review of the environmental management systems in place, namely the McMurdo Dry Valleys Antarctic Specially Managed Area (ASMA) Management Plan. Better management will safeguard the unique MDV ecosystems by using the best practice to minimise anthropomorphic impact.

Spatially concentrated krill fishing is likely to impact penguins

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Antarctic krill are important prey for Adélie, chinstrap, and gentoo penguins that breed around the Antarctic Peninsula; a commercial fishery also targets krill in this region. We used 38y of ecosystem data collected as part of the U.S. Antarctic Marine Living Resources (AMLR) Program to infer whether the krill fishery has impacted penguins. Acoustic estimates of local krill biomass in the Bransfield Strait and immediately north of the South Shetland Islands varied by as much as two orders of magnitude from 1997-2015. During most of this time (1997-2009), the krill fishery removed an average of about 34,000t of krill per year from the Antarctic Peninsula region, but, since 2010, the fishery has removed an average of about 121,000t·y-1, with a substantial proportion of this catch taken from the Bransfield Strait. Several indices of penguin performance (e.g., clutch-initiation date, foraging-trip duration, and breeding success) measured during 1978-2015 at two sites (one site each on the southern and northern shores of the South Shetland Islands) decreased (e.g., delayed clutch initiation, longer foraging trips, and decreased breeding success) when the Oceanic Niño Index (ONI) indicated that conditions were "warm." We corrected the indices of penguin performance for this climate signal, matched them to estimates of krill biomass and fishery catches in time (by season) and space (using telemetry data), and used a Bayesian random effects model to estimate first-order functional relationships between local krill biomass, local krill harvest rates, and penguin performance. Mean penguin performance decreased when krill biomass in the Bransfield Strait or immediately north of the South Shetland Islands was on the order of 104t. Mean performance also decreased when krill biomass was on the order of 105 or 106t and catches by the fishery were similar in magnitude to krill biomass. Until now, penguin performance has not been related to fishing. We hypothesize that our new result is attributable to the spatial pattern of recent krill fishing; fishing is now concentrated in locations where the prevailing circulation probably retains krill and where telemetry data demonstrate that penguins routinely forage. Given its relationship to the ONI, we expect penguin performance to decline if the frequency of warm years increases, but our results also suggest that the ecosystem effects of spatially concentrated fishing for krill may be equal to and more proximate than those of climate change.

Theme 5
Societal impact of Antarctic biological science

Research activities in Antarctica as part of the continuing education project "*Zoology in focus*" at the State University of Ponta Grossa

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The habit of just using the class room as teaching environment limits the learning conditions. The progresses related to a formative and innovative school implicates in the use of appropriate didactic resources and in an emphasis in interaction between students and teachers. In this context the continent Antarctica, is still a subject little explored in the teaching of Sciences and little commented, or even excluded of the text books in the elementary and secondary school. Based on this problem, this work had as objective to inform elementary, high school and university students and the local community in a didactic way some research activities related to the National Institute of Science and Technology on Antarctic Environmental Research (INCT-APA). The didactic activities took place at the Zoology Laboratory/Department of General Biology in the State University of Ponta Grossa, Paraná, Brazil. In 2014, a didactic exhibition on the theme "*Antarctica*" was performed, where equipment and samples of organisms collected during the Antarctic expeditions were exposed, in addition to illustrative panels related to the procedures and equipment used for sampling. The exhibition is part of the extension project of "*Zoology in Focus*", with the aid of students of the undergraduate course in Biological Sciences. The activities were accomplished in the morning, afternoon and night periods for the students of the different shifts and courses. At the same time is being worked out a collection of results of Antarctic researches obtained by the INCT-APA. Lectures on the impact of anthropic activities on Antarctic environment were carried out for the students and teachers of the post-graduate program in Biological Sciences, concentration area in Evolutionary Biology of the Ponta Grossa State University. The teachers were questioned in relation to the activities developed in the Antarctic projects, if these were expected in relation to the school activities. The participants were questioned about the degree of satisfaction and learning they acquired with the exposition. The results obtained with the exhibition demonstrated the curiosity and satisfaction on the proposed theme. As a result of the exhibition a note was published in the internet page of the University and an interview with the local Educational TV was transmitted. More than 100 visits to the exhibition by undergraduate students of different courses of UEPG, employees and local community were registered.

The UK Polar Network, who we are and our outreach activities

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The UK Polar Network was established in April 2007 as part of the 2007 – 2009 International Polar Year. We are the UK branch of the Association of Polar Early Career Scientists (APECS) and currently have over 500 members, from aspiring undergraduates to Masters and PhD students, postdoctoral researchers, and recent faculty appointees. One of our primary aims is to organise education and outreach events with regards to polar issues for young people and the general public. The UKPN Education and Outreach working group undertakes many outreach events each year including school visits and science festivals which allow pupils and students to learn more about life and research in Polar Regions, as well as the careers open to school leavers in similar fields. We have an active presence on social media sharing to advertise and share the success of our current work.

Over the last two years we have worked in conjunction with the *Our Spaces* foundation to raise awareness of Antarctica Day through an Antarctic flags project. In 2016, we sent 232 flags designed by children from 40 schools in 12 different countries to Antarctica with polar researchers. We are always interested in collaborating with other science organisations, for example recent collaborations with the International Polar Foundation have included a teaching workshop at the *Association for Science Education* annual conference and the *Sea Ice and Shackleton* workshop for school children at the Think Tank Museum in Birmingham.

In the future we hope to continue and expand our Education and Outreach work with new collaborations and workshops. Next year the UKPN will be conducting a Polar Science workshop at the @Bristol Science Center, attending the Edinburgh Science festival, running two early career workshops and visiting multiple schools around the country.

If you are interested in joining the UKPN, forming a collaboration with our team, or getting involved with our outreach activities please feel free to contact us or find out more online at http://polarnetwork.org/education-and-outreach/.

Geolocation Journeys: a Science+Arts collaboration supporting marine predator research.

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Geolocation Journeys is an innovative collaboration between marine predator scientists at the Institute for Marine and Antarctic Studies and the Tasmanian College of the Arts helping to increase public awareness and support Antarctic marine predator research. This presentation will discuss the cross-disciplinary collaboration and how the project is creatively promoting research by engaging public support.

Geolocators are tracking devices used on Southern Ocean top predators, from delicate shearwaters to imposing elephant seals. Geolocators record ambient light levels, water temperature and time enabling scientists to uncover the foraging movements of predators to identify regions that are of high ecological significance. By gaining an understanding of how marine predators use their ocean habitats, and in particular how these regions are affected by human activities such as industrial fishing and climate change, more effective management strategies can be put in place for their protection.

Geolocation Journeys brings together scientists and artists to create unique wearable artworks using 'retired' geolocators, to raise awareness of the extreme migrations these species embark on and the changing climate they are currently experiencing. With each piece comes a history of the individual animal the tag was deployed on and a printed map of the journey it undertook. These pieces are constructed using repurposed scientific materials; embossed with the unique identification number of the tagged animal.

By sharing artworks with the non-scientific community through public talks, school workshops and open days these tactile objects metaphorically transport people into the Southern Ocean, with a view from the perspective of a seabird or seal. These tiny pieces stimulate and aid critical dialogue about Antarctica and the rapid changes it is experiencing. This project not only captivates those ecologically minded, but by bridging the fields of art, ecology, physics, astronomy, engineering and mathematics it appeals to a broad, curious audience.

2016 US National Science Foundation Antarctic Biology Course: Austral winter studies in the Palmer Basin, Antarctic Peninsula

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The US National Science Foundation (NSF) Antarctic Biology Course is an advanced training program for PhD students and postdoctoral-level scientists. The intent is to engage early-career scientists in polar research through working on site in Antarctica. Since 1994 more than 240 scientists from over 130 institutions representing 24 countries have benefitted from participation in this series of training programs. The most recent NSF Antarctic Biology Course was conducted in July 2016 at Palmer Station, Anvers Island (Antarctic Peninsula) and on board the ARSV Laurence M. Gould, providing a rare opportunity for participants to work in this region during austral winter. In addition to experimental work on physiological adaptations of polar organisms and fieldwork at Palmer Station, a portion of the course was devoted to investigating winter oceanographic conditions. Data from cruise activities are presented here. Shipboard work included collecting water-column samples, phytoplankton tows, mid-water trawls, and hydrographic measurements in the Palmer Basin and adjacent waters (Biscoe Bay, Gerlache Strait, Andvord Bay). Minimum surface water temperatures were -1.7°C, increasing to 1.5°C across a thermocline that extended to 600m (~halfway to the seafloor). The vertical profile of salinity matched that of temperature, with 34.1PSU at the surface and 34.7PSU at depth. Phosphate concentrations were constant with depth (2.3±0.0µM). Silicate (82.1±7.3µM) and nitrate (33.0±0.9µM) increased with depth, while nitrite (0.2±0.1µM) and ammonia (0.6±0.5µM) decreased with depth. Higher numbers of bacteria ($9x10^6$ cells l^{-1}) occurred in surface waters, diminishing to $1x10^6$ cells l^{-1} at 1,200m. Nearly 100 taxa of phytoplankton were identified from net tows taken during the month of sampling in the region, with the large majority of species being diatoms. Estimates of phytoplankton cell densities ranged from 1,400 cells l^{-1} at the surface to 20 cells l^{-1} at 1,200m. Approximately 50% of cells observed under fluorescence were unidentified picoplankton. Chl*a* concentrations were 0.06±0.01µg.l^{-1} at the surface and 0.01±0.00µg.l^{-1} at depth. In contrast, maximum chl*a* concentrations in sea ice were >2.0µg.l^{-1}. Krill (*Euphausia antarctica*) numbers from mid-water trawls were estimated at <1 to 13 individuals m^{-3}, and 55% of krill collected were <30mm in length. In addition to enhancing education and training of early career scientists, the data collected during this training program will contribute to furthering knowledge and understanding of austral winter patterns of phytoplankton, krill, and water structure in the coastal waters of the Antarctic Peninsula.

Adaptation of microbial life to environmental extremes - Book review

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The book is at its second edition containing researches and review of environmental microbiology of extremophiles.It has 11 chapters dedicated to different environments. The book is edited by two scientist dedicated to the study of extremophilic microorganisms and the authors of chapters are well known specialists in their fields of activity.

The first chapter is dedicated to general things regarding the physico-chemical limits of life, one of the most important statement for general theoretical biology and practical importance for biological sciences, showing main factors of environments and survival and adaptation of microorganisms (Helga Stan Lotter).

The second chapter is about the life in oceans in the so called anoxic hypersaline basins (Mapelli et al.).

Chapter no. 3 is dedicated to microbial life adapted to thermal and hyperthermal water environments (Gudmundur et al).

Chapters 4 and 6 disccuss the adaptation of microbes to dry environments (Heulin et al.; Billi et al.) and their importance for space studies.

The chapters 5 (Pearce) and 7 (Fendrihan et Negoita) discuss about psychrophilic microorganisms their adaptations their habitats, and possible uses in biotechnologies in differents fields of activity - industry, food industry, light industry agriculture environment protection, medicine, and so on.

In chapter no. 8 the authors showed their experience of research of the halophiles and exteme halophilic microorgansms recovered form man made formation on the sites of salts mines - antropogenic salted lakes (Enache et al.) The Chapter nr 9 is about the acidophiles, another group of extremophilic microorganisms (Mirete et al).

The chapter 10 discuss the cases of environments with very low nutrients content as clean rooms and low humidity (Moissl-Eichinger)

The final Chapter 11 (Lee et al.) discusses the very interesting problem of meteorites as possible agents of panspermia and their role in prebiotic chemistry and origin of life in Universe.

Training 45 teachers to science from the field

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The French antarctic expeditions have reached an exceptional achievement through the project "Embarquez en Antarctique!", under the partnership of IPEV (the french polar institute), the Maison Pour La Science en Alsace, the Maison pour la Science en Bretagne (two institutions devoted to scientific and pedagogic collaborations between teachers and scientists), and the Muséum national d'Histoire naturelle (french national museum of natural history). Classically, outreach initiatives are directed towards schoolchildren. Here, for the first time the project is aimed to train teachers to Science directly from the field at Dumont d'Urville, the coastal French station. 45 teachers have been selected for their pedagogic interdisciplinary project one year and half before the cruise itself. Teachers were immersed into a zoological identification workshop of antarctic fauna gathering 10 taxonomists. The cruise itself included both a teacher's trainer on the field and a scientist, who were following the deployment of six scientific programs, and covering all aspects of professional life in an antarctic station. They produced more than 60 pedagogic documents for the trained teachers, from epistemology to technics, logistics, various skills of technical, administrative jobs that makes a scientific station work. A direct Skype event connected the teacher on the field to 500 schoolchildren. On the overall, and at the end of the process, 900 schoolchildren were initiated to science from the antarctic field and though the interdisciplinary project of their teachers. They were initiated to the diversity of jobs we find in an antarctic station as well. The project is aimed to explain how science works from the technical, logistic, sociological, epistemological points of view, to promote mutual respect and enrichment among all kind of jobs, education included. Science is not an isolated job: it is a collective enterprise.

Melting in the spotlight: Securing Antarctica's future in popular media

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As Antarctic research yields increasingly urgent warnings about our planet and major political powers embrace climate-change denial, we are called upon to seek new methods of communicating those concerns and rise above the fray. Meanwhile, popular media demonstrate themselves as effective and palatable methods of shaping popular consciousness, so much so that we've repurposed the word "binge". It is necessary to turn to the next generation of media makers to ensure that lessons learned in Antarctic research have voice.

This presentation suggests innovative academic methods that would enable and inspire researchers and students within Antarctic studies to forge a connection with students and graduates within the arts. By referring to my familiarity with Emerson College's unique interdisciplinary offerings, I will propose methods of collaboration with the goal of developing persuasive and informative media content meant to elevate the presence and impact of Antarctic stories and research through tools including fiction, television, interactive games, drama, etc. I will describe action items that I integrate into my own teaching and creative pursuits, and that may be of use to instructors, faculty members, and granters of research fellowships pertaining to arts and/or science.

Young artists and writers are often waiting impatiently for their next gig; Antarctic researchers have an opportunity to employ their talents as a platform for amplifying their own perspectives. Working across disciplines offers an opportunity to raise the alarm for climate change in a way that will make the public listen and act.

POLAR WEEKS and other education and outreach activities related to biological sciences: do, don´ts and next steps

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The successful education, outreach and communication work has been developed in the last decade in various countries, including Portugal. POLAR WEEKS (i.e. taking polar scientists into the classroom, to give talks personally or via skype; see Bulgaria et al. (2016, Portugal et al (2016)), coordinated by the Association of Polar Early Career Scientists of Portugal (APECS Portugal) and Polar Educators International (PEI), endorsed the Portuguese Polar Program PROPOLAR, have significantly contributed to bring polar science to a wide range of audiences. This initiative, in collaboration with various countries, occurs twice a year involved 17 scientists, 13 200 students and almost 700 teachers in 2016 in Portugal. In this presentation, important for SCAR Biology participants, we will review some national activities in a wider international context (e.g. Santiago et al. (2016), providing guidance to other programs on what works and what doesn´t. These include POLAR WEEKS and activities that brought a close collaboration between scientists and teachers/educators in SCAR, ATCM, APECS and PEI, such as efforts of SCAR CBET and SCAR research programs (particularly the biological science research programs), the work by Intersessional Contact Group on Education and Outreach (ATCM ICG E & O) and the main results the International PEI workshops (Bulgaria et al. (2016). Portugal has also been highly active at the Polar Educators International, throughout its presidency and the co-organization of the International Polar Science Education Workshops, including the most recent one (Italy, 2017). Various papers on the issue have started to be published aimed to bringing polar education on biodiversity (e.g. Xavier et al. 2016a), outreach (Xavier et al. 2016b) and strong links in this field with other countries have been strengthened. In conclusion, the Portuguese polar community (Polar scientists and educators) has carried out a wide range of education and outreach activities, with an international network (connecting SCAR, APECS and PEI, and numerous countries worldwide), that has produced useful methods, tools and materials that can be applied by other countries.

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Promoting science and conservation in Antarctica through collaborative innovation and active citizenship

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The oceans around Antarctica are some of the most pristine in the world. However, with parts of Antarctica undergoing rapid environmental change, the habitat and biodiversity are under increasing pressure from climate change and human activity.

Antarctica and the Southern Ocean are remote and inaccessible to the general public. Scientists and government institutions have limited funds, capability and channels for engagement of their work to connect and alert people to science and critical conservation issues in the region.

To fill this gap, responsible ecotourism can provide inspiring experiences for visitors – the majority of whom are supporting national science programmes through taxes – to become Antarctic ambassadors and informed, active citizens. In response, a number of organizations are taking a fresh, collaborative approach to ecotourism as a potential tool to conduct research, raise awareness of the importance of polar science on a global scale and ultimately achieve conservation goals.

Members of the International Association of Antarctica Tour Operators (IAATO) are working with researchers – governmental and non-governmental alike - and conservation groups such as the Antarctic and Southern Ocean Coalition (ASOC) and the WWF to promote understanding of this virtually uninhabited great wilderness. Through IAATO's framework of environmentally responsible procedures and guidelines, visitors are given an educational and potentially life-changing experience to be voices for change while actively assisting with globally recognized science projects.

Bridging the gap between polar sciences and society- an Indian initiative

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For the past decade, outreach and communication activities in polar sciences have gained momentum in India. Thirty five years ago, India started its foray in Antarctica. In order to increase and have a perceptible Indian contribution in polar sciences, Ministry of Earth Sciences (MoES), Govt. of India has established the National Centre for Antarctic and Ocean Research (NCAOR), Goa, dedicated to polar and ocean research in the year 2000. Efforts have been made by NCAOR and MoES to enhance the public understanding on polar science. The idea is to disseminate knowledge on polar regions, inculcate scientifically critical thinking and thereby making a nation of scientifically aware people.

To bridge the gap between polar sciences and society, it is the foremost to explain the relevance of Polar Regions for a country seated in tropics. Polar Regions are a key to the global ecosystem and barometer of the health of the planet (IPCCC report, 2007). These are the places where global processes connect across the earth with the far reaching effect on the atmospheric and ocean circulations (Azzolini et al., 2012). NCAOR caters to Education, Outreach and Communication (EOC). Education and outreach activities at institutional level (school/college/ university) not only make students aware of the Polar Regions but also try to change the social perception that conserving environment is only in the hands of the people. Discussion on various SSIs (Socio-scientific issues) like global warming, climate change, pollution in context with polar sciences as well as in general, motivates students to think critically and define their responsibilities in conserving the environment (**Shabudin et al., 2016)**. This also creates interest to pursue their career as researchers.

This abstract discusses the strategies being used by NCAOR to showcase the polar world to the scientific as also the non- scientific community (students, general public, etc). Example, teacher's training was conducted at NCAOR to ensure better understanding of polar regions that will further, educate students about polar sciences. Active participation in various regional and National scientific fiesta/ fairs and exhibitions provide opportunities for direct interaction with the students and general public.

These EOC efforts by NCAOR and other research institutes in India associated with Indian Antarctic Program has committed to ensure sustained public appreciation and interest on the Polar Regions and motivating young generation to be a part of polar scientist team for understanding and conserving the polar environment.

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Evaluate earth's health trough polar regions: A thematic module from IRRESISTIBLE project highlighting polar science

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IRRESISTIBLE is a European project that aims to increase students' content knowledge about research by bringing cutting edge research into the school program, and to foster the discussion among students about responsible research and innnovation (RRI) issues with the design and development of thematic modules. In each of the ten partner countries, researchers, science teachers, educational experts, exhibition experts from museums/science centres developed a thematic module on a cutting edge topic. Polar science, particularly Antarctic, was one of the cutting edge themes chose to develop a module proving to be an outstanding context for discussion of the dimensions of RRI. The module purposes the analysis of scientific papers in several areas of research, particularly in marine biology and gives students the opportunity to contact with the science that is being developed by polar scientists, its importance and the reasons why polar science should be carried out. It is intended that students conclude about the relevance of the research for the advance of knowledge in Polar Science and identify RRI practices. As product the students have to build an interactive exhibition on the theme open to the general public. In the last year, the module was applied in Portugal and The Netherlands and the best exhibits from the project were presented to the European public during the European night researchers held in September 2016 in Kiel. The module is available in the IRRESISTIBLE and SCIENTIX websites and It is expected to be applied by other countries. In this poster we wish to present the Polar Science module, as well as, the potential of scientific articles as an educational tool and as a promoter of knowledge about polar science and also a more scientifically literate and participatory society open the discussion of socio-scientific controversies.

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http://www.irresistible-project.eu/index.php/en/

Microfibers in ocean waters in Admiralty Bay, Antarctica

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An increase in the abundance of marine microplastics has been indicated in the latter years (Wright et al. 2013, Taylor et al. 2016). Marine microplastics occur in a variety of shapes from fibers to irregular fragments to spheres and rods. The aim of this study was to describe the occurrence of microfibers in ocean waters in Admiralty Bay, Antarctica. To investigate this claim samples were collected in Admiralty Bay, Antarctica during the XXIX Brazilian Antarctic Expedition (2010-2011). These samplings were compiled in four different dates (14th and 23rd of December 2010 as well as the 3rd and 10th of January 2011) with a conical net with a 150µm mesh size and mouth of 50cm diameter, equipped with a flowmeter. Samples were taken in three replicates in 5 stations from five minutes oblique tows at 2knots from the sea bottom (30m) to the water surface. The values have been standardized to 100m^3 (Freire et al. 2006). A total of 604 microfibers were collected in 60 samples, with an average density of 2.40(±4.57)microfibers.100m^{-3}. Microfibers size 10µm in diameter of various lengths and colors (blue, red, black, white opaque and clear) were collected. Most of these microfibers were entangled in various different zooplankton species. Since the equipment for sampling zooplankton had a net of 150µm probably the sampling is underestimating microfibers of smaller size that were not entangled in zooplankton.

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Thermal and other ecological preferences of native and non-native Collembolan species in Deception Island

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In this work we examine the effects of geotermalism, human footprint and other environmental variables in the distribution of native and nonnative collembola in Deception Island. Fifteen species have been found in 159 samples from 16 different island locations during four field campaigns. Two different scenarios could be observed related to temperatures. Heated grounds could act as habitat for the establishment of cosmopolitan species by sustaining milder temperatures than those limiting life on the Antarctic cold grounds. Alternatively, heated grounds could prove to be a difficult habitat to colonize and so the native species could have the upper hand to exploit this environment after a long time of exposure and adaptation to low temperatures. Nonetheless it is precisely at the low temperature soils (0-10º) where the highest richness and diversity were found. Remarkably, increased temperatures from geothermal activity have a negative effect in the diversity of species. Policy to prevent biological invasions has yet to be systematically applied. Furthermore, we describe the correlation between different species and types of microhabitats present in the island. Slope and aspect also generate effects in the abundance and diversity of collembolan species. In this context, Deception Island has been identified as one of the most densely occupied sites by humans in Antarctica and subsequently of highest risk for biological introductions. Thus, distributional information is essential to develop strategies for the effective conservation of the Antarctic biodiversity, by focusing the management on the most vulnerable spots for species invasions.

Nanoplastics impact on Antarctic organisms: preliminary data on the Antarctic sea urchin *Sterechinus neumayeri* coelomocytes

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Trillions of plastics have been estimated to float in the ocean surface[1], representing a serious threat for marine ecosystems worldwide, together with global warming and ocean acidification. Although the Antarctic Polar Front has been historically seen as strong biogeographic barrier, plastic debris have been surveyed in the Southern Ocean and recently below the 60°S[2], raising concern about their potential impact on the Antarctic marine ecosystems. Once in the marine environment, large plastic debris undergo continuous fragmentation through weathering processes[3], generating micro- (<5mm) as well as nanoplastics (<1µm)[4]. However, the identification of the smallest fraction of plastics in environmental samples is difficult due to current analytical limitations. For these reasons, polystyrene nanoparticles (PSNPs) have been recently adopted as model for nanoplastics in ecotoxicological studies. Our findings on Mediterranean sea urchin *Paracentrotus lividus* showed that PSNPs are able to accumulate in embryos, elicit developmental defects and activate apoptotic pathways, depending on PSNP surface charges[5,6]. Marine invertebrate species from remote areas are known to be more sensitive to environmental changes including pollution, since they are characterized by weak genetic differentiation[7]. The present study aims to evaluate for the first time the effects of negative carboxylated (PS-COOH, 40nm) and positive charged amino-modified (PS-NH_2, 50nm) PSNPs on Antarctic sea urchin *Sterechinus neumayeri* coelomocytes through *in vitro* exposure. Antarctic sea urchins (n=14) were collected in February 2016 in Maxwell Bay, King George Island, Antarctica and acclimatised at 0°C for 4d at the Chilean Antarctic Station "Prof. Julio Escudero". Coelomocytes (10^6cells/ml) were exposed to 0, 1 and 5µg/ml PSNP suspensions in 0.20µm natural seawater and incubated at 0°C. The experiment was repeated twice, with three to five replicates for experimental group. After 6 and 24h of exposure, cell counting and phagocytosis were determined[8]. RT-PCR analysis of target genes involved in cellular stress response (*HSP70*, *HSP90*, *Grp78*, *Grp170*, *Sod*, *Cat*, *Bcl-2*, *NF-kB*) was also performed[9]. PSNPs were able to dose-dependently decrease phagocytosis, with the strongest effect observed after 6h of exposure to positive surface charged PS-NH_2. Moreover, PSNPs induced a significant up-regulation of the selected chaperones, in particular at 1µg/ml PS-COOH after 24h. These results suggest that *in vitro* exposure of Antarctic sea urchin coelomocytes to PSNPs can lead to an impairment of the immune response and is able to modulate stress-related genes, triggering a defence cellular mechanism towards PSNPs. Our findings represent a first contribution aimed to assess the impact of nanoplastics to the Antarctic marine species.

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Distribution patterns of invertebrate species introduced into the sub-Antarctic Kerguelen Islands

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The introduction of alien species and the subsequent invasion process, can threat the sub-Antarctic biodiversity. The Kerguelen Islands (7,200 km²), which are located in the Southern Indian Ocean, are no exception to this rule. Before their regular human occupancy in the early 20th century, terrestrial ecosystems of this archipelago included 24 native invertebrate species (insects, spiders, gastropods and earthworms). Nowadays, 32 introduced species have established, of which seven are invasive. Introductions occurred into three main sites: one farm and one whaling station between 1913 and 1926, and the permanent research station from 1950s onwards.

This archipelago is conventionally divided into three main sectors according to their accessibility, ranging from easy, limited and difficult to access. None of these three sectors is free from introduced species. However, the areas furthest from the introduction sites have fewer introduced species (24-35%) than the easy access areas (34-64% of introduced species). Among the introduced species, some have strong local dynamics such as the spider *Tenuiphantes tenuis*, others have a very wide distribution and are present almost everywhere, such as the fly *Fucellia maritima* or the aphid *Myzus ascalonicus*. The predatory carabid *Merizodus soledadinus* is also distributed extensively, but the geographic expansion of this flightless insect is restricted by several geographical barriers. After their establishment, the expansion speed of invasive species depends on their dispersal capabilities and on the environmental conditions. For three out of these seven invasive insects, a few decades elapsed before they conquered their current territory: geographic expansion of *M. soledadinus* started in 1940, 1970 for *M. ascalonicus* and 1980 for the fly *Calliphora vicina* (Laparie 2011, Lebouvier et al 2011, Ouisse 2016). The rate of progression of *M. soledadinus* had tentatively been estimated at 3km/year (Chevrier, 1996).

Since the establishment of a Nature Reserve in 2006, biosecurity measures have been put in place to limit the introduction and dissemination of alien species.

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Effect of the trace element contamination over bacterial populations from Fildes Peninsula (King George Island), Antarctic.

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Soil contamination with heavy metals, such as copper (Cu) zinc (Zn), cadmiun (Cd), lead (Pb), mercury (Hg) nickel (Ni), chromium (Cr) and arsenic (As), is a widespread problem that affect several environment including pristine areas. Although Antarctica is often considered a remote and pristine environment, some ice-free areas have been subject to human impacts for 50 years or more. A high density of scientific stations is found in Arley Cove area, located on Maxwell Bay shoreline, Fildes Peninsula, King Geroge Island, make it a potentially one of the most impacted areas in Antarctica.

Recent results have been shown the trace metal contamination in surrounding areas near to the Chilean (Escudero) and Russian (Belinghousen), mainly related to high levels of Zn, Pb, Cd, Cr and Ni produced by anthropogenic sources (Padeiro et al. 2016). Little is known about the bacterial community in Fildes Peninsula in such soil and less about the taxa common to polluted soil. We wanted to know the effect of different physicochemical factors over bacterial community present on impacted and non impacted area. The use of 16S rDNA myseq illumina sequencing was performed to quantify bacterial taxa and determine variations on the bacterial community structure present in heavy metals contaminated soils from Fildes Peninsula. Most of the sequences were assigned to the Proteobacteria (Betaproteobacteria and Gammaproteobacteria) and Actinobacteria. No differences between bacterial communities of impacted and non impacted soils was found, but a decrease in bacterial diversity was observed rarefaction analysis in samples with high concentrations (81-418 µg/g-1) of lead (Pb). This study strongly points to the need for substantial efforts (starting with prevention measures and then the implementation of remediation technologies) to limit human-derived contamination impacts on the local environment and resident species and communities.

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A microplastics investigation in Arctic fish

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Microplastics (MPs) are a ubiquitous pollutant of the marine environment being found in the open ocean, deep sea sediments, on remote shorelines and in a great diversity of biota. Despite its remoteness from the main sources of microplastic pollution, recent reports have found high abundances of MPs in Artic waters which may represent a threat to this relatively pristine environment.

The present study aims to assess the ingestion of MPs by three different Arctic fish species: the sculpin *Triglops nybelini* (Jensen, 1944), the polar cod *Boreogadus saida* (Lepechin, 1774) and the capelin *Mallotus villosus* (Müller, 1776). Specimens were collected during the TUNU-VI Cruise (5-17 August 2015) onboard of R/V Helmer Hanssen (UiT), in Northeast Greenland (sampling station: lat 7614.724303 N; long 00903.272281 W). In the laboratory, a NaOH-digestion technique was applied, in order to extract microplastic items from the fish gut. Post-digestion samples were vacuum-filtered onto pre-weighed borosilicate filter with a mesh size of 0.7 µm. This process was carried out using a laminar flow to prevent contamination. Retained biological material was flushed copiously with Milli-Q and then the filters were analyzed under a stereomicroscope. Potential microplastics retained on the filters were photographed and categorized according to their shape, color and dimension. The items were then identified for their polymer composition using Fourier Transform Infrared spectroscopy (FT-IR) analysis.

Plastic fibres were detected in the three studied species. The demersal *T. nybelini* resulted the most impacted species with plastic contamination in 37% of the examined individuals, whereas 24% of the pelagic sub-Arctic fish *M. villosus,* and only 9% of the Arctic *B. saida* contained plastics.

This work documents, for the first time, the ingestion of MPs by Arctic marine fish and indirectly provides further evidence of the presence of microplastics in the Arctic region, an area where it has been recently supposed to exist a “sixth garbage patch”, as is the case of the five other major ocean basin gyres in the Atlantic, Pacific and Indian Oceans.

Further studies are needed in order to expand our understanding on the extent and meaning of the problem that, if underestimated, might represent a serious hazard for the local marine biota and ecosystem.

Marine plastic pollution in the Scotia Sea; current knowledge and future directions

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Plastic litter and other objects which have been lost or discarded at sea are recognised as a major source of marine pollution. Understanding the magnitude and significance of the effects of marine debris on the Southern Ocean ecosystem requires systematic recording and reporting of relevant data in order to establish baselines and to understand trends.

Here we present data on three decades of marine debris monitoring in the Scotia Sea at various sites on South Georgia and at the South Orkney Islands. These data are submitted annually to the Commission for the Conservation of Antarctic Marine Living Resources (CCAMLR) as part of their marine monitoring programme. We examine (a) trends in the presence of beached marine debris; (b) rates of entanglement in debris of seabirds and marine mammals, particularly the Antarctic fur seal *Arctocephalus gazella*; and (c) the presence of marine debris in association with seabird colonies.

Microplastic pollution (particles < 5mm) is increasingly recognised as an issue of global concern, but, to date, there is little information on the presence of microplastic particles in the Antarctic marine ecosystem. We review the current state of knowledge and highlight the need for focussed research and routine standardised monitoring in the Southern Ocean.

Theme 6
Human biology at the poles

Multiple faces of affect throughout Antarctic over-wintering

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Challenges imposed by Antarctic over-wintering include confinement, social isolation, altered light-dark cycles and sleep problems among others. These challenges may result in altered mood states. The most severe form of emotional problems is known as Seasonal Affective Disorder, a transient form of depression throughout the dark months. A less severe form of mood changes is referred to as the Third Quarter Phenomenon; feelings of increased discomfort past mid-term that resolves towards the end of the mission.

In a multinational, multidisciplinary project we attempt to monitor mental states of the over-wintering crews on Antarctic stations by multimodal analysis of spoken language. Oral diaries are analysed by various means of psychological content analysis. On the other hand phonological features of speech were also assessed. Furthermore we had access to the Profile of Mood States questionnaire (POMS). This paper focuses on the comparison of preliminary analyses of the above measures with respect to seasonal changes.

Computerized content analysis of diaries revealed opposing trends in the occurrence positive and negative words which together result a pattern of emotional balance consistent the Third Quarte Phenomenon. Similar analysis of POMS data however shows decreasing trend of both positive and negative affect, which is consistent with a similar finding in content analysis and could be interpreted as increasing emotional bluntness. This observation is consistent with de overall decrease of occurrence of emotional words regardless of valence. Phonological parameters of speech on the other hand show approximately linear tendencies of decreasing pitch and increasing variability which may reflect decreasing anxiety throughout the mission

Emotionality in the ICE-Group: Content Analysis of Diaries of Antarctic Winteroverers

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In the emotionality studies on polar winterovering isolated groups, the most salient model is the Third Quarter Phenomenon (third quarter emotional dysphoria), but there are three-stage, two-stage, linear, and even no-pattern models thereof. Controversial empirical results are partly due to the great variety of measures across times and settings [1,2]. Given the swift progress of Natural Language Processing technologies in our days, content analysis seems to be a promising measure for future comparison. However, content analysis in itself has well discernible, elaborated approaches to identifying and assessing psychological states and processes from bulky texts, e.g. thematic, psychological construct-based, word frequency based content analysis, etc.). In the present study, we used the latter approach, the Linquistic Inquiry and Word Count (LIWC 2015) software [3].

Sample. In an ESA coordinated multinational study, weekly diaries of two winterovering crews at the Concordia Station, Antarctica, in 2013 and 2014, were subject to word frequency based content analysis by LIWC 2015, with specific focus on emotionality patterns. A total of 18 subjects (14 males and 4 females) provided cca 20000 words as mean total word count in their respective diaries.

Method. From the more than 80 word categories in LIWC 2015, only the Affective Processes word category was analyzed for the purpose of the present study; this category is cumulative for Positive Emotion + Negative Emotion words; the latter is cumulative for Anxiety, Anger, and Sadness words. The mean percentages of the occurrence of these categories in the diaries were analyzed by Repeated Measures ANOVAs. To test the hypothesis that Q3 phenomenon is present, we introduced the Emotionality Index (Positive Emotions/Positive Emotions + Negative Emotions); further, we performed a series of paired and planned comparisons for the respective word categories.

Results. As contrasted to the other three quarters, the Emotionality Index was significantly lower in the Q3 period; within Negative Emotion words, the Anger subcategory was significantly higher, whereas Anxiety or Sadness showed no significant difference. Affective Processes, as a cumulative category for all types of emotions, showed a statistically significant decrease during the mission.

Conclusions. The presence of the Third Quarter Phenomenon was verified in the diaries of Antarctic winteroverers. Fine-grained analysis revealed the salience of Anger rather than Anxiety or Sadness in the Q3 period. Further, it was found that that overall emotional self-expression becomes poorer with advancing time in long-term isolation.

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Physiological stress during Antarctic camp in Brazilian Antarctic Program (PROANTAR) participants

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Antarctica has a very challenging environment, from a physiological perspective, since the cold, wind and sensory monotony are considered stressful stimuli for the human body. However, acclimatization can attenuate sympathetic activation and immune suppression caused by this extreme environment. In addition, considering that physical capacity reduces sympathetic activation to these same stressful stimuli, it is plausible that individual adaptation will depend of the physical aerobic capacity.

The aim of this study is to investigate biological variables (core temperature, autonomic activity, endocrine and metabolic markers) and cognitive parameters of progressive adaptation to Antarctic stress / cold and confinement, as well as the relationship between the Antarctic acclimatization and the physical aerobic capacity of Antarctic researchers. Ten volunteers from Brazilian Antarctic Program will be evaluated during 7 weeks in an extreme camp, during Brazilian Antarctic Operation in 2016-2017 summer (January to February). Initially, the volunteers will perform a maximal progressive exercise test to measure aerobic capacity (VO2max) and basal data will be collected. In Antarctic field thermoregulatory variables (internal temperature by tympanic, GI or rectal temperature and skin temperature) and autonomic balance by measuring the heart rate variability will be evaluated weekly during our permanence there. Also, mood test (Brunel Mood Scale - BRUMS) will be analyzed. Samples of blood, saliva and urine will be collected to measure inflammatory profile through immunological response in serum, catabolic state of the body by the ratio cortisol/testosterone and catecholamine's concentration.

We will test the hypothesis that biological parameters of adaptation and aerobic capacity (VO2) may influence cognitive variables of volunteers along Antarctic field stay.

Evaluation of Closed-Circuit Rebreathers for the US Antarctic Scientific Diving Program

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The use of open circuit scuba in Antarctic diving, evolving from the double-hose to single-hose regulator, and twin cylinders to large single cylinders, has been the main mode of diving in the US Antarctic Program for over 50 years. With the advent of a variety of commercially available systems at reasonable cost, the use of closed-circuit rebreathers (CCRs) has been steadily increasing in the recreational and scientific diving communities over the past decade. The aim of this study was to investigate the reliability of CCR units *in situ* at McMurdo Sound, Antarctica for potential scientific use.

The scientific advantages of rebreathers include extended range, decompression optimization, extended underwater times, reduced logistical needs at remote sites, and increased productivity. They have been shown to be particularly valuable in studies of animal behavior (quiet operation, few or no bubbles), fish population studies, bioacoustics, deep specimen collections and biodiversity studies, and studies in caves. This radically different research approach would facilitate several avenues of Antarctic research, including, but not limited to: 1) behavioral studies, 2) studies of sea ice bottom communities, where bubbles from open circuit scuba can disrupt the platelet ice community, 3) studies of highly stratified lake communities, and 4) studies that require greater depths and/or longer exposures.

During October to November 2016 we performed 116 rebreather dives using seven CCR models. We evaluated the function and reliability in air temperatures of -15˚C and water temperatures of -1.8˚C. Using small temperature sensors we measured the temperature in various parts of the breathing loop. Major findings include: scrubber canister temperatures remained near ambient temperature throughout the dives, the breathing gas was only slightly higher than ambient temperature, and rebreathers must be kept warm prior to diving. Moisture in the breathing loop promotes freezing of the automatic diluent valve or dive surface valve, and mushroom valves. Only three unit failures occurred which required bailout to the surface. One other unit had significant electronic issues. The use of rebreathers will be recommended to the Scientific Diving Control Board for use in the program.

Evaluation of Antarctica human Dose due to Cosmic Ray Exposure based on neutron spectrometer operated in the Concordia station

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Cosmic rays are one of the major sources of natural radiation exposure to humans. In the 2000 Report of the United Nations Scientific Committee of the Effects of Atomic Radiation, the annual effective dose due to cosmic ray exposure averaged over the world's population was evaluated to be 0.38 mSv. Antarctic region was characterised by its high altitude and proximity to the geomagnetic pole, which conjugate induces large dose levels. International agencies have established recommended dose limits for both workers and the general public for different types of terrestrial and atmospheric activities. Thus, national or continental regulations have been adopted in many areas based on these recommendations. Concerning the ICRP, recommendations for annual effective dose are 20 mSv and 1 mSv averaged over a five year period for aircrews and for the public, respectively. They also recommended a 2 mSv limit on the accumulated dose over nine months of pregnancy.

In the framework of the CHINSTRAP project supported by IPEV, a new cosmic ray induced neutron spectrometer has been installed in December 2015 in the inner Antarctic Plateau, at Concordia station. As detailed in [1], this instrument was composed by six Bonner sphere to record the neutron energy spectrum in the energy range from meV to GeV. The spectrometer is placed in a thermo-stabilized "Atmos" shelter, fully maintained all year-round by the Concordia station personnel. Thanks to ATMORAD method presented in [2], atmospheric shower modelling associated to a primary cosmic ray model allows for deducing the proton, muon and electron fields from cascade neutron measurements. Using the fluence to ambient dose equivalent conversions coefficients, the complementarity of measurement and modelling makes it possible to calculate the total ambient dose equivalent, but also to extrapolate it for other localization. Thus, analyses considering one-year measurements from December 2015 to 2016 (wintering workers) indicate a average dose rate and a ambient dose equivalent in Concordia around 0.47 µSv/hr and 4.1 mSv, respectively. This demonstrates that Antarctica can be a problematic environment from the point of view of the human dose, which exerts classical recommendations established for public. For comparison, this annual dose level is equivalent to approximately 40 round trip-typical transatlantic flights [3] during quiet solar period. The final work will present exhaustive analyses implying solar activity and extreme solar flare event impacts on dose level and will be extrapolate for other stations. To conclude, recommendations will be discussed.

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New possibilities in colour diagnosis of winterer's psychophysiological status in Antarctica

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In the Antarctic, it is not solved the problem of health preservation and prevention of psycho-physiological disorders. For solving this problem, it was used diagnostic method of psycho-physiological changes in the characteristics of individual color preference, which allows to evaluate early symptoms of chronic negative stress during the Antarctic expedition. For the sequences evaluation of 12 locus preferential ranking, it was defined indicators that could characterize individual physiological qualities. These indicators are consistent selection options in view of belonging to chromaticity wave spectra, which belong to the preferences of emotional, physical and intellectual factors. As a result of indicator analysis it is characterized the procedure for selecting a chromaticity within the color spectra areas of the subjective vitality assessment - color zone indicators (CZI), the combined performance color preferences (CPCP) and mixed color indicators (MCI).
During the 2014 - 2015 years at the Antarctic station "Akademik Vernadsky" was held study of color preferences in winterers (in dynamics). The goal was to determine the characteristics of changes in the individual psycho-physiological status. The results of the color test allows to determine the dynamics in the personal and group preferences and find out the presence of mutations in the balance between the emotional, intellectual and physical tone of psychophysiological state.
Thus it was defined indicators of the color preferences in person (age and biorhythmic preferences, consistency and ranking structure of chromaticity, direction the selection of locus within increasing wavelength in the visible light spectrum), the analysis of which allows to determine the characteristic manifestations of temperament types, assess the individual psycho-physiological state of living standards tone (emotional, intellectual, physical), to detect early signs of psycho-physiological disorders.

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Sleep and circadian rhythms in Antarctica: on desynchronization, winter-over syndrome and polar insomnia.

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Sleep complaints are consistently cited as the most prominent health problem in Arctic and Antarctic expeditions. Whereas the precise mechanisms underlying these disturbances are still not elucidated, several areas of research have pointed in the direction of possible causes. Firstly, chronobiology studies suggest disturbances in melatonin secretion, that might be associated with sleep disturbances. Secondly, mood disturbances are known to interact with sleep problems, both as cause and effect. With regard to Antarctic sojourns, several clusters of symptoms have been suggested to have an association with sleep disorders, such as a) the polar T3 syndrome, which mimics subclinical hypothyroidism; b) the winter-over syndrome, a term coined to describe the association of mood and sleep disturbances; or, c) a sub-syndromal seasonal affective disorder. Lastly, the lack of physical activity and the sensory deprivation due to long-duration isolation and confinement have been hypothesized to be a potential detrimental influence to sleep.

The present communication will summarize our research findings from both summer campaigns and overwintering studies at Princess Elizabeth, Concordia, Dumont d'Urville and Halley VI. Our first summer campaign showed, in addition to high sleep fragmentation, a major decrease in slow wave sleep (SWS) and an increase in stage R sleep. Furthermore, the ultradian rhythmicity of sleep was altered, with SWS occurring mainly at the end of the night and stage R sleep at the beginning. Cortisol secretion profiles were normal; melatonin secretion however showed a severe phase delay. There were no mood alterations according to the profile of mood scores, but the psychomotor vigilance task showed an impaired vigilance performance. Our overwintering studies at Concordia and Dumont d'Urville showed the prevailing disturbed sleep breathing due to altitude at Concordia, with no acclimatization over time. The disturbances showed much less at Dumont d'Urville. This comparison allowed to discard the "lack of physical activity" hypothesis to explain the lseep disturbances. The investigations at Halley VI showed a similar picture, with a higher prevalence of mood disturbances. The desynchronization of sleep as a behaviour are hypothesized to be due to both circadian desynchronization, including the unveiling of two pacemakers, one sensitive to photic cues and one to social cues. Furthermore, the pervasive effect of chronic hypobaric hypoxia at altitude is shown on sleep and exercise physiology.

Analysis of oral diaries during an Antarctic winter

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This study is part of a multinational, multidisciplinary research project measuring psychological and linguistic factors during an Antarctic winter. The full scientific team is comprised of nine senior investigators, in Canada and five European countries. Characteristics of speech are measured, using phonetic, acoustic, and content analyses. The goal is to examine the pattern of each measure as the winter progresses, their interactions, and their role in group and individual adaptation to the isolated, confined environment of the austral winter.

This paper focuses on the thematic content analysis (TCA) of video-recorded diaries from a winter-over crew (Feb. to Dec.) at Halley Station of the British Antarctic Survey. TCA is a scientifically rigorous method for converting qualitative material, such as running text, to quantitative data. Both computer and expert scoring of psychological variables such as mood, cognition, and social relationships are applied to oral diaries periodically recorded by each member of the crew. Early findings include persistent low integrative complexity; Achievement as the dominant motive overall, with major spikes in Affiliation two months after winter begins and two months before it ends, and very low Power motivation throughout; and high values for Achievement (especially in the first winter month, February to March); and Stimulation, which shows a major increase in mid-winter (July). Hedonism spikes at about the same times as Affiliation motivation; Benevolence spikes in April, then remains low; Power is at zero from April on. There is no evidence of the "third-quarter phenomenon."

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Sleep Architecture and Periodic Breathing of Chinese Expeditioners at Dome A (4093m)

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Background

Dome A (80°22′S, 77°22′E) has the highest ice peak in Antarctica, with an elevation of 4093m. It has a barometric pressure of 560-590 hpa, equivalent to about 5000m. Plenty of research at high altitude reported that hypoxia exposure is deleterious to sleep. This is the first study investigating sleep architecture and breathing disorders in healthy expeditioners from sea-level to high altitude at Dome A.

Subjects and Methods

The study was carried out on ten healthy male volunteers (mean age 28.3±5.5 years) of the 31st Chinese Antarctic expedition to Dome A. Sleep structure and breathing condition were monitored using Embltta X100 portable polysomnography (PSG) equipment at three periods: (1) at Zhongshan Station (69°22′S, 76°22′E, sea level) before departure to Dome A; (2) at 4093m on the 13rd-14th days after arriving at Dome A; (3) descent back at Zhongshan Station. All polysomnograms were analyzed upon return to China by two experienced polysomnography technologists, with the criterion of Rechtschaffen and Kale's rules for sleep staging, and the Report of the American Academy of Sleep Medicine Task Force for the diagnosis of respiratory events.

Results

The percentage of slow wave sleep significantly reduced at Dome A ($P<0.01$). There was no statistically significant difference in total sleep time, sleep latency and sleep efficiency. The total respiratory events and apnea/hypopnea index (h^{-1}) substantially increased ($P<0.001$) under high altitude. The central apnea index (h^{-1}) was normal at sea level and rose progressively to 26.0±27.3 at Dome A ($P<0.05$). Apneas were almost exclusively of periodic breathing type appearing mostly during none rapid eye movement sleep. The oxygen desaturation index (≥4% dips) greatly increased ($P<0.001$). The minimum oxygen saturation and the mean oxygen saturation during sleep significantly fell at Dome A ($P<0.001$). Also, the time spent in SaO2 below 90% was significantly increased ($P<0.001$).

Conclusion

Our field study reported novel data on sleep architecture, breathing patterns, and nocturnal oxygen saturation at Dome A (4093m) in Antarctica. High-altitude at Dome A reduced slow wave sleep and induced periodic breathing.

Acknowledgements

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SO-AntEco: Contributing information and scientific advice to the CCAMLR South Orkney Islands MPA review

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The South Orkney Islands are a small archipelago located in the Southern Ocean, 375 miles north-east of the tip of the Antarctic Peninsula. In 2009, the Commission for the Conservation of Antarctic Marine Living Resources (CCAMLR) established the South Orkney Islands Southern Shelf Marine Protected Area (SOISS MPA), the first MPA located entirely within the High Seas anywhere on the planet. The MPA is designed to contribute towards the conservation of biodiversity in the Scotia Sea region, and to protect representative examples of benthic and pelagic habitats. A review of the MPA will be undertaken by CCAMLR in 2019, and work is ongoing to further develop a system of MPAs for the southern Scotia Sea/western Antarctic Peninsula region. Such work relies on the provision of policy-relevant scientific advice on patterns of biodiversity and understanding of benthic ecosystems.

SO-AntEco (South Orkneys - State of the Antarctic Ecosystem) was a British Antarctic Survey led expedition with an international team of scientists from the SCAR AntEco research programme. The team included 22 participants from 9 different countries and 16 institutes. The expedition took place on board the RRS James Clark Ross in February-March 2016. The expedition aimed to investigate species diversity, assemblage composition, abundance and habitat zonation along the shelf break of the South Orkney Islands, and to map the locations and distribution of all species found that were identified as VME (vulnerable marine ecosystem) taxa. A total of 124 trawled gear and 34 video/camera deployments were conducted during ~17 days of science. In total, over 700 seafloor habitat photographs and 3,900 live specimen photos were taken with over 38,000 individual animals collected and preserved for future analyses. Eighteen phyla were found from depths between ~500 m and ~2000 m.

We present the policy relevant findings of the expedition, and a summary of how these results will be used to contribute information and scientific advice for the SOISS MPA review and for the development of spatial management in this region more generally.

Pocket rocket: Science in Antarctica through a small, versatile and agile vessel platform.

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Vessel support in Antarctica has traditionally been on large government-owned ships with fixed itineraries, often driven by station resupply schedules or itineraries tightly-loaded with multiple projects. Large vessels are also often limited to well-charted, fixed routes, often well away from prime study areas in shallow coastal areas.

R/V Australis is a purpose-built, 24m non-government vessel operating on the West Antarctic Peninsula and surrounding Southern Ocean. It offers a cost-effective, and more importantly, very flexible alternative to large vessels. This has the potential to broaden the scope of possibilities that can effectively be supported.

With over 20 years of Antarctic experience at the helm, Ben Wallis's detailed local knowledge, expertise and enthusiasm plays a key role in the productivity of the mission. Scientific research on board *Australis* has resulted in 27 published papers, 126 citations, five national Antarctic programs and more.

Recently *Australis* successfully supported dedicated research voyages for both the Malaysian and Turkish Antarctic programs, with the Belgium Antarctic Program scheduled for 2018.

The highly-customisable vessel accommodates tightly-focused groups of up to nine scientists. Its size allows flexible, bespoke itineraries capable of achieving specific goals as safely, and at a fraction of the cost, as traditional research support vessels.

Ocean Expeditions is proud to have supported the following institutions: Australian Antarctic Division (AAD), British Antarctic Survey (BAS), Natural Environment Research Council (NERC), National Oceanic and Atmospheric Administration (NOAA), Malaysian National Antarctic Program (YPASM), Turkish Antarctic National Program (PolReC).

The Antarctic Circumnavigation Expedition - an interdisciplinary approach

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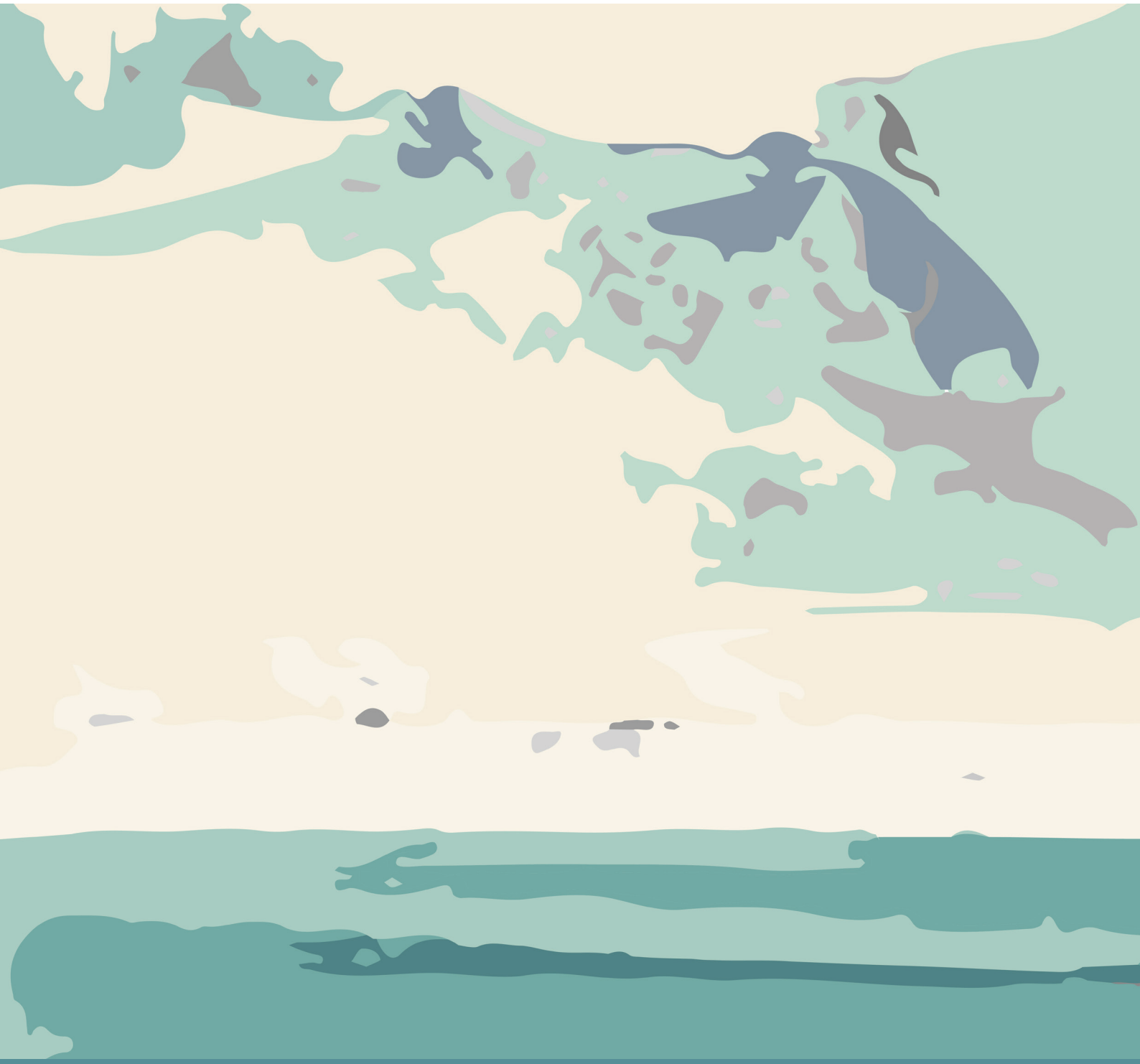
The Antarctic Circumnavigation Expedition (ACE) was organised by the new Swiss Polar Institute. It circled the Antarctic continent and most of its sub-antarctic islands over a period of 3 months from December 2016 to March 2017 supporting 22 projects and almost 150 scientists from 18 countries. Conceived as an opportunity to better characterise the role of the islands in the Southern Ocean as well as providing circumpolar measurements of many variables in a single summer the cruise offered the opportunity to link physical and biological measurements in air, water and on land.

As well as vertical profiles at fixed stations using both CTDs and radio sondes, there were also continuous underway measurements of phytoplankton, surveys of airborne particles and aerosols, collection of plastics, bird and whale surveys, measurements of trace metal availability and trace gases, studies on the evolution of flora and fauna as well as investigations into palaeoclimate from ice and peat cores. Linking of the data sets and joint analyses will promote a more holistic understanding of dynamic change in the Southern Ocean and help provide baselines for future measurements.

During the presentation we will present the vision behind the expedition and its implementation, outline the journey and main scientific experiments performed over its three months journey and give insights into the follow-up work and legacy of this unique expedition.



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